GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 14, 2006, 01:34:23 ; Search time 75 Seconds
(without alignments)
3848.671 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Perfect score: 15748
Sequence: 1 MAEAEGGASEQDDVSFLRTE.....RLADNAHDIWAKKKKEELVT 3000

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12295	78.1	5126	2	S40450	ryanodine receptor
2	6828	43.4	5107	2	T29144	partial CDS - Caen
3	6770.5	43.0	4969	2	A37113	ryanodine receptor
4	6769	43.0	4967	2	S72269	ryanodine receptor
5	6534.5	41.5	5037	1	A54161	ryanodine-binding
6	6453.5	41.0	5035	1	I46646	ryanodine receptor
7	6442.5	40.9	5032	1	A35041	ryanodine receptor
8	6439	40.9	5037	2	B35041	ryanodine receptor
9	6438.5	40.9	4859	2	S74173	ryanodine receptor
10	6423	40.8	4869	2	S66572	ryanodine receptor
11	6419	40.8	4868	2	B54161	ryanodine-binding
12	6413	40.7	4872	2	S27272	ryanodine receptor
13	538	3.4	163	2	I47214	probable brain rya
14	520	3.3	162	2	I47213	cardiac muscle rya
15	327	2.1	2783	2	T31431	inositol 1,4,5-tri
16	323	2.1	2701	2	S17796	inositol-trisphosp
17	296.5	1.9	2693	2	A40743	IP3 receptor, XIP3
18	292.5	1.9	2695	2	S54974	type 1 inositol 1,
19	290.5	1.8	2670	2	A46719	inositol 1,4,5-tri
20	289	1.8	2713	2	A55713	inositol 1,4,5-tri
21	286.5	1.8	2734	2	B36579	inositol 1,4,5-tri
22	285	1.8	2671	2	A49873	inositol 1,4,5-tri
23	284	1.8	1966	2	T32552	hypothetical prote
24	284	1.8	2848	2	T32550	hypothetical prote
25	279	1.8	2749	1	ACMSIT	inositol 1,4,5-tri
26	279	1.8	2749	2	A36579	inositol 1,4,5-tri
27	277.5	1.8	2833	2	A43360	inositol 1,4,5-tri
28	205	1.3	1676	2	E71410	probable centromer
29	203.5	1.3	2541	2	T29340	hypothetical prote
30	198	1.3	3259	1	A56539	giantin - human
31	198	1.3	5369	2	T44807	mycosubtilin synth
32	197.5	1.3	2954	2	T14156	kinesin-related pr
33	196.5	1.2	2218	2	B84683	hypothetical prote
34	192	1.2	1727	2	T50073	myosin-like coiled
35	192	1.2	3225	2	I52300	giantin - human
36	191	1.2	1882	2	T00069	hypothetical prote
37	189.5	1.2	2663	1	S28261	centromere protein
38	188.5	1.2	1642	2	T08880	NMDA receptor-bind
39	188	1.2	4540	2	T30838	cytoplasmic dynein
40	182.5	1.2	2331	2	T25410	hypothetical prote
41	182.5	1.2	3187	2	JC5837	364K Golgi complex
42	180.5	1.1	2712	2	T05113	hypothetical prote
43	179	1.1	6669	2	S55024	nebulin, skeletal
44	178	1.1	4151	2	T13734	groovin gene prote
45	177	1.1	52	2	I46644	ryanodine receptor

ALIGNMENTS

RESULT 1
S40450
ryanodine receptor/calcium release channel - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jun-1999
C;Accession: S40450
R;Takeshima, H.; Nishi, M.; Iwabe, N.; Miyata, T.; Hosoya, T.; Masai, I.; Hotta, Y.
FEBS Lett. 337, 81-87, 1994
A;Title: Isolation and characterization of a gene for a ryanodine receptor/calcium rele
A;Reference number: S40450; MUID:94102409; PMID:8276118
A;Accession: S40450
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5126 <TAK>
A;Cross-references: UNIPARC:UPI000017CF36
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homol

Query Match 78.1%; Score 12295; DB 2; Length 5126;
Best Local Similarity 77.5%; Pred. No. 0;
Matches 2348; Conservative 275; Mismatches 338; Indels 68; Gaps 22;

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Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||| |||||||||||||| ||||||||||||||||||||||||||||||:||||
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:||||||:||||||||||:||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

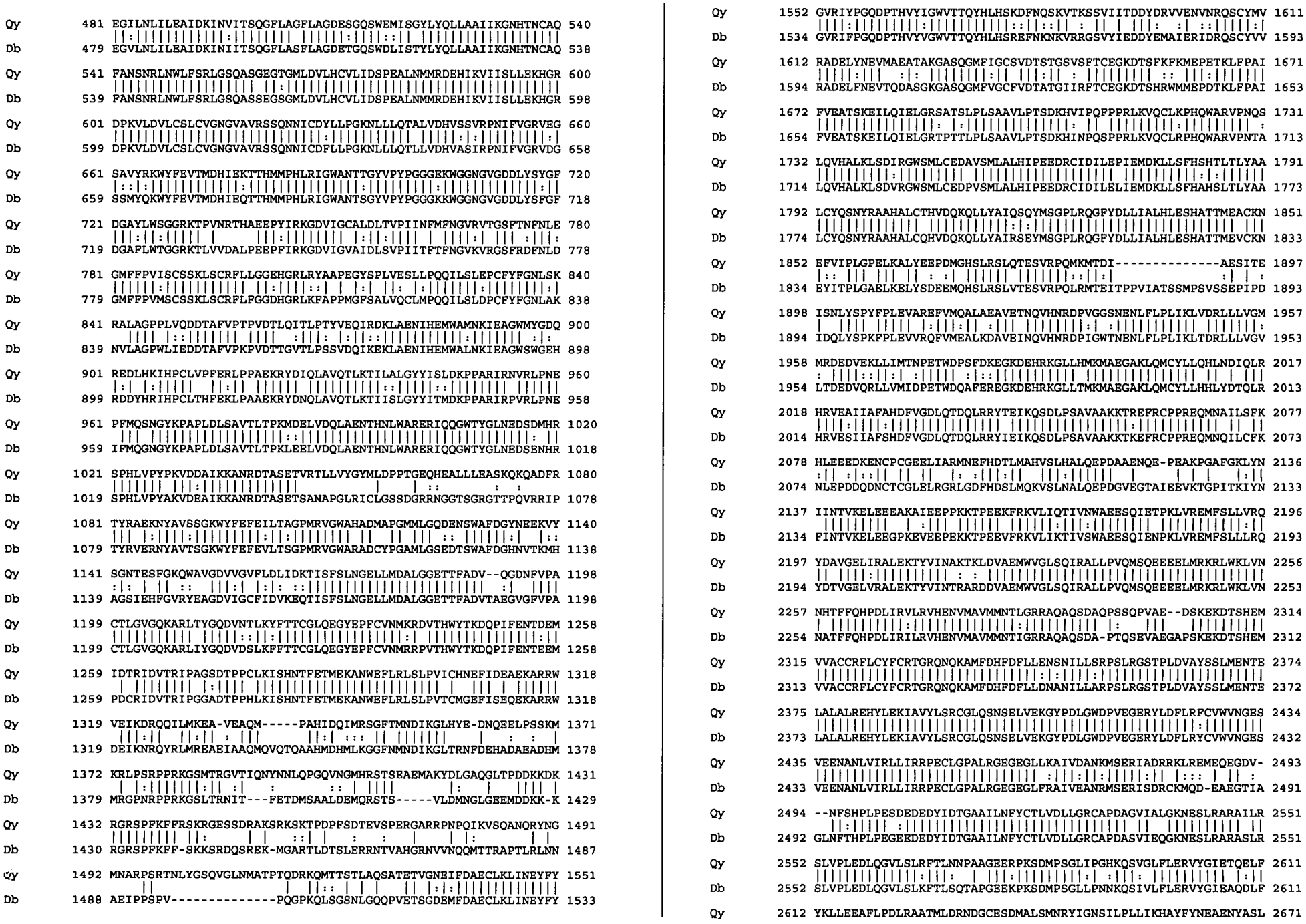
Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||||| ||||||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |   |||||:|:||||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFSW-QEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||||||||||||||| ||||||||||:|||||||||||:||   |
Db        359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 418

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| |||||:|| ||| ||||||||||||:||::|||||||||:|||||||||||||||
Db        419 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 478
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```
Db       2612 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2671

Qy       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731

Db       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2731

Qy       2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791

Db       2732 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2790

Qy       2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851

Db       2791 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2848

Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911

Db       2849 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2908

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969

Db       2909 KGLLAIGWTVEHSEVEVPLNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2963

Qy       2970 TLSREMQNMAERLADNAHDIWAKKKKEEL 2998

Db       2964 TLSREMQNMAERLAENSHDIWAKKKNEEL 2992


RESULT 2
T29144
partial CDS - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29144
R;Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid K11C4.
A;Reference number: Z20577
A;Accession: T29144
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5107 <PAU>
A;Cross-references: UNIPROT:Q94279; UNIPARC:UPI000011013D; EMBL:U64854; PIDN:AAB18318.1;
A;Experimental source: strain Bristol N2; clone K11C4
C;Genetics:
A;Gene: CESP:unc-68
A;Map position: 5
A;Introns: 27/1; 64/3; 92/3; 127/1; 158/2; 1222/2; 1300/2; 1347/2; 1391/1; 1419/3; 1517/
/3; 3269/2; 3313/2; 3466/1; 3519/3; 3615/3; 3629/3; 3658/2; 3710/1; 3741/3; 3779/2; 3810
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo

  Query Match             43.4%;  Score 6828;  DB 2;  Length 5107;
  Best Local Similarity   45.0%;  Pred. No. 0;
  Matches 1407;  Conservative  519;  Mismatches  850;  Indels  350;  Gaps   52;

Qy        113 MYLACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVAT 172

Db          1 MYLACLSSCSSNDKLAFDVGVQETNEGEACWWTIHPASKQRSEGEKVRVGDDVILVSVAT 60

Qy        173 ERYLHTTK---ENEVSI----------------------VNASFHVTHWSVQPYGTGI 205

Db         61 ERYLHLKKGKTEEEASLMLLFCGRNVLLLFHQHMAYSKGYMVIASFHQTLWNIQSVSSGS 120

Qy        206 SRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELA 265

Db        121 MRTRNMGFLFGNDVLRLFHGNDECLTIPENWSEHPQHNMVIYEGGAAVTQARSLWRVELI 180

Qy        266 RTKWAGGPINWYHPMRIRHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQ 325

Db        181 RMKWHGALVGWEQVFRIKHITSGRYLGVLD-NSVQLYHKEKADFDLTAFVMCQNKDPKKQ 239

Qy        326 VLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGK 385

Db        240 MLDEKEEEGMGNATIRYGETNAFIQHVKTQLWLSYQTTEVTKKGLGKVEEKKAVALKDGH 299

Qy        386 MDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEMVMCL 445

Db        300 MDDCYTFFMALEEESKSARVIRKCSSVLNKFLKGIDALQLEGNQSTDWTRVDLNEVLKLM 359

Qy        446 EDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAG 505

Db        360 EDLIEYFAQPNDEQDFEEKQNHLRALRSRQDLFQEEGVLNMILDTIDKFSQMEALPDFAG 419

Qy        506 FLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGM 565

Db        420 -LIGEETHVKWEQISTYLYLLVAAMIKGNHYNCAQFASAQRLDWLFGRLSNPQSAE--GI 476

Qy        566 LDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNN 625

Db        477 LDVLYCVLTESPEALNMINEGHIRSVISLLEKVGRDPKVLDVLSSLCEGNGMAVRSSQNL 536

Qy        626 ICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEKTTHMMPH 685

Db        537 ITQYLLPGKDLLLQTSMRDHVSSMMPNVMLGVVEGSALFRKWYFEAEVEHIETMTKQTPY 596

Qy        686 LRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIR 745

Db        597 LRIGWANSVGFKPFPGSGDKMGCNGVGDDFYSYGFDGKSMYFGGKSRRVG-----HKLLE 651

Qy        746 KGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGR 805

Db        652 KGDVIGCSIDLTIPEIKFSVNGTYMSGSFKKFNIDGYFFPVMSLSAKVSCRFILGGNQGR 711

Qy        806 LRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSKRALAGPPLVQDD-TAFVPTPVDTLQ 864

Db        712 LRYGPPTGFSAVVEAVNGE--LQITDCLSFGDLGKNIFSGPQTIFNNLEPPIPTPIDVSA 769

Qy        865 ITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRY 924

Db        770 TQLNHHATEMHQKYAENLHELWAMRKIELGWSYGETRSETSRKHPCLTKFEYLPETEKKY 829

Qy        925 DIQLAVQTLKTILALGYYISLDKPPARIRNVRL-PNEPFMQSNGYKPAPLDLSAVTLTPK 983

Db        830 NILLALTTMKTIEALGYHLITEDPPCRLRAVRLGPN--FQQQNGYKPGPLDTHEIQLPAE 887

Qy        984 MDELVDQLAENTHNLWARERIQQGWTYGLNE--DSDMHRSPHLVPYPKVDDAIKKANRDT 1041

Db        888 LQPLTEALARNTHNIWAKEKIKRGWTFGLSEHVDATQKRSPHLVPYEQVDERIKQANRES 947

Qy       1042 ASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEI 1101

Db        948 AAENIRALQLFGIFLEPPAHE-HDEVAEKELRARKDNTRTYRAEATYAVCGGKWYFEFEI 1006

Qy       1102 LTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFL 1161

Db       1007 LTAGYMKIGWMDIGSTPEIQLGADDRSYAFDGYLGRKWHQG-AETYGKEWKIGDVVGCFL 1065

Qy       1162 DLIDKTISFSLNGELLMDALGGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKY 1220

Db       1066 DLNDRTISFSLNGELLLDPSGSEMAFDNVVCGDGLVPAMTLGSGQRGRLNFGQQSNSLKF 1125

Qy       1221 FTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMIDTRI-DVTRIPAGSDTPPCLK 1279

Db       1126 FTTCGLQEGYEPFCVNMYRTMPMWFAKQLPRFEDISTLKSGSILEVSRIPATGNSPPCLK 1185

Qy       1280 ISHNTFET----MEKANWEFLRLSLPVICHNEFIDEAEK---ARRWVEIKDRQQILMKEA 1332

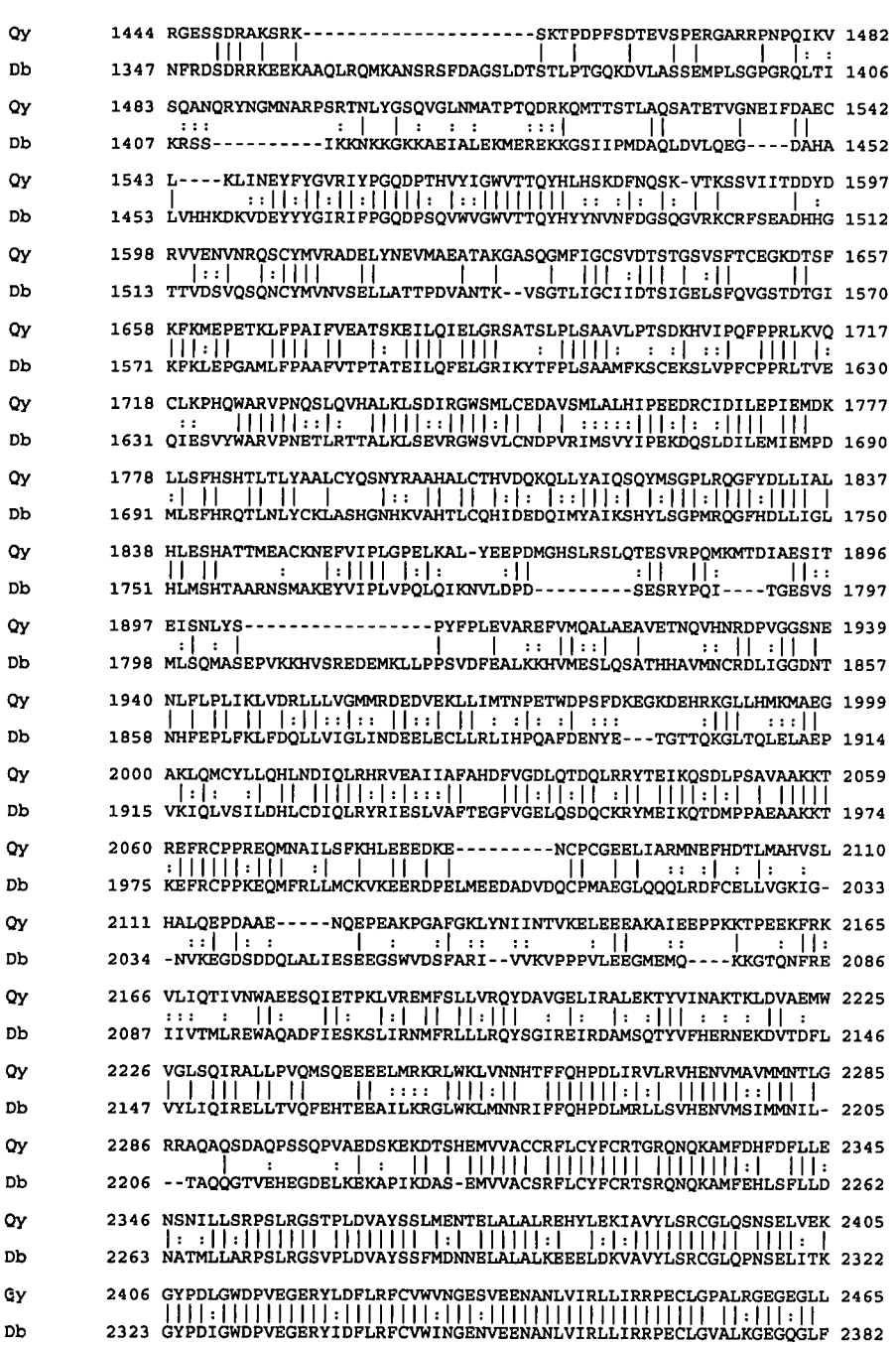
Db       1186 ILQKVTISEGGPSEKAKMEYIKLSLPVKCNDTFVKNKDKETIRRQLQEYKPRSQSVVSQI 1245

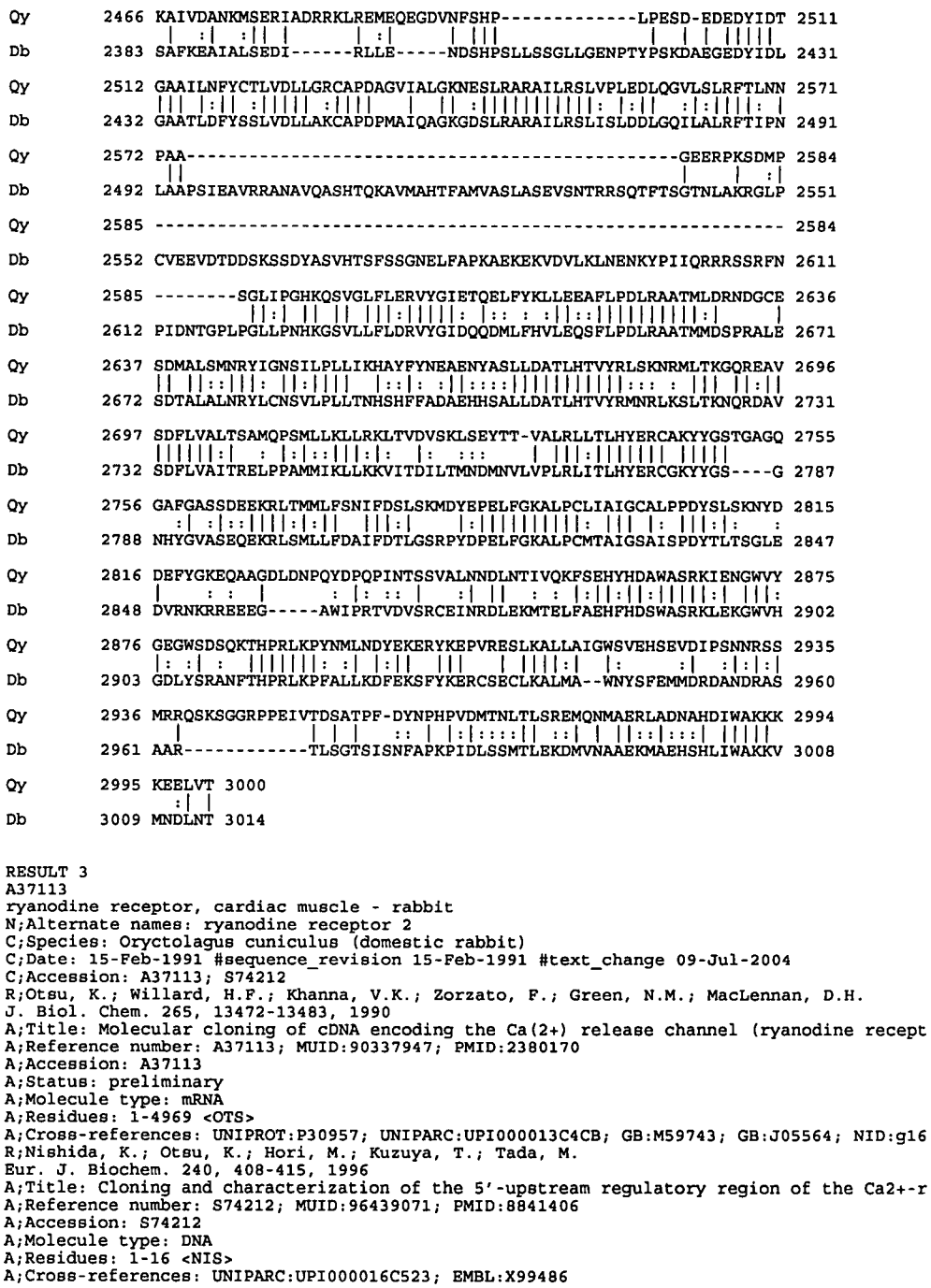
Qy       1333 VEAQMPAHIDQIM-RSGFTMNDIKGLHYEDNQEELPSSKMKRLPS----RPPRKGSMTRG 1387

Db       1246 RAPGIPKEFDDNKEKKGFLRSMLGSKDSHESDDDRRSRTNSKQPSVDGDEPPA------- 1298

Qy       1388 VTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFFRS----K 1443

Db       1299 --------VRRSLLELPHDERQIAEDSMRDLNDR----HSEKPKKGGLLSRLRDSSNTRK 1346
```





RESULT 3
A37113
ryanodine receptor, cardiac muscle - rabbit
N;Alternate names: ryanodine receptor 2
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 09-Jul-2004
C;Accession: A37113; S74212
R;Otsu, K.; Willard, H.F.; Khanna, V.K.; Zorzato, F.; Green, N.M.; MacLennan, D.H.
J. Biol. Chem. 265, 13472-13483, 1990
A;Title: Molecular cloning of cDNA encoding the Ca(2+) release channel (ryanodine recept
A;Reference number: A37113; MUID:90337947; PMID:2380170
A;Accession: A37113
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4969 <OTS>
A;Cross-references: UNIPROT:P30957; UNIPARC:UPI000013C4CB; GB:M59743; GB:J05564; NID:g16
R;Nishida, K.; Otsu, K.; Hori, M.; Kuzuya, T.; Tada, M.
Eur. J. Biochem. 240, 408-415, 1996
A;Title: Cloning and characterization of the 5'-upstream regulatory region of the Ca2+-r
A;Reference number: S74212; MUID:96439071; PMID:8841406
A;Accession: S74212
A;Molecule type: DNA
A;Residues: 1-16 <NIS>
A;Cross-references: UNIPARC:UPI000016C523; EMBL:X99486

A;Experimental source: strain New Zealand White
C;Genetics:
A;Gene: RYR2
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo
C;Keywords: cardiac muscle; heart; phosphoprotein; transmembrane protein

Query Match 43.0%; Score 6770.5; DB 2; Length 4969;
Best Local Similarity 45.6%; Pred. No. 0;
Matches 1401; Conservative 530; Mismatches 851; Indels 291; Gaps 58;

```
Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP  58
              |:||  | |:: ||||:| | | ||||     :::|||||||||| ||||: :: ||:||
Db          2 ADGGEGE-DEIQFLRTDDEVVLQCTATIHKEQQKLCLAAEGFGNRLCFLESTSNSKNVPP  60

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKG-------------TGSGHRTLLYGNAI 104
              ||| | ||:||:| ||||||:: |   | :|               | ||||||||:||
Db         61 DLSICTFVLEQSLLVRALQEML-ANTVEKSEGQVDVEKWKFMMKTAQGGGHRTLLYGHAI 119

Qy        105 LLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGD 163
              |||| | ||| ||||| || ||||||||||: : |||||||:|||||||||||||||||
Db        120 LLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVRVGD 179

Qy        164 DLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFF 223
              |||||||::||||| :  |     |:|:|  | ||| |  :|    :  ||: ||||||
Db        180 DLILVSVSSERYLHLSYGNGSLHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVLRLL 237

Qy        224 HGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRI 282
              ||  |||||:||    :  :  | ||||:|   |||||||  |  |:|  | |  | |:
Db        238 HGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGSHIRWGQPFRL 297

Qy        283 RHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKY 342
              ||:|||:|| : :   | |: :|:|   | ||  |  |:     :  |::: :|   |||
Db        298 RHVTTGKYLSLMEDKNLLLMDKEKADVKSTAFTFRSSKEKLDGGVR-KEVDGMGTSEIKY 356

Qy        343 GDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRT 402
              |||   :|| :|||||:|:| : |   :| :: | ||:| || |||||: |||| ||||| 
Db        357 GDSICYIQHVDTGLWLTYQSVDVKSVRMGSIQRK-AIMHHEGHMDDGLNLSRSQHEESRT 415

Qy        403 ARVIRKCSSLFTKFINGLETLQENRRHSMPFASVNL--GEMVMCLEDLINYFAQPDEDME 460
              |||||    || :|| ||: | :  : |    ||:|    : : |:||| ||  ||| :|
Db        416 ARVIRSTVFLFNRFIRGLDALSKKAKAS----SVDLPIESVSLSLQDLIGYFHPPDEHLE 471

Qy        461 HEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMIS 520
              ||:||: |||:|||:|||||::||:|| ||:::| :|     |  :|| |:|:||: |
Db        472 HEDKQNRLRALKNRQNLFQEEGMINLVLECIDRLHVYSSAAHFAD-VAGREAGESWKSIL 530

Qy        521 GYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEAL 580
              ||:||||:|:||  |||||: |  |:|| |||  :     :|:|:|||||::|||||
Db        531 NSLYELLAALIRGNRKNCAQFSGS--LDWLISRL--ERLEASSGILEVLHCVLVESPEAL 586

Qy        581 NMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQT 640
              |:::: ||| |||||:||||: |||||||||| :|||||:|: ||| ||||::|||||
Db        587 NIIKEGHIKSIISLLDKHGRNHKVLDVLCSLCVCHGVAVRSNQHLICDNLLPGRDLLLQT 646

Qy        641 ALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPY 699
              ||:|||||:|||||:|  |||| |:|||:|: :|| |   |    |||:|||:| || ||
Db        647 RLVNHVSSMRPNIFLGVSEGSAQYKKWYYELMVDHTEPFVTAEATHLRVGWASTEGYSPY 706

Qy        700 PGGGBEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVP 759
              |||||:||||||||||:|||||| :||||      |:  :  :  :|  ||| | |||: |
Db        707 PGGGEEWGGNGVGDDLFSYGFDGLHLWSGCIARTVSSPN--QHLLRTDDVISCCLDLSAP 764

Qy        760 IINFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVE 819
              |:|  ||  | | | |||::|:||||:| |: :  ||||| ||  ::  | ||:|  |
Db        765 SISFRINGQPVQGMPENFNIDGLFFPVVSFSAGIKVRFLLGGRHGEFKFLPPPGYAPCYE 824

Qy        820 SLLPQQILSLEPC--FYFGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDK 877
              ::||:: | :|    :      | | || :     || | |||| || || ::|:|:|:|
Db        825 AVLPKEKLKVEHSREYKQERTYTRDLLGPTVSLTQAAFTPIPVDTSQIVLPPHLERIREK 884

Qy        878 LAENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTIL 937
              |||||||:| ||||| || ||  |:|  : |||| | :||  |: |::|::::||||:|
Db        885 LAENIHELWVMNKIELGWQYGPVRDDNKRQHPCLVEFSKLPEQERNYNLQMSLETLKTLL 944

Qy        938 ALGYYISLDKPPA--RIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENT 995
              ||| :: :    | ::: ::||   :  ::|||||:||| : |||  : :||:||||
Db        945 ALGCHVGISDEHAEEKVKKMKLPKN-YQLTSGYKPAPMDLSFIKLTPSQEAMVDKLAENA 1003

Qy        996 HNLWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYM 1055
              ||:|||:||:|||||: :|    |:| ||||  :||  ||:|:|:  | ||||| |||
Db       1004 HNVWARDRIRQGWTYGIQQDVKNRRNPRLVPYTLLDDRTKKSNKDSLREAVRTLLGYGYN 1063

Qy       1056 LDPPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHAD 1115
              |: |  :|  |    |          || :|||| ||| :|:|||||| :|:| |||||:
Db       1064 LEAP--DQDHAARAEVCSGTGERFRIFRAEKTYAVKAGRWYFEFEAVTSGDMRVGWSRPG 1121

Qy       1116 MAPGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGE 1175
                |   || || ::|||||:  :: : || | :|: |  |||||  :|: : |: |:|||| 
Db       1122 CQPDQELGSDERAFAFDGFKAQRWHQGN-EHYGRSWQAGDVVGCMVDMNEHTMMFTLNGE 1180

Qy       1176 LLMDALGGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFC 1234
              :|:|  | |  | |   || |:| |:||| |  |: :|:||:|||||| ||||||||||
Db       1181 ILLDDSGSELAFKDFDVGDGFIPVCSLGVAQVGRMNFGKDVSTLKYFTICGLQEGYEPFA 1240

Qy       1235 VNMKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE 1294
              ||  ||:| | :|  | |       :  |:|||    |: ||||::  :| : : :| :
Db       1241 VNTNRDITMWLSKRLPQFLQVPSNHE-HIEVTRIDGTIDSSPCLKVTQKSFGS-QNSNTD 1298

Qy       1295 --FLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMN 1352
                | |||:|: |   |
Db       1299 IMFYRLSMPIECAEVF---------------------------------------------- 1314

Qy       1353 DIKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAE 1412
                                | :|  | |                  | | :    ::::
Db       1315 ------------------SKTVPGGLPGAGLF-------------GPKNDLEDYDADSD 1342

Qy       1413 MAKYDLGAQG-LTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPER 1471
                  | | | |                          ||   |  |   |::
Db       1343 FEVLMKTAHGHLVP----------------------DRVDKDKETTKAEFNN------- 1372

Qy       1472 GARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATE 1531
                :  | | |:  ||:     :|                          :|| |:  :
Db       1373 --HKDYAQEKPSRLKQRFLLRRTKP---------------------DYSTSHSARLTED 1408

Qy       1532 TVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVI 1591
                : ::  | : |   : |:| |||:|||:| :|::||:|: :| :   |:  :|   :|
Db       1409 VLADDRDDYDFLMQTSTYYYSVRIFPGQEPANVWVGWITSDFHQYDTGFDLDRVRTVTVT 1468

Qy       1592 ITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCE 1651
                : |:  :| |:: | :|||| |    | |:    :  : |: ||| || ::| ::|
Db       1469 LGDEKGKVHESIKRSNCYMVCA----GESMSPGQGRN-NNGLEIGCVVDAASGLLTFIAN 1523

Qy       1652 GKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFP 1711
                ||: |  :::|| ||||||:| :|||  : | ||||    :|||| :  :  |: :|| |
Db       1524 GKELSTYYQVEPSTKLFPAVFAQATSPNVFQFELGRIKNVMPLSAGLFKSEHKNPVPQCP 1583

Qy       1712 PRLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILE 1771
                ||| || |    |:|:||| |:|   ::|: :|| : | | :  ::|||||:| :||||
Db       1584 PRLHVQFLSHVLWSRMPNQFLKVDVSRISERQGWLVQCLDPLQFMSLHIPEENRSVDILE 1643

Qy       1772 PIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFY 1831
                | ::|| || ||| ||:|:|    |:| |||||:|||: ||||||:::|| | || |:|
Db       1644 LTEQEELLKFHYHTLRLYSAVCALGNHRVAHALCSHVDEPQLLYAIENKYMPGLLRTGYY 1703

Qy       1832 DLLIALHLESHATTMEACKNEFVIPLGPELKA--LYEEPDMGHSLRSL-QTESVRPQMKM 1888
                |||| :|| |:||        |||::|:  | |:  |: : :  | |  :  : |:|:|:
Db       1704 DLLIDIHLSSYATARLMMNNEFIVPMTEETKSITLFPDENKKHGLPGIGLSTSLRPRMQF 1763

Qy       1889 TDIAESITEISN---LYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPL 1945
                :  : |   |:|    ||| |||:: :   :| | |||:   :| ||||||: | ||:||
Db       1764 S--SPSFVSINNECYQYSPEFPLDILKAKTIQMLTEAVKEGSLHGRDPVGGTTEFLFVPL 1821

Qy       1946 IKLVDRLLLVGMMRDEDVEKLLIMTNPETW--------------DPSFDK---EGKDEH 1987
                |||   ||::|:  :||:  :| :  |  :                :|| :   ||  |
Db       1822 IKLFYTLLIMGIFHNEDLRHILQLIEPSVFKDAATPEEEGDTLEEEPSVEDTKLEGAGEE 1881
```

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Qy       1988 --------RKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQL 2039
                    ::||| ||: |  ||||| |||:| | |:|||:|||:||: |||  || :|
Db       1882 EAKVGKRPKEGLLQMKLPEPVKLQMCLLLQYLCDCQVRHRIEAIVAFSDDFVAKLQDNQR 1941

Qy       2040 RRYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMN 2098
                || |: |: :: :|: |:||:||| ||:||:| :|:||    :||  ||| ||:  ::
Db       1942 FRYNEVMQALNMSAALTARKTKEFRSPPQEQINMLLNFK----DDKSECPCPEEIRDQLL 1997

Qy       2099 EFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEE--AKAIEEPPK 2156
                :||: || |  :   ::      | :   :    |:| :::  |  |:::   | :|   :
Db       1998 DFHEDLMTHCGIELDEDGSLDGNSDLTIR----GRLLSLVEKVTYLKKKQTEKPVESDSR 2053

Qy       2157 KTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAK 2216
                |:     :::: :|:| ||:|| || |:||| || || |||| :| |:||| ||| ||
Db       2054 KS--STLQQLISETMVRWAQESVIEDPELVRAMFVLLHRQYDGIGGLVRALPKTYTINGV 2111

Qy       2217 TKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENV 2276
                :  |   :   | |||:|| |:| :|||:|| : |  ::||  |:|||:|:| | :|| |
Db       2112 SVEDTINLLASLGQIRSLLSVRMGKEEEKLMIRGLGDIMNNKVFYQHPNLMRALGMHETV 2171

Qy       2277 MAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAM 2336
                | ||:| ||                  :||| |  :||  |||||||||  |||||||
Db       2172 MEVMVNVLG----------------GGESKE-ITFPKMVANCCRFLCYFCRISRQNQKAM 2214

Qy       2337 FDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAV-YLSRCG 2395
                |||  :|||||:: |: |::|||||||||| :|:|:| |||||||  |||: | ||: ||
Db       2215 FDHLSYLLENSSVGLASPAMRGSTPLDVAAASVMDNNELALALREPDLEKVVVRYLAGCG 2274

Qy       2396 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2455
                |||   || |||||:||:|||||||||||||| |: ||||||||||:|:|||||||| ||
Db       2275 LQSCQMLVSKGYPDIGWNPVEGERYLDFLRFAVFCNGESVEENANVVVRLLIRRPECFGP 2334

Qy       2456 ALRGE-GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPES---------DED 2505
                ||||| | ||| |: :| |::|                | :   | | |         :|:
Db       2335 ALRGEGGNGLLAAMEEAIKIAE--------------DPSRDGPSPTSGSSKTLDTEEEE 2379

Qy       2506 EDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL 2565
                :| |  | ||: ||  |:|||||||:  :|  || |::| |:|||||:|| || ||:|:
Db       2380 DDTIHMGNAIMTFYAALIDLLGRCAPEMHLIHAGKGEAIRIRSILRSLIPLGDLVGVISI 2439

Qy       2566 RFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRA 2625
                | :   |      : || :|  | || :: |||:|||||| |:    |||  |||||||
Db       2440 AFQMPTIAKDGNVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRA 2499

Qy       2626 ATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKN 2685
                |  ||      :||||::|||:  ::|||| : |  :   |::|||:|: |||||||||
Db       2500 AASLDTAALSATDMALALNRYLCTAVLPLLTRCAPLFAGTEHHASLIDSLLHTVYRLSKG 2559

Qy       2686 RMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745
                   ||| ||:::   |:::   ::|||:  |||:|  ||  |:|:  : |:||| |||||
Db       2560 CSLTKAQRDSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCW 2619

Qy       2746 KYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALP 2805
                |||    | | | |||:|:||  |:  ||  |||:||:  || |||  |||||  |:  |||
Db       2620 KYYCLPG-GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALP 2678

Qy       2806 PDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWA 2865
                ||| :  ||       ::|:: | :   ::|||::||:: :    |   : |::|| || |:
Db       2679 PDY-MESNYVSMM--EKQSSMDSEG-NFNPQPVDTSNIIIPEKLEYFINKYAEHSHDKWS 2734

Qy       2866 SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE 2925
                |: |||:||| :||| |  | :||| :|:: ||| |: |::|||| :|| || :| :
Db       2735 MDKLANGWIYGEIYSDSSKIQPLMKPYKLLSEKEKEIYRWPIKESLKTMLAWGWRIERTR 2794

Qy       2926 VDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADN 2985
                    :  ::  :::   :  ::  |:|    |:|  :||:|:||||::  ||| :|:|
Db       2795 ----EGDSMALYNRTRRISQTSQVSVDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAEN 2848

Qy       2986 AHDIWAKKKKEEL 2998
                |:|||||| ||
Db       2849 YHNIWAKKKKLEL 2861
```

```
RESULT 4
S72269
ryanodine receptor isoform 2, cardiac muscle - human
N;Alternate names: calcium release channel protein isoform 2
C;Species: Homo sapiens (man)
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
C;Accession: S72269
R;Tunwell, R.E.A.; Wickenden, C.; Bertrand, B.M.A.; Shevchenko, V.I.; Walsh, M.B.; Allen
Biochem. J. 318, 477-487, 1996
A;Title: The human cardiac muscle ryanodine receptor-calcium release channel: identific
A;Reference number: S72269; MUID:96404895; PMID:8809036
A;Accession: S72269
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-4967 <TUN>
A;Cross-references: UNIPROT:Q92736; UNIPARC:UPI0000013594; EMBL:X98330; NID:g1526977; PI
A;Experimental source: cardiac muscle; sarcoplasmic reticulum
C;Genetics:
A;Gene: RyR-2
C;Complex: homotetramer
C;Function:
A;Description: mediates rapid release of Ca2+ ions from intracellular stores during car
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo
C;Keywords: alternative splicing; calcium channel; cardiac muscle; glycoprotein; heart;
F;710-715/Region: adenine nucleotide binding #status predicted
F;1148-1153/Region: adenine nucleotide binding #status predicted
F;2338-2342/Region: adenine nucleotide binding #status predicted
F;2626-2631/Region: adenine nucleotide binding #status predicted
F;4030-4048/Domain: calcium binding #status predicted <CA1>
F;4499-4519/Domain: transmembrane #status predicted <TM01>
F;4572-4593/Domain: transmembrane #status predicted <TM02>
F;4719-4744/Domain: transmembrane #status predicted <TM03>
F;4767-4789/Domain: transmembrane #status predicted <TM04>
F;4809-4829/Domain: transmembrane #status predicted <TM05>
F;4844-4867/Domain: transmembrane #status predicted <TM06>
F;140,301/Binding site: phosphate (Thr) (covalent) (by cAMP-and calmodulin-dependent kin
F;2808/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status
F;4794/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            43.0%;  Score 6769;  DB 2;  Length 4967;
  Best Local Similarity  45.6%;  Pred. No. 0;
  Matches 1399;  Conservative  536;  Mismatches  854;  Indels  276;  Gaps   58;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
                |:||  | |:: |||||:| | | ||||     :::|||||||||| ||||: :: ||:||
Db          2 ADGGEGE-DEIQFLRTDDEVVLQCTATIHKEQQKLCLAAEGFGNRLCFLESTSNSKNVPP 60

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKG-------------TGSGHRTLLYGNAI 104
                ||| | ||:||:|||||||:: |   |  :|               | |||||||:||
Db         61 DLSICTFVLEQSLSVRALQEML-ANTVEKSEGQVDVEKWKFMMKTAQGGGHRTLLYGHAI 119

Qy        105 LLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGD 163
                ||||  | ||| ||||| || ||||||||||: : |||||||:||||||||||||||||
Db        120 LLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVRVGD 179

Qy        164 DLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFF 223
                |||||||:|||||  :  |    |:|:|  | ||| |  :|    :  ||: ||||||
Db        180 DLILVSVSSERYLHLSYGNGSLHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVLRLL 237

Qy        224 HGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRI 282
                ||  ||||:||    :  :  | ||||:|   ||||||||  |  |:|  | |  | |:
Db        238 HGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGSHIRWGQPFRL 297

Qy        283 RHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKY 342
                ||:|||:|| : :   | |: :|:|   | ||  |  | ::  |  |::: :|  |||
Db        298 RHVTTGKYLSLMEDKNLLLMDKEKADVKSTAFTFRSSK-EKLDVGVRKEVDGMGTSEIKY 356

Qy        343 GDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRT 402
                |||   :|| :|||||:|:| : |   :| :: | ||:| || ||||:  |||| |||||
Db        357 GDSVCYIQHVDTGLWLTYQSVDVKSVRMGSIQRK-AIMHHEGHMDDGISLSRSQHEESRT 415

Qy        403 ARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHE 462
                |||||    || :|| ||: | :  : |     : :  : : |:||| ||  ||| :|||
```



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Qy       2574 AGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRND 2633
Db       2447 KDGNVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRAAASLDTAA 2506

Qy       2634 GCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQR 2693
Db       2507 LSATDMALALNRYLCTAVLPLLTRCAPLFAGTEHHASLIDSLLHTVYRLSKGCSLTKAQR 2566

Qy       2694 EAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGA 2753
Db       2567 DSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCWKYYCLPG- 2625

Qy       2754 GQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKN 2813
Db       2626 GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALPPDY-MESN 2684

Qy       2814 YDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGW 2873
Db       2685 YVSMM--EKQSSMDSEG-NFNPQPVDTSNITIPEKLEYFINKYAEHSHDKWSMDKLANGW 2741

Qy       2874 VYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNR 2933
Db       2742 IYGEIYSDSSKVQPLMKPYKLLSEKEKEIYRWPIKESLKTMLARTMRTERTR----EGDS 2797

Qy       2934 SSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKK 2993
Db       2798 MALYNRTRRISQTSQVSVDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAENYHNIWAKK 2855

Qy       2994 KKEEL 2998
Db       2856 KKMEL 2860
```

RESULT 5
A54161
ryanodine-binding protein alpha form - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A54161
R;Oyamada, H.; Murayama, T.; Takagi, T.; Iino, M.; Iwabe, N.; Miyata, T.; Ogawa, Y.; End
J. Biol. Chem. 269, 17206-17214, 1994
A;Title: Primary structure and distribution of ryanodine-binding protein isoforms of the
A;Reference number: A54161; MUID:94274714; PMID:8006029
A;Accession: A54161
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-5037 <OYA>
A;Cross-references: UNIPROT:Q91313; UNIPARC:UPI0000110258; GB:D21070; NID:g1856972; PIDN
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo

 Query Match 41.5%; Score 6534.5; DB 1; Length 5037;
 Best Local Similarity 44.3%; Pred. No. 0;
 Matches 1371; Conservative 539; Mismatches 875; Indels 311; Gaps 64;

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Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
Db          2 AEGGEGE-DEIQFLRTEDVVVLQCSATIRKENLKMCMGVEGFGNRLCYLESTSNAQNAPP 60

Qy         59 DLSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYL 115
Db         61 DLAICCFILEQSLSVRALQEMLANTVEMGSESSQ--GGGHRTLLYGHAILLRHCHSDMYL 118

Qy        116 ACLSTSSS-QDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATER 174
Db        119 CCLTTSRSLTDKLAFDVGLQEDASGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSER 178

Qy        175 YLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGG-DECLTIP 233
Db        179 YLHLSTASGDLQVDASFMQTLWNMNPITSGCEIAE--GYVTGGDVLRLFHGHMDECLTIS 236

Qy        234 STWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGV 293
Db        237 STDQGEEQRRIPHYEGGAVCSHARSLWRSEPLRISWSGSHMRWGMPFRARHVTTGRYLAR 296

Qy        294 NDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSE 353
Db        297 EEERGLVLVDAEKANTKATAFCFRISK-EKLDVAPKRDIEGMGPADIKYGESMCFVQHVN 355

Qy        354 TGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
Db        356 SGLWLTYAAADSKVARLGPLKRK-AILHQEGHMDDALSLSRSQREESQAARMIYSTAGLF 414

Qy        414 TKPINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRN 473
Db        415 NIFIKGLDSLNGKNKPSKPI-SLPLDMVVLTLQDLIGYFQHPEEELQHEEKQTKLRSLKN 473

Qy        474 RQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKG 533
Db        474 RQNLFQEEGIISQVLDCIDRLNVYSTAAHFAEF-AGEEAAESWKEIVNLLYELLASLIRG 532

Qy        534 NHTNCAQFANSNRLNWLFSRLGS-QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVII 592
Db        533 NRSNCALF--SNNLDWVVSKLDRLEAS---SGILEVLYCVLIESPEVLNIIKKNHIKSII 587

Qy        593 SLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPN 652
Db        588 SLLDKHGRNHKVLDVLCSLCVCNGVAVRSNQNLITENLLPRRDLLLQTRMVNYVTSMRPN 647

Qy        653 IFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGV 711
Db        648 IYFGTCEGSTQFKKWYFEVIVDQVEPFVTAEATHLRVGWALTEGYSPYPGAGEGWGANGA 707

Qy        712 GDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVT 771
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Qy        772 GSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEP 831
Db        766 GMFENFNLDGLFFPVSSFSPGIKIRFLLGGRHGEFKFLPPPGYAPAYEALLPRDRMRVEP 825

Qy        832 CFYF----GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWA 887
Db        826 IKEYKHDVGDI--RNLLGPTKSLSHTSFVPCPVDTVQIVLPPHLERIREKLAENIHELWA 883

Qy        888 MNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISL-- 945
Db        884 LTRIEQGWTYGPIRDDNKRLHPCLLDFHSLPEPERNYNLLMSGETLKTLLALGCHVGMAD 943

Qy        946 DKPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQ 1005
Db        944 EKAEENLKKIKLP-KTYMMSNGYKPAPLDLSHVKLTPAQNTLVDKLAENGHNVWARDRVQ 1002

Qy       1006 QGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHE 1065
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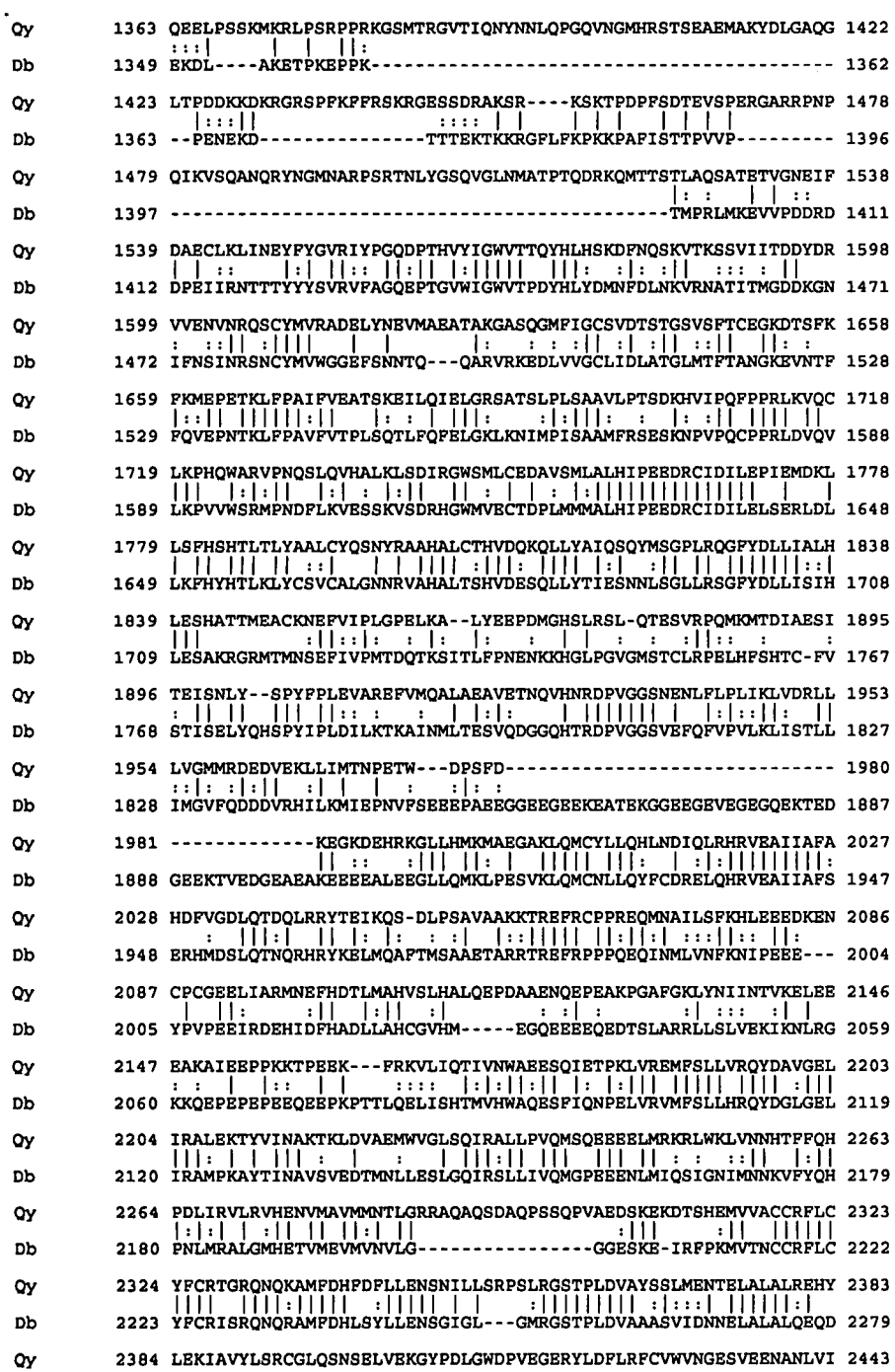
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Qy       1126 ENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGET 1185
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Qy       1245 YTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE--FLRLSLPV 1302
Db       1240 FSKSLPQFANV-SADHGHIEVSRIDGTVDNPPCLKVTHKTFGS-QNSNTDMLFFRLSMPV 1297

Qy       1303 ICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDN 1362
Db       1298 ----EFYETFKCTPGATPLTRSFTIVEEEVQDVDMDSEF-EVLKKSAARKEIEA----TN 1348
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RESULT 6
I46646
ryanodine receptor, skeletal muscle - pig
N;Alternate names: calcium release channel protein
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I46646; I46645; S31395; I47133; S26624; A37105; I47212; S18135
R;Fujii, J.; Otsu, K.; Zorzato, F.; De Leon, S.; Khanna, V.K.; Weiler, J.E.; O'Brien, P
Science 253, 448-451, 1991
A;Title: Identification of a mutation in porcine ryanodine receptor associated with mal
A;Reference number: I46645; MUID:91320118; PMID:1862346
A;Accession: I46646
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5035 <FUJ>
A;Cross-references: UNIPROT:Q29105; UNIPARC:UPI00001101C2; GB:M91452; NID:g164647; PIDN
A;Accession: I46645
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-614,'C',616-5035 <FU2>
A;Cross-references: UNIPARC:UPI00001101C1; GB:M91451; NID:g164645; PIDN:AAA31118.1; PID
R;Leeb, T.; Brem, G.; Brenig, B.
submitted to the EMBL Data Library, November 1992
A;Description: Genomic organization of porcine skeletal muscle ryanodine receptor gene
A;Reference number: S31395
A;Accession: S31395
A;Molecule type: DNA
A;Residues: 1542-2643 <LEE>
A;Cross-references: UNIPARC:UPI00001741C8; EMBL:X69465

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R;Leeb, T.; Schmoelzl, S.; Brem, G.; Brenig, B.
Genomics 18, 349-354, 1993
A;Title: Genomic organization of the porcine skeletal muscle ryanodine receptor (RYR1) g
A;Reference number: A48915; MUID:94117003; PMID:8288238
A;Contents: annotation
R;Harbitz, I.; Kristensen, T.; Bosnes, M.; Kran, S.; Davies, W.
Anim. Genet. 23, 395-402, 1992
A;Title: DNA sequence of the skeletal muscle calcium release channel cDNA and verificati
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A;Reference number: I47133; MUID:93036581; PMID:1329581
A;Accession: I47133
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 2-2091,'A',2093-3494,'L',3496-4163,'S',4165-4182,'R',4184-4411,'W',4413-4971
A;Cross-references: UNIPARC:UPI000016B7C5; EMBL:X62880; NID:g1936; PIDN:CAA44674.1; PID:
R;Harbitz, I.; Kristensen, T.; Kran, T.; Davies, W.
submitted to the EMBL Data Library, August 1992
A;Reference number: S26624
A;Accession: S26624
A;Molecule type: DNA
A;Residues: 482-706 <HAW>
A;Cross-references: UNIPARC:UPI00001741C9; EMBL:X68247
R;Harbitz, I.; Chowdhary, B.; Thomsen, P.D.; Davies, W.; Kaufmann, U.; Kran, S.; Gustavs
Genomics 8, 243-248, 1990
A;Title: Assignment of the porcine calcium release channel gene, a candidate for the mal
A;Reference number: A37105; MUID:91065640; PMID:2174405
A;Accession: A37105
A;Status: preliminary
A;Molecule type: mRNA
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A;Cross-references: UNIPARC:UPI000016C6A7; GB:M32501; NID:g164428; PIDN:AAA31022.1; PID:
R;Ledbetter, M.W.; Preiner, J.K.; Louis, C.F.; Mickelson, J.R.
J. Biol. Chem. 269, 31544-31551, 1994
A;Title: Tissue distribution of ryanodine receptor isoforms and alleles determined by re
A;Reference number: A55660; MUID:95081095; PMID:7989322
A;Accession: I47212
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Keywords: calcium channel

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Db          3 DGGEGE-DEVQFLRTDDEVVLQCNATVLKEQLKLCLAAEGFGNRLCFLEPTSNAQNVPPD 61

Qy         60 LSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLA 116
              |: | ||:||:||||||||::     || |: :  | ||||||||:|||||| :| |||:
Db         62 LAICCFVLEQSLSVRALQEMLANTVEAGVESSQ--GGGHRTLLYGHAILLRHAHSGMYLS 119

Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
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Db        120 CLTTSRSMTDKLAFDVGLQEDATGEACWWTTHPASKQRSEGEKVRVGDDLILVSVSSERY 179

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGG-DECLTIPS 234
              || :  :    |:|||  | |:: |  :|       ||| || ||| |||  |||||| |
Db        180 LHLSTASGELQVDASFMQTLWNMNPICSGCEE----GYVTGGHVLRLFHGHMDECLTI-S 234

Qy        235 TWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVN 294
                  | : :| |||||| : ||||||||  |  |:|  : |  |:||||:|||||| :
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Qy        295 DQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSET 354
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Db        295 EDQGLVVVDASKAHTKATSFCFRISK-EKLDTAPKRDVEGMGPPEIKYGESLCFVQHVAS 353

Qy        355 GLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFT 414
              ||||:| : : |   :| | :|:||||:|| ||| |  :| |:|||: ||:|   : |:
Db        354 GLWLTYAAPDPKALRLG-VLKKKAILHQEGHMDDALSLTRCQQEESQAARMIYSTAGLYN 412

Qy        415 KFINGLETLQENRRHSMFFA--SVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALR 472
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Qy        473 NRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIK 532
              ||| ||||||:|:|:|  ||::|| |:    | | ||:|: :||: |   ||::||::|:
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Qy        533 GNHTNCAQFANSNRLNWLFSRLGS-QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVI 591
              ||  ||| |  || |:|| |:|   :||   :|:|:||:||||:||| ||:::: ||| |
Db        532 GNRANCALF--SNNLDWLVSKLDRLEAS---SGILEVLYCVLIESPEVLNIIQENHIKSI 586

Qy        592 ISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRP 651
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Qy        711 VGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRV 770
              |||||||||||| :||:|     |    |  :  :   ||: | |||:|| |:|  ||  |
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Qy        771 TGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLE 830
              | |  ||| |:||||:| |: :  ||||| ||  ::  | ||:|  |::||:: | ||
Db        765 QGVFEAFNLNGLFFPVVSFSAGVKVRFLLGGRHGEFKFLPPPGYAPCHEAVLPRERLRLE 824

Qy        831 PCFYFGNLSKRA--LAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAM 888
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Db        825 PIKEYRREGPRGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPHLERIREKLAENIHELWAL 884

Qy        889 NKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISL--D 946
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Qy        947 KPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQ 1006
              |    :|  :|| : :| ||||||||||||| | |||    |||:|||| ||:|||:|: |
Db        945 KAEDNLRKTKLP-KTYMMSNGYKPAPLDLSHVRLTPAQTTLVDRLAENGHNVWARDRVAQ 1003

Qy       1007 GWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEA 1066
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Qy       1067 LLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDE 1126
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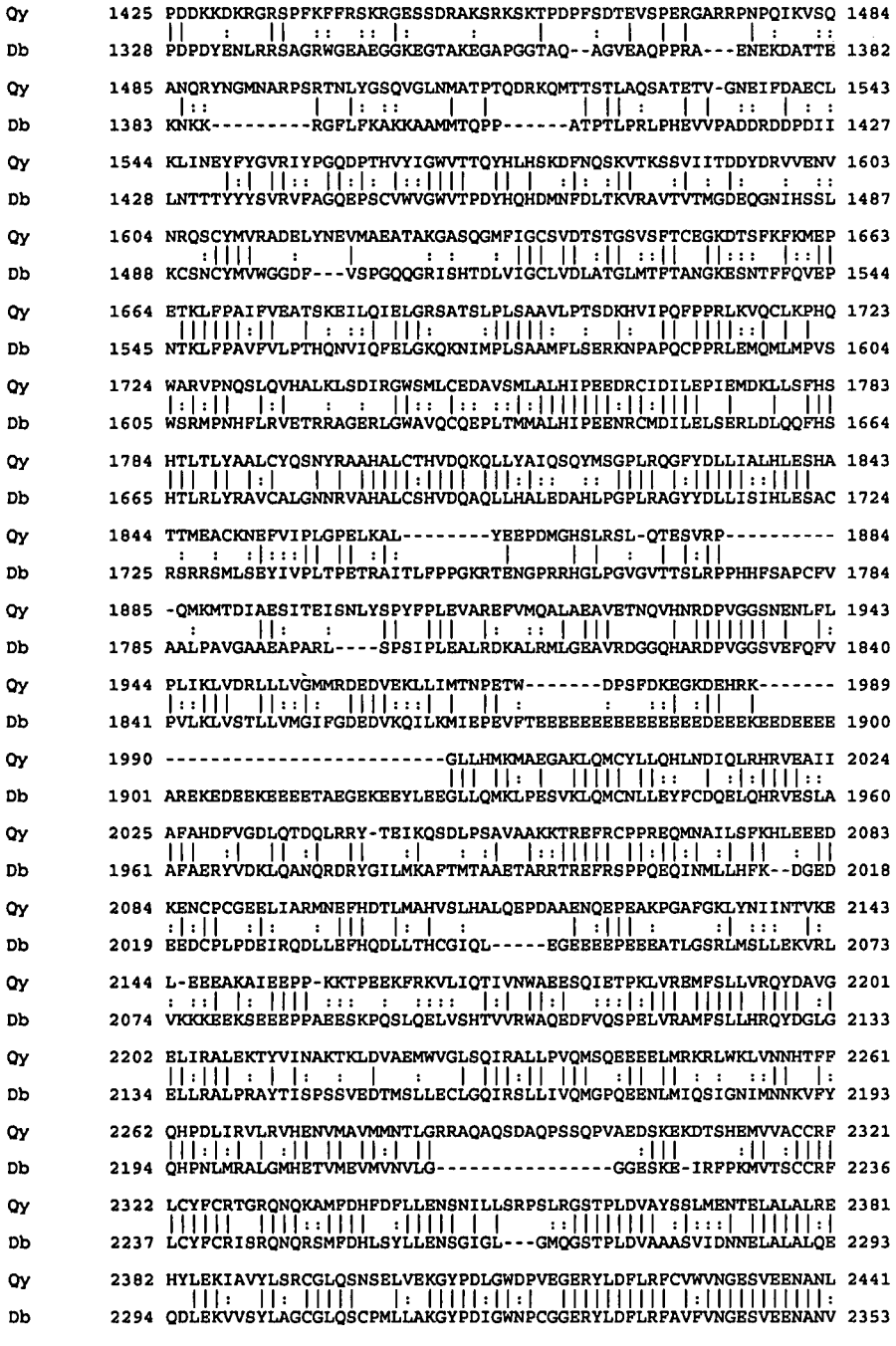
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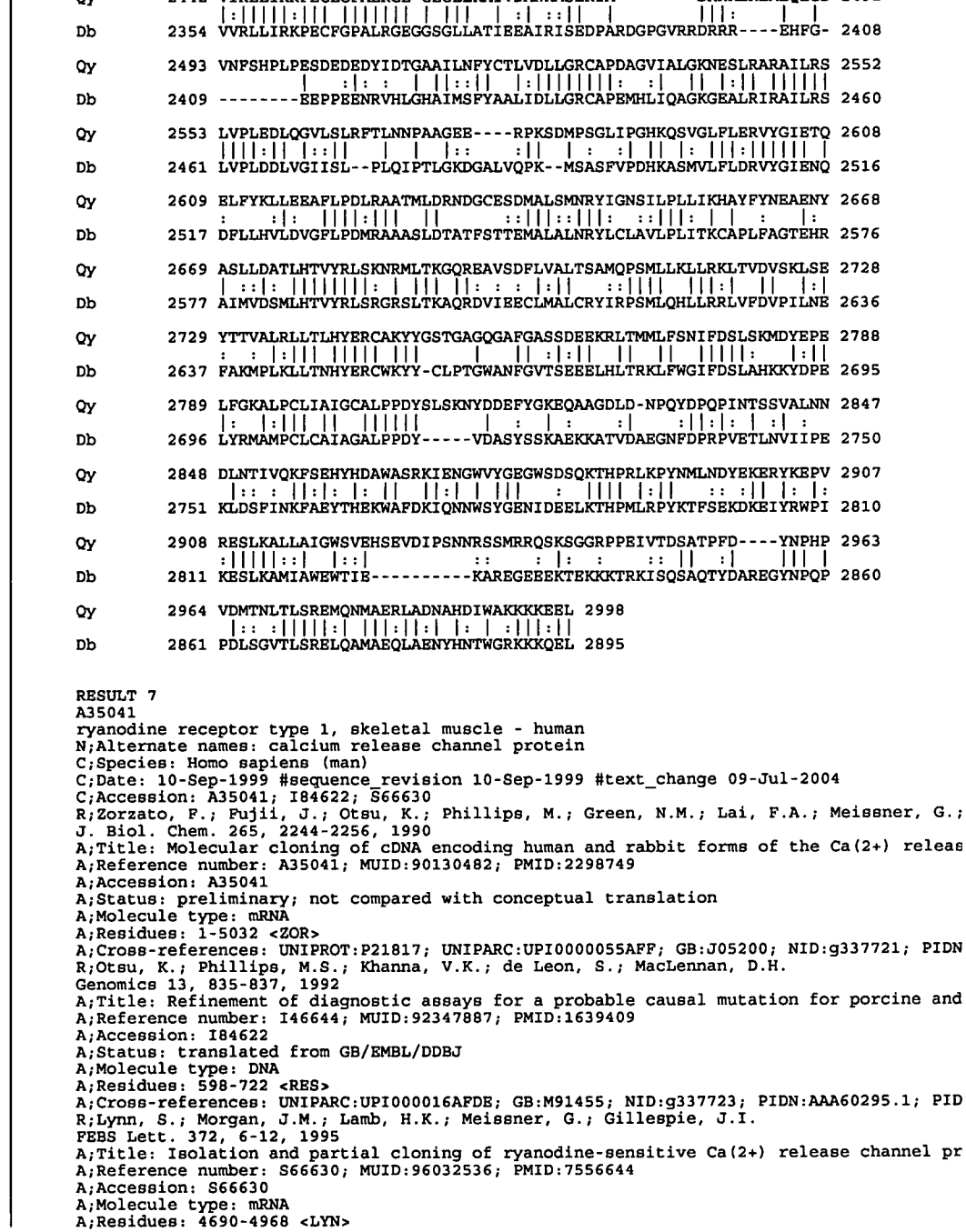
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              | |:: || |:| |:|| ||    |  ||||::|::|  ||||||:||| :||:| || |:
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Qy       1246 TKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEK-ANWEFLRLSLPVIC 1304
              :|  | ||    :    :|:|:    ||||||:::| |: :        ||||||||
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Qy       1305 HNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQE 1364
              |  |  |                                    | |
Db       1298 HQHFRCTA----------------------------------GAT-------------- 1308

Qy       1365 ELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLT 1424
                    |  ||                  |||           :| |        |:
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RESULT 7
A35041
ryanodine receptor type 1, skeletal muscle - human
N;Alternate names: calcium release channel protein
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35041; I84622; S66630
R;Zorzato, F.; Fujii, J.; Otsu, K.; Phillips, M.; Green, N.M.; Lai, F.A.; Meissner, G.;
J. Biol. Chem. 265, 2244-2256, 1990
A;Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) releas
A;Reference number: A35041; MUID:90130482; PMID:2298749
A;Accession: A35041
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-5032 <ZOR>
A;Cross-references: UNIPROT:P21817; UNIPARC:UPI0000055AFF; GB:J05200; NID:g337721; PIDN
R;Otsu, K.; Phillips, M.S.; Khanna, V.K.; de Leon, S.; MacLennan, D.H.
Genomics 13, 835-837, 1992
A;Title: Refinement of diagnostic assays for a probable causal mutation for porcine and
A;Reference number: I46644; MUID:92347887; PMID:1639409
A;Accession: I84622
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: UNIPARC:UPI000016AFDE; GB:M91455; NID:g337723; PIDN:AAA60295.1; PID
R;Lynn, S.; Morgan, J.M.; Lamb, H.K.; Meissner, G.; Gillespie, J.I.
FEBS Lett. 372, 6-12, 1995
A;Title: Isolation and partial cloning of ryanodine-sensitive Ca(2+) release channel pr
A;Reference number: S66630; MUID:96032536; PMID:7556644
A;Accession: S66630
A;Molecule type: mRNA
A;Residues: 4690-4968 <LYN>

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A;Experimental source: myometrial smooth muscle
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A;Gene: GDB:RYR1
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A;Map position: 19q13.1-19q13.1
A;Introns: 642/2
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Qy         56 IPPDLSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLYGNAILLRHLNSD 112
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Qy        113 MYLACLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVA 171
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Db        408 GLYNQFIKSLDSFSGKPRGSGPPAGTALPIEGVILSLQDLIIYFEPPSEDLQHEEKQSKL 467

Qy        469 RALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLA 528
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Db        468 RSLRNRQSLFQEEGMLSMVLNCIDRLNVYTTAAHFAEF-AGEEAAESWKEIVNLLYELLA 526

Qy        529 AIIKGNHTNCAQFANSNRLNWLFSRLGS-QASGEGTGMLDVLHCVLIDSPEALNMMRDEH 587
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Db        527 SLIRGNRSNCALF--STNLDWLVSKLDRLEAS---SGILEVLYCVLIESPEVLNIIQENH 581

Qy        588 IKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVS 647
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Qy        648 SVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYPGGGEKW 706
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Qy        707 GGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFN 766
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Db        702 GGNGVGDDLYSYGFDGLHLWTGHVARPV--TSPGQHLLAPEDVISCCLDLSVPSISFRIN 759

Qy        767 GVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQI 826
              |  | | |  :|||:|:||||:| |: :  |||||| ||  ::  | ||:|  |::||::
Db        760 GCPVQGVFESFNLDGLFFPVVSFSAGVKVRFLLGGRHGEFKFLPPPGYAPCHEAVLPRER 819

Qy        827 LSLEPCFYFGNLSKRA--LAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHE 884
              | |||   :     |   | ||      | ||| |||||:|| || ::|:||:|||||||||

Db        820 LHLEPIKEYRREGPRGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPHLERIREKLAENIHE 879

Qy        885 MWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYIS 944
              :||: :|| || ||  |:|  ::||||| |  ||  |: |::|:: :||||:|||| ::
Db        880 LWALTRIEQGWTYGPVRDDNKRLHPCLVDFHSLPEPERNYNLQMSGETLKTLLALGCHVG 939

Qy        945 L--DKPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARE 1002
              :  :|    ::  :|| : :| ||||||||||| | |||     |||:|||| ||:|||:
Db        940 MADEKAEDNLKKTKLP-KTYMMSNGYKPAPLDLSHVRLTPAQTTLVDRLAENGHNVWARD 998

Qy       1003 RIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGE 1062
              |: |||:|   :|    |:| ||||  :|:| |::|||:  : |||||  ||| ::||  |
Db        999 RVGQGWSYSAVQDIPARRNPRLVPYRLLDEATKRSNRDSLCQAVRTLLGYGYNIEPPDQE 1058

Qy       1063 QHEALLLEASKQKQAD-FRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMM 1121
                    :   | : |  | :||||:| | ||:|||||| :| | |||||  :: | :
Db       1059 PS-----QVENQSRCDRVRIFRAEKSYTVQSGRWYFEFEAVTTGEMRVGWARPELRPDVE 1113

Qy       1122 LGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDAL 1181
              || || :: |:|:  :: : | :| ||: |  |||||  :|| : || |:||||:||
Db       1114 LGADELAYVFNGHRGQRWHLG-SEPFGRPWQPGDVVGCMIDLTENTIIFTLNGEVLMSDS 1172

Qy       1182 GGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRD 1240
              | || | ::: || |:| |:|| ||    |  ||||::|::|  ||||||:||| :||:|
Db       1173 GSETAFREIEIGDGFLPVCSLGPGQVGHLNLGQDVSSLRFFAICGLQEGFEPFAINMQRP 1232

Qy       1241 VTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEK-ANWEFLRLS 1299
              || |::|  | ||     :  :|:|:   ||||||:::| |: :      |||||
Db       1233 VTTWFSKGLPQFEPV-PLEHPHYEVSRVDGTVDTPPCLRLTHRTWGSQNSLVEMLFLRLS 1291

Qy       1300 LPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHY 1359
              |||  |  |  |                                  | |   ||
Db       1292 LPVQFHQHFRCTA----------------------------------GATPLAPPGL-- 1314

Qy       1360 EDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRST---SEAEMAKY 1416
                          :|| :          :| ||:        ||    ||||  |
Db       1315 -----------------QPPAEDEARAAEPDPDYENLR--------RSAGGWSEAENGKE 1349

Qy       1417 DL---GAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGA 1473
                 || | ||                ::  ||  :  ||:: |  |       || : :||
Db       1350 GTAKEGAPGGTP--------------QAGRGAPA-RAENEKDAT------TEKNKKRGF 1387

Qy       1474 RRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETV 1533
                 ::          |  :|          ||||  |          |
Db       1388 LFKAKKV----------AMMTQPP------------ATPTLPR-------LPHDVVPAD 1417

Qy       1534 GNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIIT 1593
                :  | | :      |:| ||:: ||:|: |: |||| || |   |: |||   :| :
Db       1418 NRD--DPEIILNTTTYYYSVRVFAGQEPSCVWAGWVTPDYHQHDMSFDLSKVRVVTVTMG 1475

Qy       1594 DDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGK 1653
              |:   |  ::   :|||  :   |      : :   : ||| || :|| ::|| ||
Db       1476 DEQGNVHSSLKCSNCYMVWGGDF---VSPGQQGRISHTDLVIGCLVDLATGLMTFTANGK 1532

Qy       1654 DTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPR 1713
              :::  |::|| ||||||:||  | : ::| |||:    :|||||:  :  |:  || |||
Db       1533 ESNTFFQVEPNTKLFPAVFVLPTHQNVIQFELGKQKNIMPLSAAMFQSERKNPAPQCPPR 1592

Qy       1714 LKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPI 1773
              |::| | |  |:|:||  |||   :  :  ||:: |:: ::|:|||||||:||:||||
Db       1593 LEMQMLMPVSWSRMPNHFLQVETRRAGERLGWAVQCQEPLTMMALHIPEENRCMDILELS 1652

Qy       1774 EMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDL 1833
              |   |  |||||| || |:|   | | |||||:|||| ||||:|::  :: |||| |:|||
Db       1653 ERLDLQRFHSHTLRLYRAVCALGNNRVAHALCSHVDQAQLLHALEDAHLPGPLRAGYYDL 1712

Qy       1834 LIALHLESHATTMEACKNEFVIPLGPELKALYEEP-----DMGHSLRSLQ----TESVRP 1884
              ||::||||   :  :  :|:::|| || :|:  |     :  ||     |  |:||
Db       1713 LISIHLESACRSRRSMLSEYIVPLTPETRAITLFPPGRSTENGHPRHGLPGVGVTTSLRP 1772

Qy       1885 QMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGS 1937
                 :          |    |      ||  |||  |:  :: | |||      | ||||| |
Db       1773 PHHFSPPCFVAALPAAGAAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHARDPVGAS 1832
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Qy       1938 NENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW-------DPSFDKEGKDEHRK- 1989
Db       1833 VEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEEDEEEEGEEEDEEEKE 1892

Qy       1990 -------------------------------GLLHMKMAEGAKLQMCYLLQHLNDIQLRH 2018
Db       1893 EDEEETAQEKEDEEKEEEEAAEGEKEEGLEEGLLQMKLPESVKLQMCHLLEYFCDQELQH 1952

Qy       2019 RVEAIIAFAHDFVGDLQTDQLRRY-TEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db       1953 RVESLAAFAERYVDKLQANQRSRYGLLIKAFSMTAAETARRTREFRSPPQEQINMLLQFK 2012

Qy       2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNI 2137
Db       2013 --DGTDEEDCPLPEEIRQDLLDFHQDLLAHCGIQL-----DGEEEEPEEETTLGSRLMSL 2065

Qy       2138 INTVK-------ELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMF 2190
Db       2066 LEKVRLVKKKEEKPEEERSAEESKPRSLQE-----LVSHMVVRWAQEDFVQSPELVRAMF 2120

Qy       2191 SLLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKR 2250
Db       2121 SLLHRQYDGLGELLRALPRAYTISPSSVEDTMSLLECLGQIRSLLIVQMGPQEENLMIQS 2180

Qy       2251 LWKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDT 2310
Db       2181 IGNIMNNKVFYQHPNLMRALGMHETVMEVMVNVLG----------------GGESKE-IR 2223

Qy       2311 SHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLM 2370
Db       2224 FPKMVTSCCRFLCYFCRISRQNQRSMFDHLSYLLENSGIGL---GMQGSTPLDVAAASVI 2280

Qy       2371 ENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWV 2430
Db       2281 DNNELALALQEQDLEKVVSYLAGCGLQSCPMLVAKGYPDIGWKPCGGERYLDFLRFAVFV 2340

Qy       2431 NGESVEENANLVIRLLIRRPECLGPALRGE-GEGLLKAIVDANKMSERIA--------DR 2481
Db       2341 NGESVEENANVVVRLLIRKPECFGPALRGEGGSGLLAAIEEAIRISEDPARDGPGIRRDR 2400

Qy       2482 RKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKN 2541
Db       2401 RR----EHFG---------EEPPEENRVHLGHAIMSFYAALIDLLGRCAPEMHLIQAGKG 2447

Qy       2542 ESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEE----RPKSDMPSGLIPGHKQSVGL 2597
Db       2448 EALRIRAILRSLVPLEDLVGIISL--PLQIPTLGKDGALVQPK--MSASFVPDHKASMVL 2503

Qy       2598 FLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIK 2657
Db       2504 FLDRVYGIENQDFLLHVLDVGFLPDMRAAASLDTATFSTTEMALAVNRYLCLAVLPLITK 2563

Qy       2658 HAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLR 2717
Db       2564 CAPLFAGTEHRAIMVDSMLHTVYRLSRGRSLTKAQRDVIEDCLMSLCRYIRPSMLQHLLR 2623

Qy       2718 KLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIF 2777
Db       2624 RLVFDVPILNEFAKMPLKLLTNHYERCWKYY-CLPTGWANFGVTSEEELHLTRKLFWGIF 2682

Qy       2778 DSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLD-NPQYDPQ 2836
Db       2683 DSLAHKKYDPELYRMAMPCLCAIAGALPPDY-----VDASYSSKAEKKATVDAEGNFDPR 2737

Qy       2837 PINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLN 2896
Db       2738 PVETLNVIIPEKLDSFINKFAEYTHEKWAFDKIQNNWSYGENIDEELKTHPMLRPYKTFS 2797

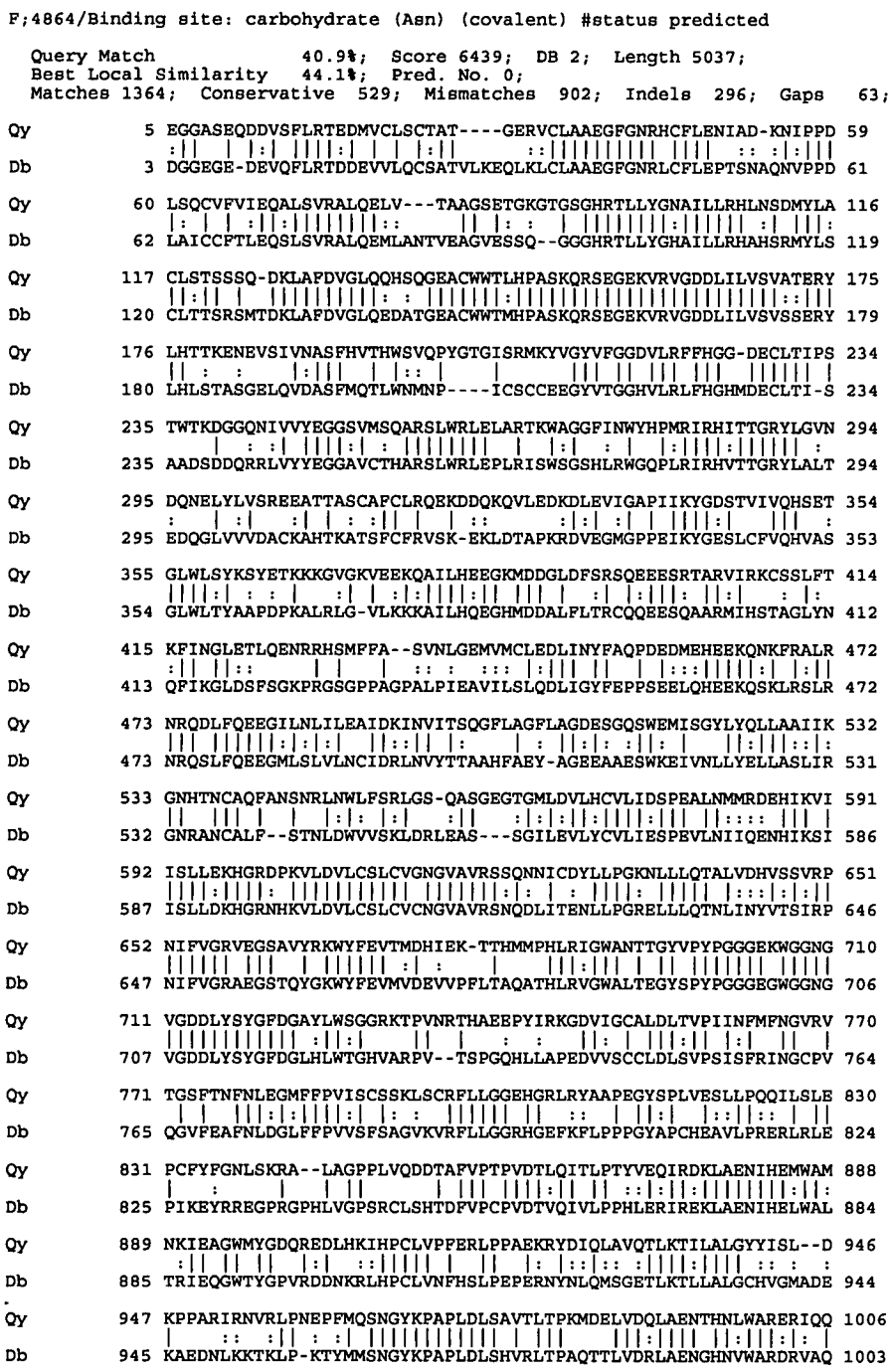
Qy       2897 DYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATP 2956
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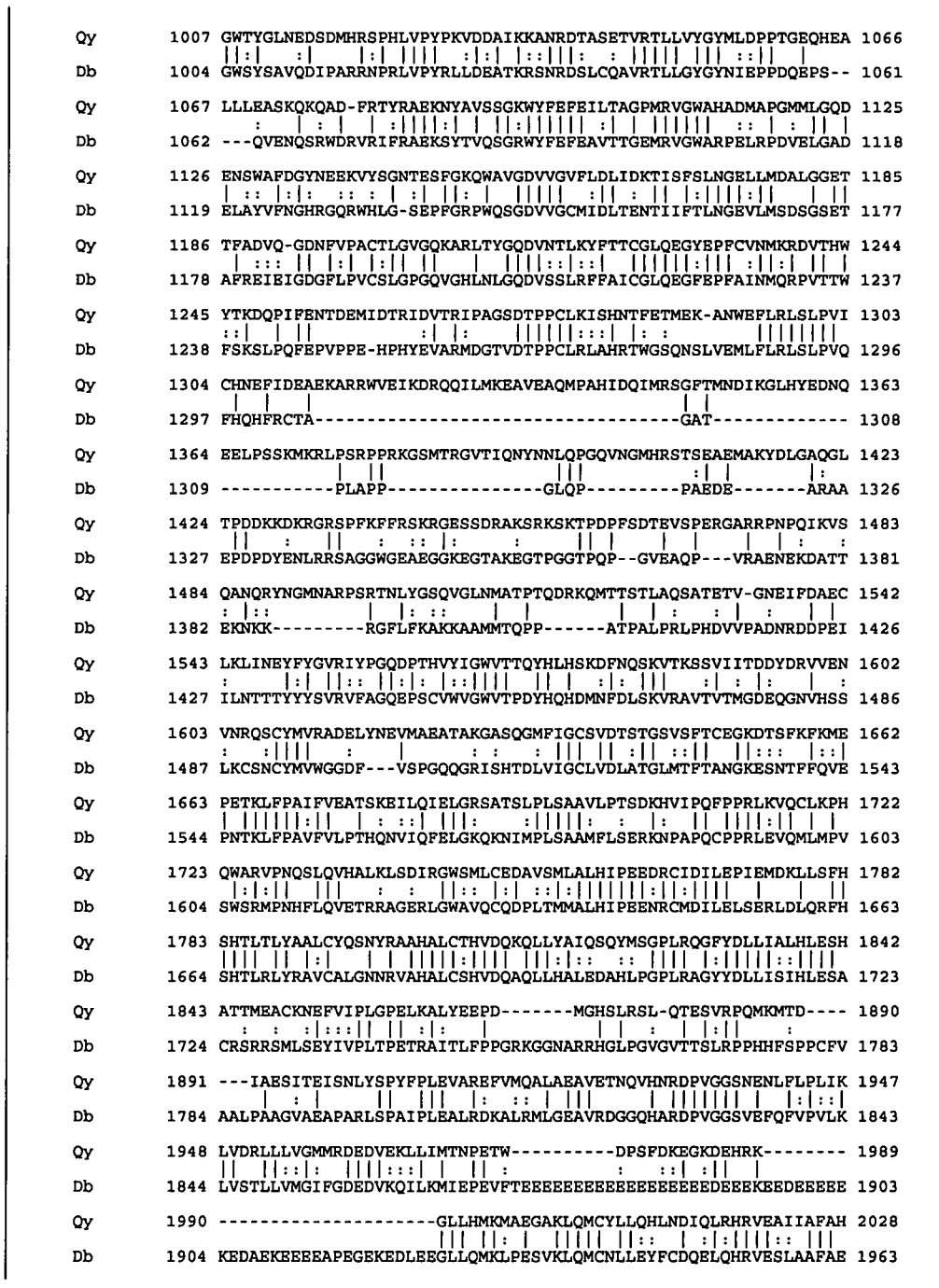
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Qy       2957 FD----YNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEEL 2998
Db       2848 YDPREGYNPQPPDLSAVTLSRELQAMAEQLAENYHNTWGRKKKQEL 2893
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RESULT 8
B35041
ryanodine receptor, skeletal muscle - rabbit
N;Alternate names: calcium-release channel protein; junctional channel complex
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 27-Jul-1990 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: S04654; B35041; A36181; S53794; S32504
R;Takeshima, H.; Nishimura, S.; Matsumoto, T.; Ishida, H.; Kangawa, K.; Minamino, N.; M
Nature 339, 439-445, 1989
A;Title: Primary structure and expression from complementary DNA of skeletal muscle rya
A;Reference number: S04654; MUID:89262082; PMID:2725677
A;Accession: S04654
A;Molecule type: mRNA
A;Residues: 1-5037 <TAK>
A;Cross-references: UNIPROT:P11716; UNIPARC:UPI000013C4CA; EMBL:X15750; NID:g1709; PIDN
A;Note: part of this sequence was confirmed by protein sequencing
R;Zorzato, F.; Fujii, J.; Otsu, K.; Phillips, M.; Green, N.M.; Lai, F.A.; Meissner, G.;
J. Biol. Chem. 265, 2244-2256, 1990
A;Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) releas
A;Reference number: A35041; MUID:90130482; PMID:2298749
A;Accession: B35041
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-66,'Y',68-2014,'D',2016-3246,'E',3248-3480,3486-4497,'LE',4498-4521,'Q',4
,4748-4758,'N',4760-5037 <ZOR>
A;Cross-references: UNIPARC:UPI000017CF33
R;Marks, A.R.; Tempst, P.; Hwang, K.S.; Taubman, M.B.; Inui, M.; Chadwick, C.; Fleische
Proc. Natl. Acad. Sci. U.S.A. 86, 8683-8687, 1989
A;Title: Molecular cloning and characterization of the ryanodine receptor/junctional ch
A;Reference number: A36181; MUID:90046857; PMID:2813419
A;Accession: A36181
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 'X',1223-1235,'XX',1238-1251;1334-1348;1566-1569,'X',1571,'X',1573;1597-160
-4679,'X',4681-4689,'X',4691-4693,'X',4695,'X',4697-4700 <MAR>
A;Cross-references: UNIPARC:UPI0000177940; UNIPARC:UPI0000177941; UNIPARC:UPI0000177942
947
A;Note: the proteolytic fragments sequenced here from the junctional channel complex as
R;Varsanyi, M.; Meyer, H.E.
Biol. Chem. Hoppe-Seyler 376, 45-49, 1995
A;Title: Sarcoplasmic reticular Ca(2+) release channel is phosphorylated at serine 2843
A;Reference number: S53794; MUID:95336639; PMID:7612188
A;Accession: S53794
A;Molecule type: protein
A;Residues: 2841-2852 <VAR>
A;Cross-references: UNIPARC:UPI0000177948
R;Takeshima, H.; Nishimura, S.; Nishi, M.; Ikeda, M.; Sugimoto, T.
FEBS Lett. 322, 105-110, 1993
A;Title: A brain-specific transcript from the 3'-terminal region of the skeletal muscle
A;Reference number: S32504; MUID:93245969; PMID:8097730
A;Accession: S32504
A;Molecule type: mRNA
A;Residues: 4163-5037 <TAW>
A;Cross-references: UNIPARC:UPI0000177949
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homol
C;Keywords: calcium channel; glycoprotein; phosphoprotein; skeletal muscle; transmembra
F;699-704/Region: adenine nucleotide binding
F;841-954,955-1068/Region: 114-residue repeats
F;1344-1359,1371-1386/Region: 16-residue repeats
F;1789-1985/Domain: transcription initiation factor sigma region 1 homology <SR1>
F;2370-2375/Region: adenine nucleotide binding
F;2725-2844,2845-2958/Region: 120-residue repeats
F;4564-4580/Domain: transmembrane #status predicted <TM1>
F;4641-4664/Domain: transmembrane #status predicted <TM2>
F;4836-4859/Domain: transmembrane #status predicted <TM3>
F;4918-4937/Domain: transmembrane #status predicted <TM4>
F;128,286/Binding site: phosphate (Thr) (covalent) (by cAMP- and calmodulin-dependent k
F;2843/Binding site: phosphate (Ser) (covalent) #status experimental

F;4864/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.9%; Score 6439; DB 2; Length 5037;
Best Local Similarity 44.1%; Pred. No. 0;
Matches 1364; Conservative 529; Mismatches 902; Indels 296; Gaps 63;





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Qy       2029 DFVGDLQTDQLRRYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENC 2087
Db       1964 RYVDKLQANQRSRYALLMRAFTMSAAETARRTREFRSPPQEQINMLLHFK--DEADEEDC 2021

Qy       2088 PCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEE 2147
Db       2022 PLPEDIRQDLQDFHQDLLAHCGIQL-----EGEEEEPEEETSLSSRLRSLLETVRLVKKK 2076

Qy       2148 AKAIEE--PPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIR 2205
Db       2077 EEKPEEELPAEEKKPQSLQELVSHMVVRWAQEDYVQSPELVRAMFSLLHRQYDGLGELLR 2136

Qy       2206 ALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTPFQHPD 2265
Db       2137 ALPRAYTISPSSVEDTMSLLECLGQIRSLLIVQMGPQEENLMIQSIGNIMNNKVFYQHPN 2196

Qy       2266 LIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYF 2325
Db       2197 LMRALGMHETVMEVMVNVLG----------------GGETKE-IRFPKMVTSCCRFLCYF 2239

Qy       2326 CRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLE 2385
Db       2240 CRISRQNQRSMFDHLSYLLENSGIGL---GMQGSTPLDVAAASVIDNNELALALQEQDLE 2296

Qy       2386 KIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRL 2445
Db       2297 KVVSYLAGCGLQSCPMLLAKGYPDIGWNPCGGERYLDFLRFAVFVNGESVEENANVVVRL 2356

Qy       2446 LIRRPECLGPALRGE-GEGLLKAIVDANKMSERIA--------DRRKLREMEQEGDVNFS 2496
Db       2357 LIRKPECFGPALRGEGGSGLLAAIEEAIRISEDPARDGPGVRRDRRR----EHFG----- 2407

Qy       2497 HPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPL 2556
Db       2408 ----EEPPEENRVHLGHAIMSFYAALIDLLGRCAPEMHLIQAGKGEALRIRAILRSLVPL 2463

Qy       2557 EDLQGVLSLRFTLNNPAAGEE----RPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFY 2612
Db       2464 DDLVGIISL--PLQIPTLGKDGALVQPK--MSASFVPDHKASMVLFLDRVYGIENQDFLL 2519

Qy       2613 KLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLL 2672
Db       2520 HVLDVGFLPDMRAAASLDTATFSTTEMALALNRYLCLAVLPLITKCAPLFAGTEHRAIMV 2579

Qy       2673 DATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTV 2732
Db       2580 DSMLHTVYRLSRGRSLTKAQRDVIEDCLMALCRYIRPSMLQHLLRRLVFDVPILNEFAKM 2639

Qy       2733 ALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGK 2792
Db       2640 PLKLLTNHYERCWKYY-CLPTGWANFGVTSEEELHLTRKLFWGIFDSLAHKKYDQELYRM 2698

Qy       2793 ALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLD-NPQYDPQPINTSSVALNNDLNT 2851
Db       2699 AMPCLCAIAGALPPDY-----VDASYSSKAEKKATVDAEGNFDPRPVETLNVIIPEKLDS 2753

Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
Db       2754 FINKFAEYTHEKWAFDKIQNNWSYGENVDEELKTHPMLRPYKTFSEKDKEIYRWPIKESL 2813

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFD----YNPHPVDMT 2967
Db       2814 KAMIAWEWTIEKAREG--EEERTEKKKTRK--------ISQTAQTYDPREGYNPQPPDLS 2863

Qy       2968 NLTLSREMQNMAERLADNAHDIWAKKKKEEL 2998
Db       2864 GVTLSRELQAMAEQLAENYHNTWGRKKKQEL 2894


RESULT 9
S74173
ryanodine receptor 3 - Mustela sp.
C;Species: Mustela sp.
C;Date: 23-Apr-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004
C;Accession: S74173
R;Marziali, G.; Rossi, D.; Giannini, G.; Charlesworth, A.; Sorrentino, V.
FEBS Lett. 394, 76-82, 1996
A;Title: cDNA cloning reveals a tissue specific expression of alternatively spliced tra
A;Reference number: S74173; MUID:97074208; PMID:8925932
A;Accession: S74173
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-4859 <MAR>
A;Cross-references: UNIPROT:Q7M2T9; UNIPARC:UPI000017CF34
A;Experimental source: mink lung epithelial cell line CCL64
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homol
C;Keywords: alternative splicing; calcium channel; glycoprotein; phosphoprotein; transm
F;697-702/Region: adenine nucleotide binding #status predicted
F;849-934/Domain: repeat #status predicted <RPT1>
F;963-1048/Domain: repeat #status predicted <RPT2>
F;1134-1139/Region: adenine nucleotide binding #status predicted
F;2234-2239/Region: adenine nucleotide binding #status predicted
F;2521-2526/Region: adenine nucleotide binding #status predicted
F;2596-2681/Domain: repeat #status predicted <RPT3>
F;2714-2792/Domain: repeat #status predicted <RPT4>
F;3834-3854/Domain: transmembrane #status predicted <TM1>
F;3862-3880/Domain: transmembrane #status predicted <TM2>
F;3914-3932/Domain: calcium binding #status predicted <CA1>
F;4119-4142/Domain: transmembrane #status predicted <TM3>
F;4184-4204/Domain: transmembrane #status predicted <TM4>
F;4399-4420/Domain: transmembrane #status predicted <TM5>
F;4471-4494/Domain: transmembrane #status predicted <TM6>
F;4611-4642/Domain: transmembrane #status predicted <TM7>
F;4659-4678/Domain: transmembrane #status predicted <TM8>
F;4701-4720/Domain: transmembrane #status predicted <TM9>
F;4736-4759/Domain: transmembrane #status predicted <TM10>
F;130,290,1243/Binding site: phosphate (Thr) (covalent) (by cAMP- and calmodulin-depend
F;2706/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #statu
F;4686/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             40.9%;  Score 6438.5;  DB 2;  Length 4859;
  Best Local Similarity   43.7%;  Pred. No. 0;
  Matches 1336;  Conservative  513;  Mismatches  843;  Indels  363;  Gaps   50;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
Db          2 AEGGEGGEDEIQFLRTEDEVVLQCIANIHKEQRKFCLAAEGLGNRLCFLEPTSEAKYVPP 61

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKGT--GSGHRTLLYGNAILLRHLNSDMYLA 116
Db         62 DLCVCNFVLEQSLSVRALQEMLANTGENGGEGAAQGGGHRTLLYGHAILLRHSFSGMYLT 121

Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
Db        122 CLTTSRSQTDKLAFDVGLRENATGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSERY 181

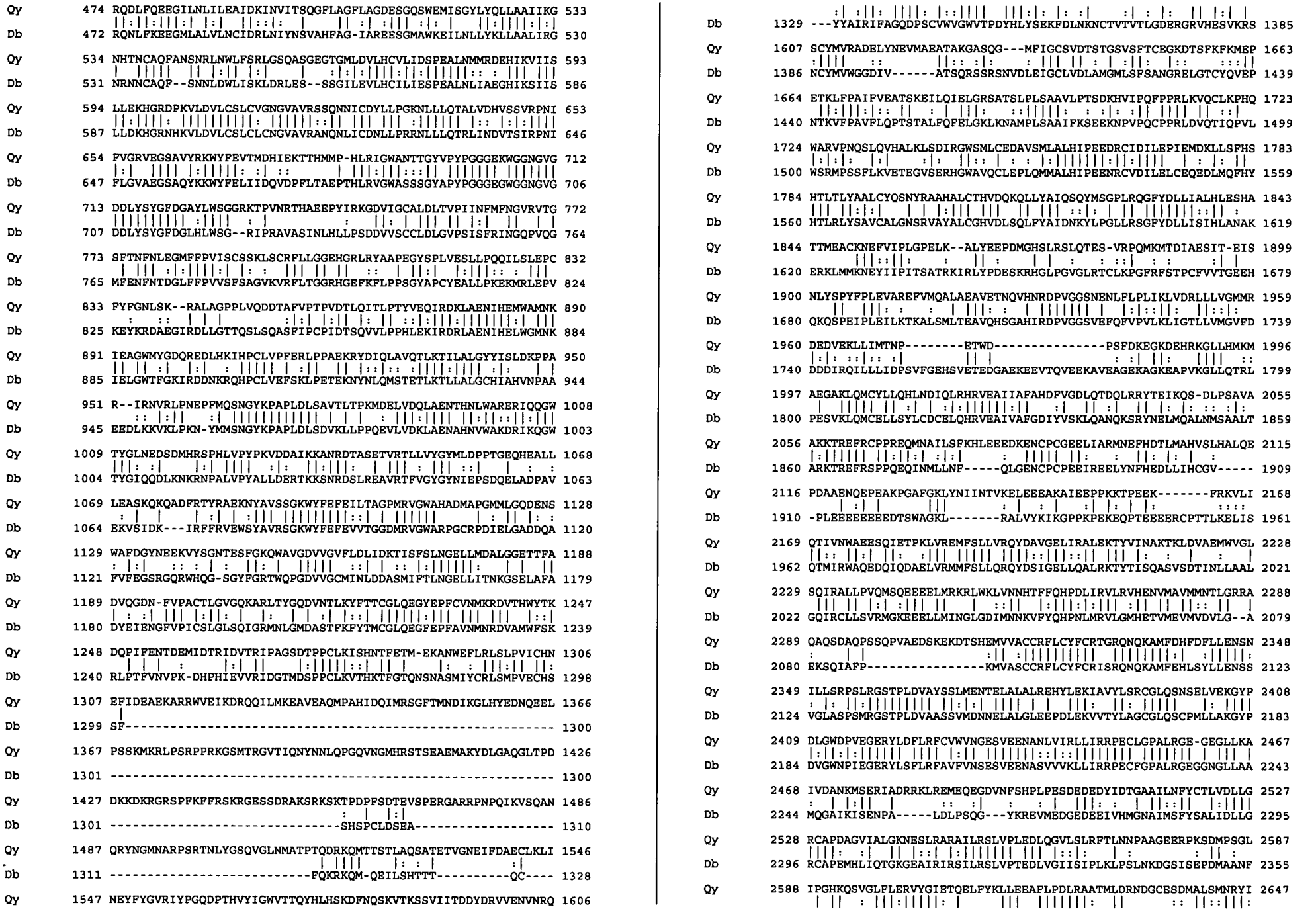
Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
Db        182 LHLSVSNGNVQVDASFMQTLWNVHPTCSGSSIEE--GYLLGGHVVRLFHGHDECLTIPST 239

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
Db        240 DQNDAQHRRIFYEAGGAGTRARSLWRVDPLRISWSGSNIRWGQAFRLRHITTGHYLALTE 299

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQV--LEDKDLEVIGAPIIKYGDSTVIVQHSE 353
Db        300 DQGLLLQDRAKSDTKSTAFSFRASKEIKEKLDSSHKRDIEGMGVPEIKYGDSVCFVQHIA 359

Qy        354 TGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
Db        360 SGLWVTYKAQDAKTSRLGPLKRK-VILHQEGHMDDGLTLQRCQREESQAARIIRNTTALF 418

Qy        414 TKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRN 473
Db        419 SQFVSG-----NNRAAAP--VTLPIQEVLQTLQDLIAYFQPPEEEMQHEDKQNKLRSLKN 471
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Db       2356 CPDHKAPMVLFLDRVYGIKDQTFLLHLLEVGFLPDLRASASLDTVSLSTTEAALALNRYL 2415

Qy       2648 GNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAM 2707
              :::|||| : |  :   |:| ||:|:|| |:||||| | ||| ||: : : |:|: : :
Db       2416 CSAVLPLLTRCAPLFAGTEHYTSLIDSTLQTIYRLSKGRSLTKAQRDTIEECLLAICNHL 2475

Qy       2708 QPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKR 2767
              :|||| :|||:|  || :|:|||  : |:||| |||:| |||    :| |::| : :||
Db       2476 RPSMLQQLLRRLVFDVPQLNEYCKMPLKLLTNHYEQCWKYY-CLPSGWGSYGLAVEEELH 2534

Qy       2768 LTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDY---SLSKNYDDEFYGKEQA 2824
              ||  ||  ||||||   |:|:||  ||||| ||  ||||||    :|   :      :|
Db       2535 LTEKLFWGIFDSLSHKKYDPDLFRMALPCLSAIAGALPPDYLDTRISATLE------KQI 2588

Qy       2825 AGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQK 2884
              : | |   :||:|||| : :|      || |::|| || ||  | :||| ||    :: |
Db       2589 SVDADG-NFDPKPINTMNFSLPEKWEYIVTKYAEHSHDKWACDKSQNGWKYGISLDENVK 2647

Qy       2885 THPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHS-EVDIPSNNRSSMRRQSKSG 2943
              ||| ::|:  | : ||| |: | ||||| :||:||||| : | :      | : : :|
Db       2648 THPLIRPPKTLTEKEKEIYRWPARESLKTMLAVGWSVERTKEGEALVQQRENEKLRS--- 2704

Qy       2944 GRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEEL 2998
                 |: ::    |:| |:|::|: ||||:| | | :|:| |:|||||| ||
Db       2705 ------VSQASQGNSYSPAPLDLSNVVLSRELQGMVEVVAENYHNIWAKKKKLEL 2753


RESULT 10
S66572
ryanodine receptor type 3 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66572
R;Ottini, L.; Marziali, G.; Conti, A.; Charlesworth, A.; Sorrentino, V.
Biochem. J. 315, 207-216, 1996
A;Title: Alpha and beta isoforms of ryanodine receptor from chicken skeletal muscle are
A;Reference number: S66572; MUID:96207583; PMID:8670108
A;Accession: S66572
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-4869 <OTT>
A;Cross-references: UNIPROT:Q90985; UNIPARC:UPI000017CF35; EMBL:X95267; NID:g1212911; PI
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo

  Query Match             40.8%;  Score 6423;  DB 2;  Length 4869;
  Best Local Similarity   43.7%;  Pred. No. 0;
  Matches 1339;  Conservative  498;  Mismatches  849;  Indels  380;  Gaps   50;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
              ||||   :|:: ||||:| | | | ::      : |||||| ||| ||||  :: | :||
Db          2 AEGGEGGEDEIQFLRTDDEVVLQCVSSIHKEQRKFCLAAEGLGNRLCFLEPTSEAKYVPP 61

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKGTG-SGHRTLLYGNAILLRHLNSDMYLAC 117
              ||  | ||:||:|||||||::|  |    :|    ||||||||:||||||  |:||| |
Db         62 DLCICNFVLEQSLSVRALQEMLTNTGDNASEGAAQGGHRTLLYGHAILLRHSFSEMYLTC 121

Qy        118 LSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYL 176
              |::| || |||||||||:::: |||||||:|||||||||||||:|||||||||::||||
Db        122 LTSSRSQTDKLAFDVGLRENAAGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSERYL 181

Qy        177 HTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTW 236
              | :  |    |:||| | |:| |  :| :  :  ||: || |:| ||| || ||||||
Db        182 HLSMSNGSIQVDASFMQTLWNVHPTCSGSNITE--GYLLGGHVVRLFHGHDEYLTIPSTD 239

Qy        237 TKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQ 296
              |  |  |:|| |    :||||||:|  |  |:|  | |  | |:|||||| || :||
Db        240 QNDSQQKKVLYETGGAGVRARSLWRVEPLRISWSGSNIRWGQPFRLRHITTGMYLALNDD 299

Qy        297 NELYLVSREEATTASCAFCLRQEKD--DQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSET 354
                | :: ||:: | | ||| |  |:  :::     :|:: :| | ||||||   :|| :
Db        300 EGLVMLDREKSDTTSSAFCFRASKELKEKQDSTLKRDIDGMGVPEIKYGDSVCFIQHVAS 359

Qy        355 GLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFT 414
                                                                        |||:||: : |   :| :: |  |||:|| |||||   | | |||: ||:||  :|||:
Db        360 ALWLTYKAPDAKSARLGLLKRK-VILHQEGHMDDGLTLQRCQHEESQAARIIRNTTSLFS 418

Qy        415 KFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNR 474
              :||:|     || |      |   ||   :|||| ||  | ||:|||:|||| |:|:||
Db        419 QFISG-----NNRTLSPIALPVE--EMAQTLQDLIKYFQPPGEDLEHEDKQNKLRSLKNR 471

Qy        475 QDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGN 534
              |:||::||:|  |:|  ||::|    |     |  ::  |:| :|: |   ||:||||:|:||
Db        472 QNLFKDEGMLALVLNCIDRLNDYNSAAHFAE-ISRVENGTAWKEILNLLYELLAALIRGN 530

Qy        535 HTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISL 594
              || ||  |: |:|| |:|    |   :|:|:|||||:||:||||||:: :|||| ||||
Db        531 RNNCTQF--SSNLDWLISKLDRLES--SSGILEVLHCILIESPEALNIIAEEHIKSIISL 586

Qy        595 LEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIF 654
              |:|||: |||||||||| ||||||::|| ||| ||| ::|||| |:: |:|:|||||
Db        587 LDKHGRNYKVLDVLCSLCVCNGVAVRANQNLICDNLLPRRDLLLQTRLINDVTSIRPNIF 646

Qy        655 VGRVEGSAVYRKWYFEVTMDHIEKTTHMMP-HLRIGWANTTGYVPYPGGGEKWGGNGVGD 713
              :|  |||| |:|||||: :|  ::       | |||:|||:|:|| |||||||  ||||||||
Db        647 LGVAEGSAQYKKWYFELIIDQVDPFLTAEPTHLRVGWASTSGYAPYPGGGEGWGGNGVGD 706

Qy        714 DLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGS 773
              ||||:|||| :|||| : |       :  :   ||: | ||| || |:|  ||  | |
Db        707 DLYSFGFDGLHLWSG--RVPRAVASVNQHLLSSDDVVSCCLDLGVPSISFRINGQPVQGM 764

Qy        774 FTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCF 833
              | ||  || |||||:| |: :  ||||| ||  ::  | ||:|  |:|||:: : |||
Db        765 FENFCTEGFFFPVVSLSAGVKARFLLGGRHGEFKFLPPTGYAPCYEALLPKEKMKLEPVK 824

Qy        834 YFGNLSK--RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKI 891
              :   |  | | |         :|:| |:|| || || ::|:|||||||||||:| ||||
Db        825 EYKRDSDGVRDLLGTTQFLSQASFIPCPIDTSQIALPFHLEKIRDKLAENIHELWGMNKI 884

Qy        892 EAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPAR 951
              | || ||  |:|  : ||||| | :||  || |::|:: :||||:|||| :|   | |
Db        885 ELGWTYGKIRDDNKRHHPCLVEFSKLPETEKNYNLQMSTETLKTLLALGCHIVHANPAAE 944

Qy        952 --IRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWT 1009
                :: |:||   :: |||||||||||| | | |  : ||::|||| ||:||::||:||||
Db        945 EDLKKVKLPKN-YIMSNGYKPAPLDLSEVKLLPSQEFLVNKLAENAHNVWAKDRIKQGWT 1003

Qy       1010 YGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLL 1069
              ||: :|    |:| |||| :|:  ||:|||:  | |||   ||| ::||  | :  :
Db       1004 YGIQQDLKNKRNPRLVPYDLLDERTKKSNRDSLREAVRTFAGYGYNVEPPDQEIADQTVE 1063

Qy       1070 EASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSW 1129
              : |  |    | || |::||| ||||||||| :| | ||||||     | : || |: ::
Db       1064 KVSIDK---IRFYRVEQSYAVKSGKWYFEFEAVTGGDMRVGWARPGCRPDIELGADDQAF 1120

Qy       1130 AFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFAD 1189
              |:|   :: : | :  ||: |  ||||  ::| ||:|  |:|||||: : | |  |||
Db       1121 VPEGSKGQRWHQG-SGFFGRSWQPGDVVGCMINLDDKSIIFTLNGELLITSKGSELAFAD 1179

Qy       1190 VQGDN-FVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPPFCVNMKRDVTHWYTKD 1248
              ::  ||| |:||: |  |:  | | :|  ||:| ||||||:||| ||| |||  |::|
Db       1180 FGIESGFVPICSLGLSQIGRMNLGMDASTFKYYTMCGLQEGFEPPFAVNMNRDVAMWFSKR 1239

Qy       1249 QPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETM-EKANWEFLRLSLPVICHNE 1307
                | | |  :     |:: ||    ::|| ||::|  |  |    ::  : |||:|:    |
Db       1240 LPTFVNVPKN-HPHIEIWRIDGTIESPPRLKVTHKTLGTQNSNSDMIYCRLSMPI----E 1294

Qy       1308 FIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELP 1367
              |                                    || |
Db       1295 F-----------------------------------RSSFNF---------------- 1301

Qy       1368 SSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDD 1427
                                    || ::|
Db       1302 ------------------GVGVEN---------------------------------- 1307

Qy       1428 KKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQ 1487
                                    |||  : ||     | | |
```

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Db       1308 ------------------ASSDALQKRKHSQEFPASST---------------------- 1327

Qy       1488 RYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLIN 1547

Db       1328 ------------------------------------------------------TC----- 1329

Qy       1548 EYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQS 1607

Db       1330 --FYSLRIFAGQDPSSVWVGWVTPDYHFYSENFDINKNCTVTVTLGDERGRVHESVKRSN 1387

Qy       1608 CYMVRADELYNEVMAEATAKGASQ-GMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETK 1666

Db       1388 CYMVWG----GDIAANSQRSGRSNVDLEIGCFVDLATGMLSFTANGKELGTCYQVEPNTK 1443

Qy       1667 LFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWAR 1726

Db       1444 LFPAAFVQPTSTNLIQFELGKLKNTMPLSAAIFKSEERNPVPQCPPRLDVQTITPVLWSR 1503

Qy       1727 VPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTL 1786

Db       1504 MPNSFLKVETERVSERHGWVVQCLEPLQMMALHIPEENRCVDILELCEQEDLMKFHYHTL 1563

Qy       1787 TLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTM 1846

Db       1564 KLYSSVCALGNTRVAYALCSHVDISQLFYTIDNQYLPGLLRSGFYDLLISIHLDHAKQAK 1623

Qy       1847 EACKNEFVIPLGPELKA--LYEEPDMGHSLRSLQTES-VRPQMKMTDIAESIT-EISNLY 1902

Db       1624 LMMNNEFIIPVTEETRTIKLYPDETKKHGLPGVGLSTCLKPSFNFSTPCFIVTSEEHQTS 1683

Qy       1903 SPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDED 1962

Db       1684 SPDIPLDTLKSKAISMLTEAVQCSGSHIRDPVGGHIAFQFVPVLKLIATLLVMGVFDDDD 1743

Qy       1963 VEKLLIMTNPETW-DPSFDKEGKDEHR------------------------KGLLHMKMA 1997

Db       1744 VKQVLILIDPNVFGDHKEEAEEKTEKEEVTQVEEKAVEAGEKAVKETKAPTKGLLQTRLP 1803

Qy       1998 EGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQS-DLPSAVAA 2056

Db       1804 ESVKLQMCHLLNYFCDCELQHRVEAIVSFADHYVSKLQYNQKYRYNELMQALNMSAALTA 1863

Qy       2057 KKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEP 2116

Db       1864 KKTKEFRSPPQEQINMLLNF-----QLGEDCPCPEEIRDELYDFHDDLLIHCGI------ 1912

Qy       2117 DAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPEEK-------FRKVLIQ 2169

Db       1913 PLEEEEEEEEDSSLTGKLRSLIYKI-------KGPPKPEKIEPREEEDKSPTTLKELISQ 1965

Qy       2170 TIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLS 2229

Db       1966 TMVRWSQEDQIQDPELVRIMYTLLRRQYDSIGELLQALRKAYTISAASVKDTINLLAALG 2025

Qy       2230 QIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQ 2289

Db       2026 QIRSLLSVRMGKEEELLMINGLGDIMNNKVFYQHPNLMRVLGMHETVMDVMVNVLG---- 2081

Qy       2290 AQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNI 2349

Db       2082 --------------GDKSQIAFPKMVASCCRFLCYFCRISRQNQKAMFEHLSYLLENSSV 2127

Qy       2350 LLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPD 2409

Db       2128 GLAFPSMRGSTPLDVAAASVMDNNELALALEEPDLDKVVTYLAGCGLQSCPVLLAKGYPD 2187

Qy       2410 LGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE-GEGLLKAI 2468

Db       2188 IGWNPIEGERYLSFLRFAVFVNSESVEENASVVVKLLIRRPECFGPELRGEGGNGLLAAM 2247

Qy       2469 VDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGR 2528

Db       2248 QEAIRISENPTRDLPSQGYKREGD-------EEEEEEEEIVHMGNAIMSFYSALIDLLGR 2300

Qy       2529 CAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLI 2588

Db       2301 CAPEMHLIQSGKGEAIRIRSILRSLVPTEDLVGIISIPLKLSTVNKDGTVNEPDMSANFC 2360

Qy       2589 PGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIG 2648

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Qy       2649 NSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQ 2708

Db       2421 SAVFPLLKRCAPLFSGTEHHASLVDSMLHTIYRLSKGRSLTKAQRDTIEECLLAICHHLR 2480

Qy       2709 PSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRL 2768

Db       2481 PSMLQQLLRRLVFDVPLLNEYCKMPLKLLTNHYEQCWKYY-CLPSGMGSYGIAAEDELHL 2539

Qy       2769 TMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDY-------SLSKNYDDEFYGK 2821

Db       2540 TEKLFWGIFDSLSHKKYDPELFRMALPCLSAIAGALPPDYLDTRIRSTLEK--------- 2590

Qy       2822 EQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSD 2881

Db       2591 -QTSVDPEG-NFDPKPVNTANLVLPEKLEYIVSKYAEHSHDKWAFDKTNNGWKYGVSLDE 2648

Qy       2882 SQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSK 2941

Db       2649 NTKTHPLIRPFKTLTEKEKEIYRWPVRESLKTMLAMGWSLE----------------RTK 2692

Qy       2942 SGG------RPPE---IVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAK 2992

Db       2693 EGGEGMLHQRENEKLRSISQSSQGNGYSPAPLDLTNVVLSRELQGMVEVMAENYHNIWAK 2752

Qy       2993 KKKEEL 2998

Db       2753 KKKMEL 2758


RESULT 11
B54161
ryanodine-binding protein beta form - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: B54161
R;Oyamada, H.; Murayama, T.; Takagi, T.; Iino, M.; Iwabe, N.; Miyata, T.; Ogawa, Y.; En
J. Biol. Chem. 269, 17206-17214, 1994
A;Title: Primary structure and distribution of ryanodine-binding protein isoforms of th
A;Reference number: A54161; MUID:94274714; PMID:8006029
A;Accession: B54161
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-4868 <OYA>
A;Cross-references: UNIPROT:Q91319; UNIPARC:UPI0000110256; GB:D21071; NID:g1856973; PID
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homol

  Query Match             40.8%;  Score 6419;  DB 2;  Length 4868;
  Best Local Similarity   43.8%;  Pred. No. 0;
  Matches 1339;  Conservative  517;  Mismatches  845;  Indels  354;  Gaps   51;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58

Db          2 AEGGEVE-DEIQFLRTDDEVVLQCIATIHKEQRKFCLAAEGLGNRLCFLEPTSEAKYVPP 60

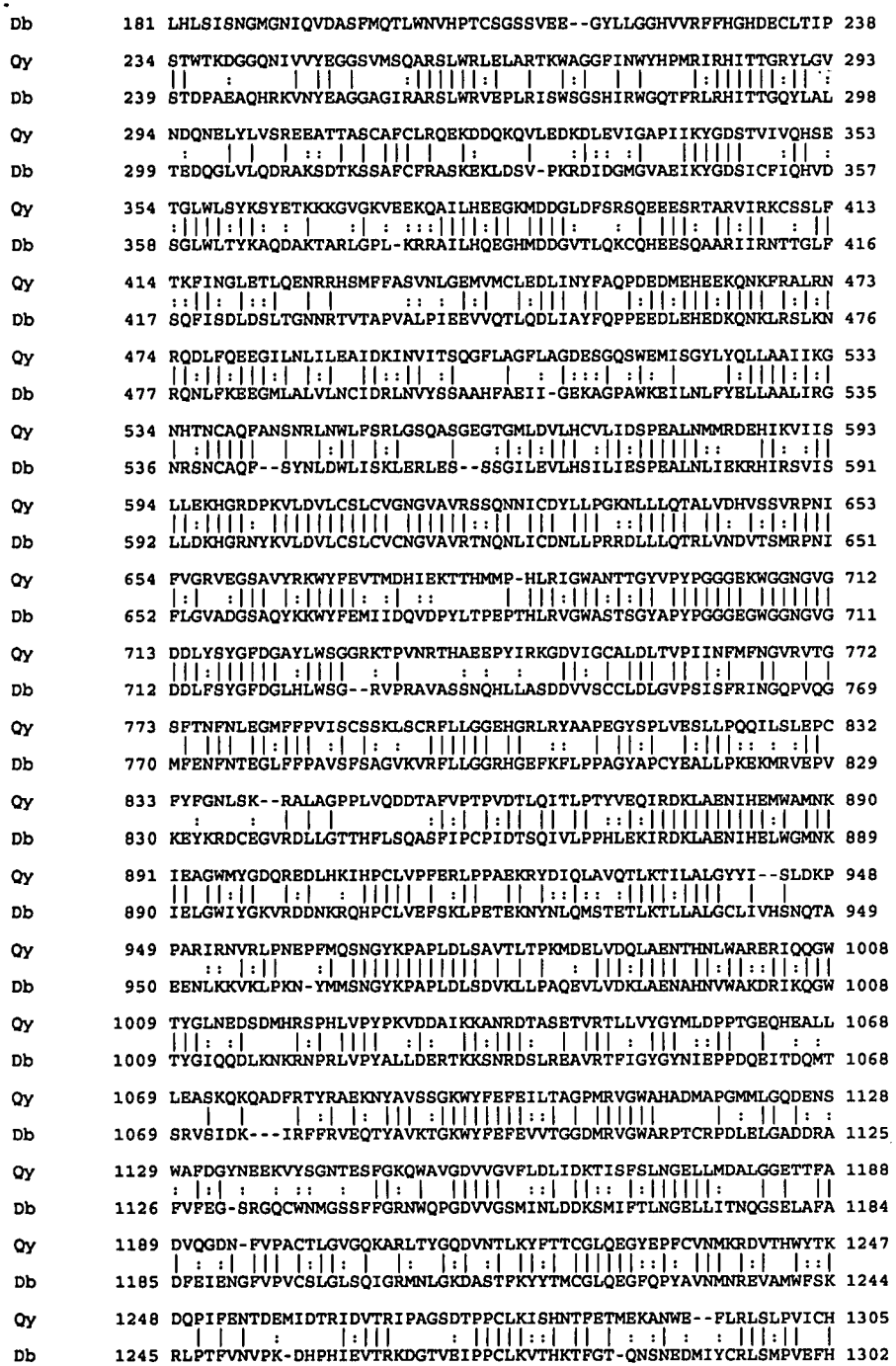
Qy         59 DLSQCVFVIEQALSVRALQELV--TAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLA 116

Db         61 DLCICNFVLEQSLSVRALQEMLANTIANGNEGASQGGGHRTLLYGHAILLRHSFSGMYLT 120

Qy        117 CLSTSSS-QDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175

Db        121 CLTTSRSLTDKLAFDVGLQDTATGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSERY 180

Qy        176 LHTTKENEVS--IVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIP 233
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Db 181 LHLSISNGMGNIQVDASFMQTLWNVHPTCSGSSVEE--GYLLGGHVVRFFHGHDECLTIP 238
Qy 234 STWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGPINWYHPMRIRHITTGRYLGV 293
Db 239 STDPAEAQHRKVNYEAGGAGIRARSLWRVEPLRISWSGSHIRWGQTFRLRHITTGQYLAL 298
Qy 294 NDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSE 353
Db 299 TEDQGLVLQDRAKSDTKSSAFCFRASKEKLDSV-PKRDIDGMGVAEIKYGDSICFIQHVD 357
Qy 354 TGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
Db 358 SGLWLTYKAQDAKTARLGPL-KRRAILHQEGHMDDGVTLQKCQHEESQAARIIRNTTGLF 416
Qy 414 TKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRN 473
Db 417 SQFISDLDSLTGNNRTVTAPVALPIEEVVQTLQDLIAYFQPPEEDLEHEDKQNKLRSLKN 476
Qy 474 RQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKG 533
Db 477 RQNLFKEEGMLALVLNCIDRLNVYSSAAHFAEII-GEKAGPAWKEILNLFYELLAALIRG 535
Qy 534 NHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIIS 593
Db 536 NRSNCAQF--SYNLDWLISKLERLES--SSGILEVLHSILIESPEALNLIEKRHIRSVIS 591
Qy 594 LLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNI 653
Db 592 LLDKHGRNYKVLDVLCSLCVCNGVAVRTNQNLICDNLLPRRDLLLQTRLVNDVTSMRPNI 651
Qy 654 FVGRVEGSAVYRKWYFEVTMDHIEKTTHMMP-HLRIGWANTTGYVPYPGGGEKWGGNGVG 712
Db 652 FLGVADGSAQYKKWYFEMIIDQVDPYLTPEPTHLRVGWASTSGYAPYPGGGEGWGGNGVG 711
Qy 713 DDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTG 772
Db 712 DDLFSYGFDGLHLWSG--RVPRAVASSNQHLLASDDVVSCCLDLGVPSISFRINGQPVQG 769
Qy 773 SFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPC 832
Db 770 MFENFNTEGLFFPAVSFSAGVKVRFLLGGRHGEFKFLPPAGYAPCYEALLPKEKMRVEPV 829
Qy 833 FYFGNLSK--RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNK 890
Db 830 KEYKRDCEGVRDLLGTTHFLSQASFIPCPIDTSQIVLPPHLEKIRDKLAENIHELWGMNK 889
Qy 891 IEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYI--SLDKP 948
Db 890 IELGWIYGKVRDDNKRQHPCLVEFSKLPETEKNYNLQMSTETLKTLLALGCLIVHSNQTA 949
Qy 949 PARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGW 1008
Db 950 EENLKKVKLPKN-YMMSNGYKPAPLDLSDVKLLPAQEVLVDKLAENAHNVWAKDRIKQGW 1008
Qy 1009 TYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALL 1068
Db 1009 TYGIQQDLKNKRNPRLVPYALLDERTKKSNRDSLREAVRTFIGYGYNIEPPDQEITDQMT 1068
Qy 1069 LEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENS 1128
Db 1069 SRVSIDK---IRFFRVEQTYAVKTGKWYFEFEVVTGGDMRVGWARPTCRPDLELGADDRA 1125
Qy 1129 WAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFA 1188
Db 1126 FVFEG-SRGQCWNMGSSFFGRNWQPGDVVGSMINLDDKSMIFTLNGELLITNQGSELAFA 1184
Qy 1189 DVQGDN-FVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTK 1247
Db 1185 DFEIENGFVPVCSLGLSQIGRMNLGKDASTPKYYTMCGLQEGFQPYAVNMNREVAMWFSK 1244
Qy 1248 DQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE--PLRLSLPVICH 1305
Db 1245 RLPTFVNVPK-DHPHIEVTRKDGTVEIPPCLKVTHKTFGT-QNSNEDMIYCRLSMPVEFH 1302
Qy 1306 NEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEE 1365
Db 1303 SAFINE---------- 1308
Qy 1366 LPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTP 1425
Db 1309 ----------ENF---------- 1311
Qy 1426 DDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQA 1485
Db 1312 ----------QKRNQLQD---------- 1319
Qy 1486 NQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKL 1545
Db 1320 ----------ASSHTTTL---------- 1327
Qy 1546 INEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNR 1605
Db 1328 ---YYYSVRIFAGQDPSSVWVGWVTPDYHFYSENFDLSKNCTVTVTLGDERGRVHESVKR 1384
Qy 1606 QSCYMVRADELYNEVMAEATAKGASQ-GMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPE 1664
Db 1385 SNCYMVWGGDL----STGSQRSGRSNVDIDIGCLVDLATGLLSFTANGKDLGTCYQVEPN 1440
Qy 1665 TKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQW 1724
Db 1441 TKLFPAVFLQPTSTNLFQFELGKLKNTMPLSAAIFKSEEKNPVSQCPPRLDVQTITPVLW 1500
Qy 1725 ARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSH 1784
Db 1501 SRMPNMFLKVETERVSERHGWVVQCLEPLQMLALHIPEENRCIDILELSEQEDLMKFHYH 1560
Qy 1785 TLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHAT 1844
Db 1561 TLKLYCAVCALGNNRVAHALCSHVDQSQLLYTIDNQYLPGLLRSGFFNLLISIYLESAKE 1620
Qy 1845 TMEACKNEFVIPLGPELKALYEEPDMG--HSLRSL-QTESVRPQMKMTDIAESIT-EISN 1900
Db 1621 GKLMMNNEFIIPITDETRKIRLFPDESKRHGLPGVGRSTCLKSDLHFTAPCFVLTGEERQ 1680
Qy 1901 LYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRD 1960
Db 1681 QHGPEIPVDILKSKAISMLTEAVQSSGDHIRDPVGGKAEFQFVPVLKLIATLLIMGVFED 1740
Qy 1961 EDVEKLLIMTNPETWDPSFDKEGKDEHR----------KGLLHM 1994
Db 1741 EDVRQILLLIDPNVFGDHKEEEAEENGEKEDVAQIEEKAVEAGEKPTRDAKAPAKGLLQT 1800
Qy 1995 KMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQS-DLPSA 2053
Db 1801 RLPESVKLQMCELLHYFCDCELKHRVESIVAFSDKYVSKLQYNQKFRYNELMLALNMSAA 1860
Qy 2054 VAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHAL 2113
Db 1861 LTAKKTREFRSPPQEQINMLLNFQMQEES-----PCPEEIRDELYEFHEDLLIHCGI--- 1912
Qy 2114 QEPDAAENQEPEAKPGAFGKLYNIINTVK---ELEEEAKAIEEPPKKTPEEKFRKVLIQT 2170
Db 1913 --PLEEEEQEEEDTSWT-GRLRSLVYKIKGRPKAEEQAPQEEE--EKSP-TTLKELISQT 1966
Qy 2171 IVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQ 2230
Db 1967 MVRWAQEDHIQDPELVRIMFSLLRLQYDSIGELLRAMRKTYTISAASVEDTINLLASLGQ 2026
Qy 2231 IRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQA 2290
Db 2027 IRSLLSVRMGKEEEMLMIDGLGDIMNNKVFYQHPNLMRVLGMHETVMEVMVDVLGGN-KS 2085
Qy 2291 QSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNIL 2350
Db 2086 QQIAFP----------KMVASCCRFLCYFCRISRQNQKAMFEHLAYLLENSSVG 2129

```
Qy       2351 LSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDL 2410
             |: ||:|||||||||| :|:|:| ||||||:|  |||:  ||: |||||   |: |||||:
Db       2130 LASPSMRGSTPLDVAAASVMDNNELALALQEPDLEKVVTYLAGCGLQSCLMLITKGYPDI 2189

Qy       2411 GWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE-GEGLLKAIV 2469
             ||:|:|||||| |||| |:|| |||||||::|::|||||||| ||:|||| | ||| |:
Db       2190 GWNPIEGERYLSFLRFAVFVNCESVEENASVVVKLLIRRPECFGPSLRGEGGNGLLAAMQ 2249

Qy       2470 DANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRC 2529
             :|  :||  |     :  ::|       : | :|:|: :  | ||::||  |:|||||
Db       2250 EAINISENPALDLPSQGYQRE-------VVEEDEEEEEIVHMGNAIMSFYSALIDLLGRC 2302

Qy       2530 APDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERP--KSDMPSGL 2587
             ||:  :|  || |::| |||||||||| ||| |::|:   |  ||  ::    : || :
Db       2303 APEPHLIQAGKGEAIRIRAILRSLVPTEDLVGIISIPLKL--PAFNKDGTVFEPDMAASF 2360

Qy       2588 IPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYI 2647
              | ||  : |||:|||||: |     ||| |||||||:  ||       ::|||::||||
Db       2361 CPDHKAPMVLFLDRVYGIKDQSFLLHLLEVAFLPDLRASASLDTASLSVTEMALALNRYI 2420

Qy       2648 GNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAM 2707
              :::|||| : |  ::  |:||:|:|:||||:||||| | ||| ||: : : |:::   |
Db       2421 CSAVLPLLTRCAPLFSGTEHYAALIDSTLHTIYRLSKGRSLTKAQRDTIEECLLSICHHM 2480

Qy       2708 QPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKR 2767
             :|||| :|||:|  ||  |||| : |:||| |||:| |||    :| |:::| :|:||
Db       2481 RPSMLQQLLRRLVFDVPLLSEYCKMPLKLLTNHYEQCWKYY-CLPSGWGSYGLASEEELH 2539

Qy       2768 LTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGD 2827
             ||  ||  ||||||   |: |||   :||| ||  ||||||       |        :
Db       2540 LTEKLFWGIFDSLSHKKYDAELFRMCMPCLSAIAGALPPDY-----VDTRIKATPEKQMS 2594

Qy       2828 LD-NPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTH 2886
             :|   :||:|:||::: |   |  || ||:|| || ||  |: :|| ||    :: |:|
Db       2595 VDAEGNFDPKPVNTANLTLPEKLEYIVNKFAEHSHDKWAYDKLHSGWKYGTTLDENTKSH 2654

Qy       2887 PRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHS-EVDIPSNNRSSMRRQSKSGGR 2945
              | |:|:  | : ||| |: |:|||:| :|||||||| : | :  : :| : : :|
Db       2655 PLLRPFKTLAEKEKEIYRWPIRESVKTMLAIGWSVERTKEGEALALHRENEKMRS----- 2709

Qy       2946 PPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000
                 :: ::    | | |:|::|: ||||:| | | :|:| |:|||||| :| |
Db       2710 ----ISQTSQGNGYTPVPIDLSNVVLSRELQGMVEVMAENYHNIWAKKKKMDLET 2760


RESULT 12
S27272
ryanodine receptor, brain - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S27272
R;Hakamata, Y.; Nakai, J.; Takeshima, H.; Imoto, K.
FEBS Lett. 312, 229-235, 1992
A;Title: Primary structure and distribution of a novel ryanodine receptor/calcium releas
A;Reference number: S27272; MUID:93050200; PMID:1330694
A;Accession: S27272
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4872 <HAK>
A;Cross-references: UNIPROT:Q9TS33; UNIPARC:UPI00001101C5; EMBL:X68650
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo

  Query Match           40.7%;  Score 6413;  DB 2;  Length 4872;
  Best Local Similarity  43.5%;  Pred. No. 0;
  Matches 1333;  Conservative  508;  Mismatches  844;  Indels  382;  Gaps   52;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
              ||||   :|:: |||||| | | | ||      : |||||| ||| |||| ::  | |||
Db          2 AEGGEGGEDEIQFLRTEDEVVLQCIATVHKEQRKFCLAAEGLGNRLCFLEPTSEAKFIPP 61

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKGT--GSGHRTLLYGNAILLRHLNSDMYLA 116
              ||  | ||:||:|||||||::   |   |:|   | |||||||:||||||  | |||
Db         62 DLCVCNFVLEQSLSVRALQEMLANTGENGGEGAAQGGGHRTLLYGHAILLRHSFSGMYLT 121

Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              ||:|| || |||||||||::|: |||||||:|||||||||||||:|||||||::|||
Db        122 CLTTSRSQTDKLAFDVGLREHATGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSERY 181

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVPGGDVLRFFHGGDECLTIPST 235
              || :  |   |:||| | |:| |  :| |  :  || || |:| ||| |||||||||
Db        182 LHLSISNGNIQVDASFMQTLWNVHPTCSGSSIEE--GYLLGGHVVRLFHGHDECLTIPST 239

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
                 :  || |   ::|||||:|  |  |:|  | |    |:||:||| || : :
Db        240 DQNDSQHRRIFYEAGGAGTRARSLWRVEPLRISWSGSNIRWGQAFRLRHLTTGHYLALTE 299

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQV--LEDKDLEVIGAPIIKYGDSTVIVQHSE 353
                | |  | :| | | ||  |  |: ::::     :|:| :| | ||||||   |||
Db        300 DQGLLLQDRGKADTKSTAFSFRPSKETKEKLDSSHKRDIEGMGVPEIKYGDSVCFVQHIA 359

Qy        354 TGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
             :|||::||: : |   :| | :: |  |||:|| |||||   | | |||: ||:||  ::||
Db        360 SGLWVTYKAQDAKTSRLGPLKRK-VILHQEGHMDDGLTLQRCQREESQAARIIRNTTALF 418

Qy        414 TKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRN 473
             ::|::|      || :    :: : |::  | ||| ||  |:|:|:||:|||| |:|:|
Db        419 SQFVSG-----NNRTAAP--VTLPIEEVLQTLHDLIAYFQPPEEEMQHEDKQNKLRSLKN 471

Qy        474 RQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKG 533
             ||:||:|||:| |:|  ||::|:  |    || :| :||| :|: :   ||:||||:|:|
Db        472 RQNLFKEEGMLALVLNCIDRLNIYNSVAHFAG-IAREESGMAWKEVLSLLYKLLAALIRG 530

Qy        534 NHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIIS 593
             |   |||| || |:|| |:|    |   :|:|:|||||:||:||||||:: : ||| |||
Db        531 NRNTCAQF--SNNLDWLISKLDRLES--SSGILEVLHCILIESPEALNLIAEGHIKSIIS 586

Qy        594 LLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNI 653
             ||:||||: |||||||||: ||||||::|| ||| ||| :|||||  |:: |:|:||||
Db        587 LLDKHGRNHKVLDVLCSLCLCNGVAVRANQNLICDNLLPRRNLLLQTRLINDVTSIRPNI 646

Qy        654 FVGRVEGSAVYRKWYFEVTMDHIEKTTHMMP-HLRIGWANTTGYVPYPGGGEKWGGNGVG 712
             |:|  |||| |:|||||: :| ::       | |||:|||:::|| ||||||| |||||||
Db        647 FLGVAEGSAQYKKWYFELIIDQVDPFLTAEPTHLRVGWASSSGYAPYPGGGEGWGGNGVG 706

Qy        713 DDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTG 772
             |||||||||| :|||  | |        :  ::  ||: | ||| || |:|  ||  | |
Db        707 DDLYSYGFDGLHLWSG--RIPRAVASINQHLLKSDDVVSCCLDLGVPSISFRINGQPVQG 764

Qy        773 SFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPC 832
              | ||| :|:||||:| |: :  |||:|| ||  ::  | ||:|  |:|||:: : |||
Db        765 MFENFNTDGLFFPVMSFSAGVKVRFLMGGRHGEFKFLPPSGYAPCYEALLPKEKMRLEPV 824

Qy        833 FYFGNLSK--RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNK 890
             :   ::  | | |         :|:| |:|| |: || ::|:|||:|||||||:| |||
Db        825 KEYKRDAEGVRDLLGTTQFLSQASFIPCPIDTSQVVLPPHLEKIRDRLAENIHELWGMNK 884

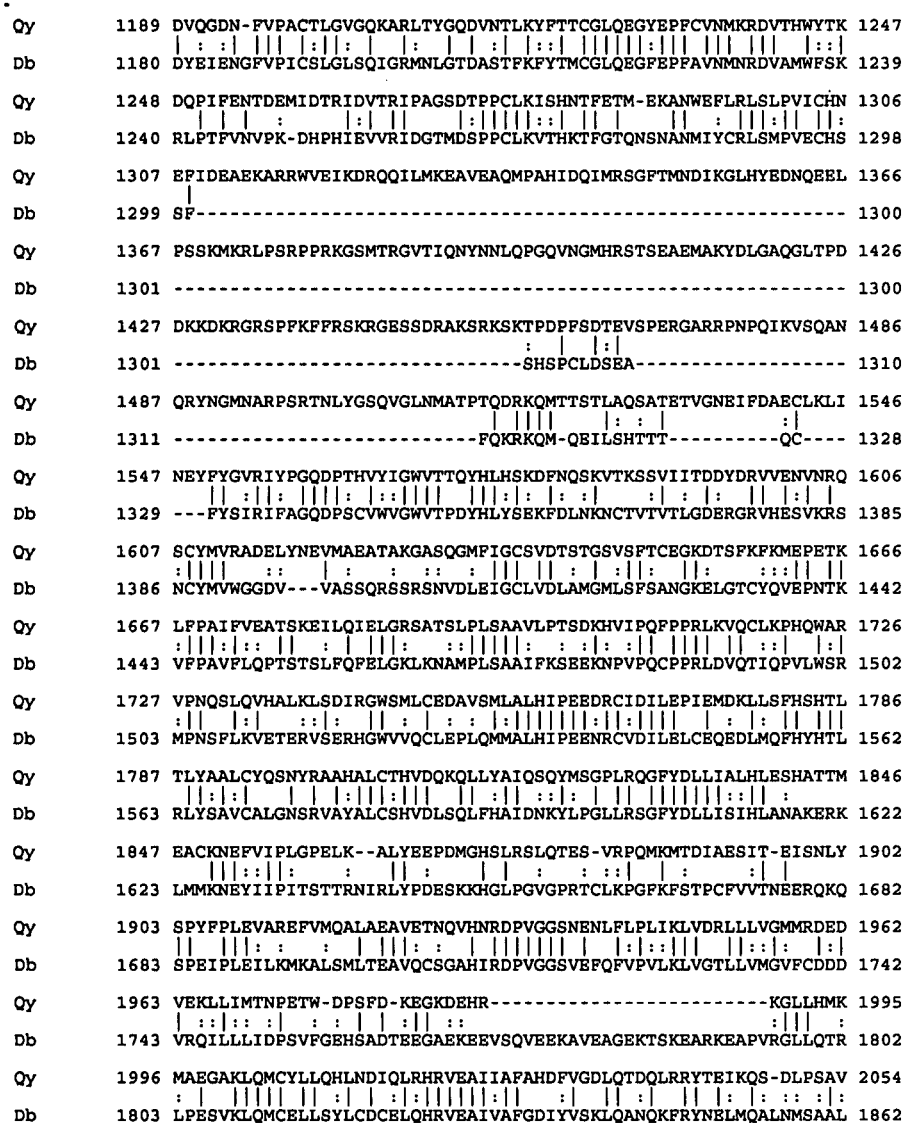
Qy        891 IEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPA 950
             || || :|  :|  : ||||| | :||  || |::|:: :||||:|||| :|:   | |
Db        885 IELGWTFGKMRDDNKRQHPCLVEFSKLPETEKNYNLQMSTETLKTLLALGCHIAHVNPAA 944

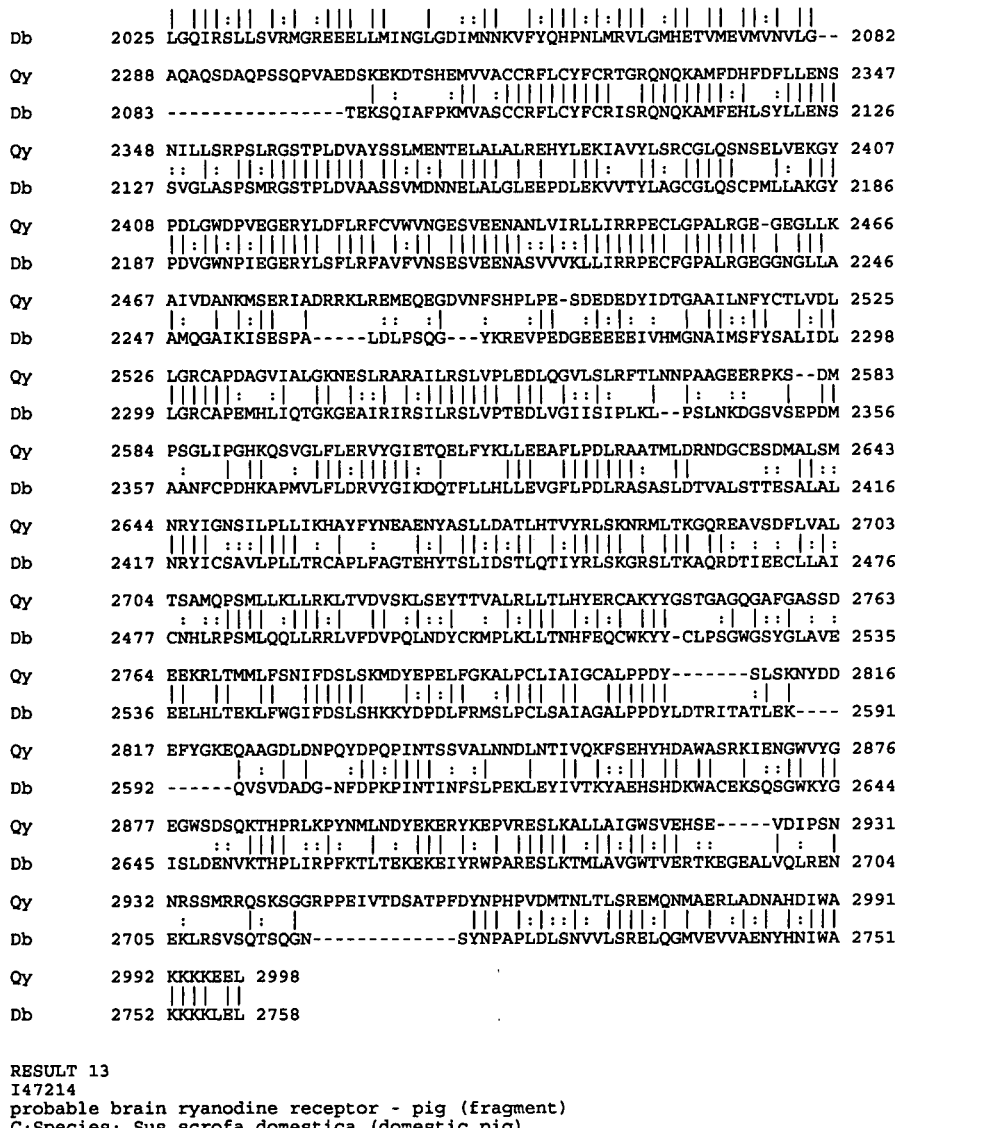
Qy        951 R--IRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGW 1008
             :: |:||   :| |||||||||||| | | |  : |||:|||| ||:||::||:|||
Db        945 EEDLKKVKLPKN-YMMSNGYKPAPLDLSDVKLLPPQEILVDKLAENAHNVWAKDRIKQGW 1003

Qy       1009 TYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALL 1068
             |||: :|    :| |||| :|:  ||:|||:  | ||| : ||| ::|    |  :  :
Db       1004 TYGIQQDLKNKRNPRLVPYALLDERTKKSNRDSLREAVRTFVGYGYNIEPSDQELADPAV 1063

Qy       1069 LEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENS 1128
              : |  |   | :| |::||| ||||||||::| | ||||||     | :  ||
Db       1064 EKVSIDK---IRFFRVERSYAVRSGKWYFEFEVVTGGDMRVGWARPGCRPDIELGPMTKP 1120

Qy       1129 WAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFA 1188
                  | :      |  |||||  ::| | :: |:||||||:    | |  ||
Db       1121 LCLKAAG-ASVGTKVVGILGVPWQPGDVVGCMINLDDASMIFTLNGELLITNKGSELAFA 1179
```





RESULT 13
I47214
probable brain ryanodine receptor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I47214
R;Ledbetter, M.W.; Preiner, J.K.; Louis, C.F.; Mickelson, J.R.
J. Biol. Chem. 269, 31544-31551, 1994
A;Title: Tissue distribution of ryanodine receptor isoforms and alleles determined by r
A;Reference number: A55660; MUID:95081095; PMID:7989322
A;Accession: I47214
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-163 <LED>
A;Cross-references: UNIPROT:Q28954; UNIPARC:UPI0000087F9F; EMBL:U15975; NID:g562099; PI
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homol

```
  Query Match             3.4%;  Score 538;  DB 2;  Length 163;
  Best Local Similarity   61.7%;  Pred. No. 1.8e-26;
  Matches  103;  Conservative   31;  Mismatches   29;  Indels    4;  Gaps    2;

Qy        510 DESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVL 569
              :||| :|: |   ||:||||:|:||  |||||  || |:|| |:|    |   :|:|:||
Db          1 EESGMAWKEILNLLYKLLAALIRGNRNNCAQF--SNNLDWLISKLDRLES--SSGILEVL 56

Qy        570 HCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDY 629
              ||:||:|||||:: : ||| |||||:||||: ||||||||||: ||||||::|| |||
Db         57 HCILIESPEALNLIAEGHIKSIISLLDKHGRNHKVLDVLCSLCLCNGVAVRANQNLICDN 116

Qy        630 LLPGKNLLLQTALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHI 676
              ||| :|||||| |:: |:|:|||||:|  |||| |:|||||: :| :
Db        117 LLPRRNLLLQTRLINDVTSIRPNIFLGVAEGSAQYKKWYFELIIDQV 163


RESULT 14
I47213
cardiac muscle ryanodine receptor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I47213
R;Ledbetter, M.W.; Preiner, J.K.; Louis, C.F.; Mickelson, J.R.
J. Biol. Chem. 269, 31544-31551, 1994
A;Title: Tissue distribution of ryanodine receptor isoforms and alleles determined by re
A;Reference number: A55660; MUID:95081095; PMID:7989322
A;Accession: I47213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-162 <LED>
A;Cross-references: UNIPROT:Q28953; UNIPARC:UPI0000087B98; EMBL:U15966; NID:g562097; PID
C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo
C;Keywords: cardiac muscle; heart

  Query Match             3.3%;  Score 520;  DB 2;  Length 162;
  Best Local Similarity   65.2%;  Pred. No. 2.4e-25;
  Matches  101;  Conservative   29;  Mismatches   21;  Indels    4;  Gaps    2;

Qy        523 LYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNM 582
              ||:||||:|:||  |||||: |  |:|| |||  :     :|:|:||||||::||||||:
Db          7 LYELLAALIRGNRKNCAQFSGS--LDWLISRL--ERLEASSGILEVLHCVLVESPEALNI 62

Qy        583 MRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTAL 642
              ::: ||| |||||:||||: |||||||||||| :||||||:|: ||| ||||::||||| |
Db         63 IKEGHIKSIISLLDKHGRNHKVLDVLCSLCVCHGVAVRSNQHLICDNLLPGRDLLLQTRL 122

Qy        643 VDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIE 677
              |:||||:|||||:|  |||| |:|||:|: :|| |
Db        123 VNHVSSMRPNIFLGVSEGSAQYKKWYYELMVDHTE 157


RESULT 15
T31431
inositol 1,4,5-trisphosphate receptor, localized in plasma membrane - Panulirus argus
C;Species: Panulirus argus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: T31431
R;Munger, S.D.; Ache, B.W.; Greenberg, R.M.
submitted to the EMBL Data Library, March 1998
A;Description: Plasma membrane localization of an olfactory inositol 1,4,5-trisphosphate
A;Reference number: Z21030
A;Accession: T31431
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2783 <MUN>
A;Cross-references: UNIPROT:O77089; UNIPARC:UPI00000773E6; EMBL:AF055079; NID:g3660666;
C;Superfamily: inositol-trisphosphate receptor

  Query Match             2.1%;  Score 327;  DB 2;  Length 2783;
  Best Local Similarity   17.9%;  Pred. No. 6.5e-11;
  Matches  520;  Conservative  416;  Mismatches  980;  Indels  990;  Gaps  136;

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Db          4 EGSA------SFLHMGDIVSLYAEGSVSG---FISTLGLVDARCVVNPEAGDLSTPPKKF 54

Qy         61 SQCVFVI--------------------EQALSVRALQELVTAAGSETGKGTGSGHR---- 96
               |:| |                          |  |  || :|  :       :
Db         55 RDCLFSICPSNRYSAQKQFWKAAKHSGNSTTDPSLLNRLHDAAKTEKRQNEAESKKLMGT 114

Qy         97 TLLYGNAILLRHLNSDMYLAC-LSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSE 155
              : ||  | | || |: ||       :  :| |  | |  :   |  |: ::|  | |:
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Qy        156 GEKVRVGDDLILVSVATERYLHTTKEN---------EVSIVNASFHVTHWSVQPYGTGIS 206
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Db        174 GDNVVVGDKVILSPVNAGQQLHVSSTHDLRDHPGCKEVNVLNSN---TCWKISLFLEHKE 230

Qy        207 RMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDGGQNIVVYEGG----SVMSQARSLWRL 262
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Db        231 NLE--GVLKGGDVIRLFHAEQEKFLTMDEYKKK--QHVFLRTTGRTTATAATSSKALWEV 286

Qy        263 ELAR-TKWAGGFINWYHPMRIRHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKD 321
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Db        287 EVVQHDPSRGGAGHWNSLFRFKHLATGHYLAAEIDDD------------------PTPD 327

Qy        322 DQKQVLEDKD----LEVIGAPI-------------IKYGDST------VIVQHSETGLW 357
               :  | | :     :::  |:              :  |||       | ::|  |  |
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Qy        358 LSYKSY----ETKKKGVGKV------EEKQAI----LHEEGKMDDGLDFSRSQEEESRTA 403
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Qy        404 RVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEE 463
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Qy        464 KQNKFRAL--------RNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESG-- 513
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Qy        514 --QSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHC 571
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Qy        572 VLIDSPEALNM-MRDEHIKVIISLLEK--HGRDPKVLDVLCSLCVGNGVAVRSSQNNICD 628
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Db        593 LLHNNRKLLEIHITATEIETFVGLVRKNMHKWDWRFLDYLKVLCISNNQAIPRTQELICK 652

Qy        629 YLLPGKN--LLLQTALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEKTTHMMPHL 686
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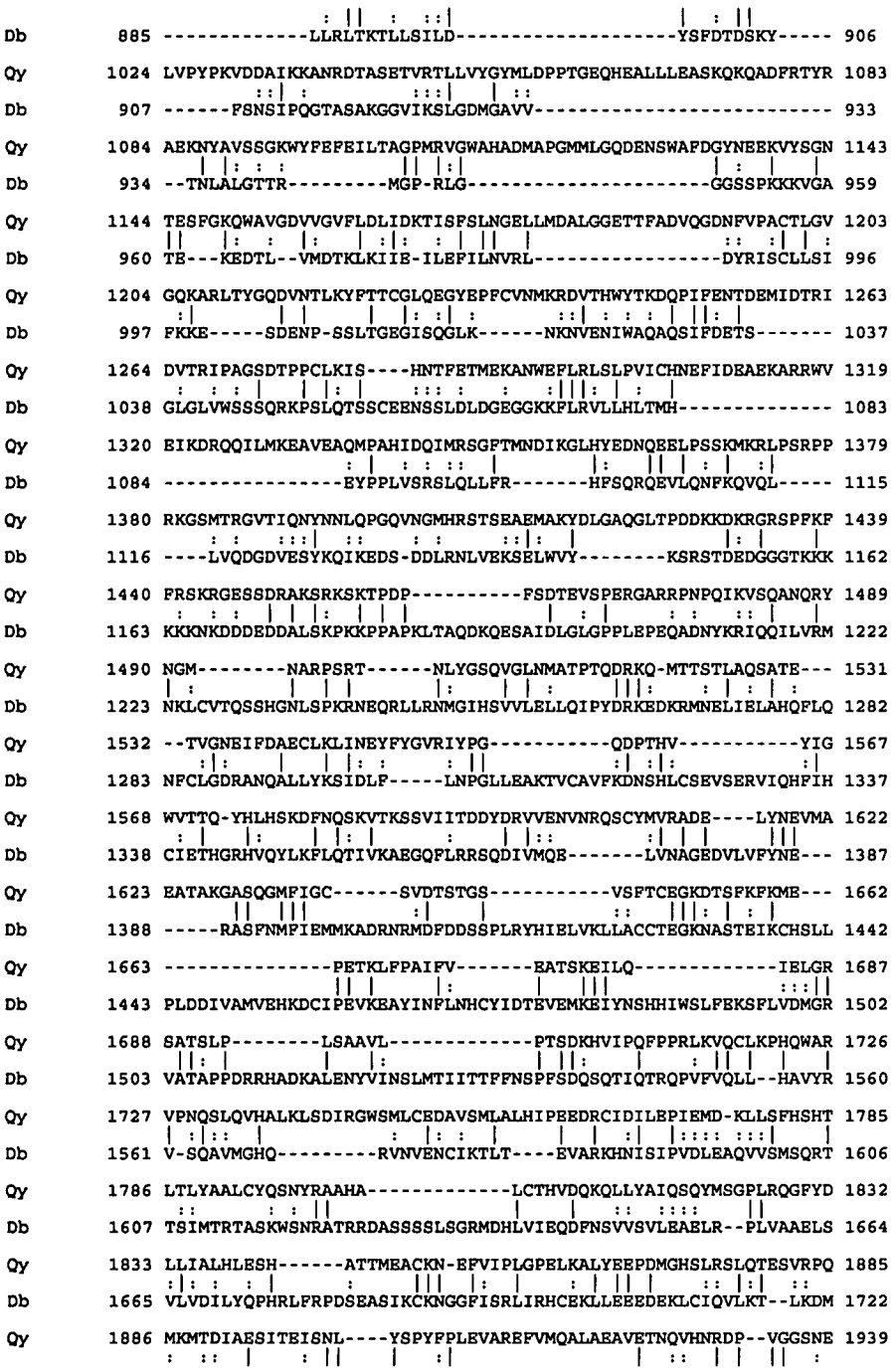
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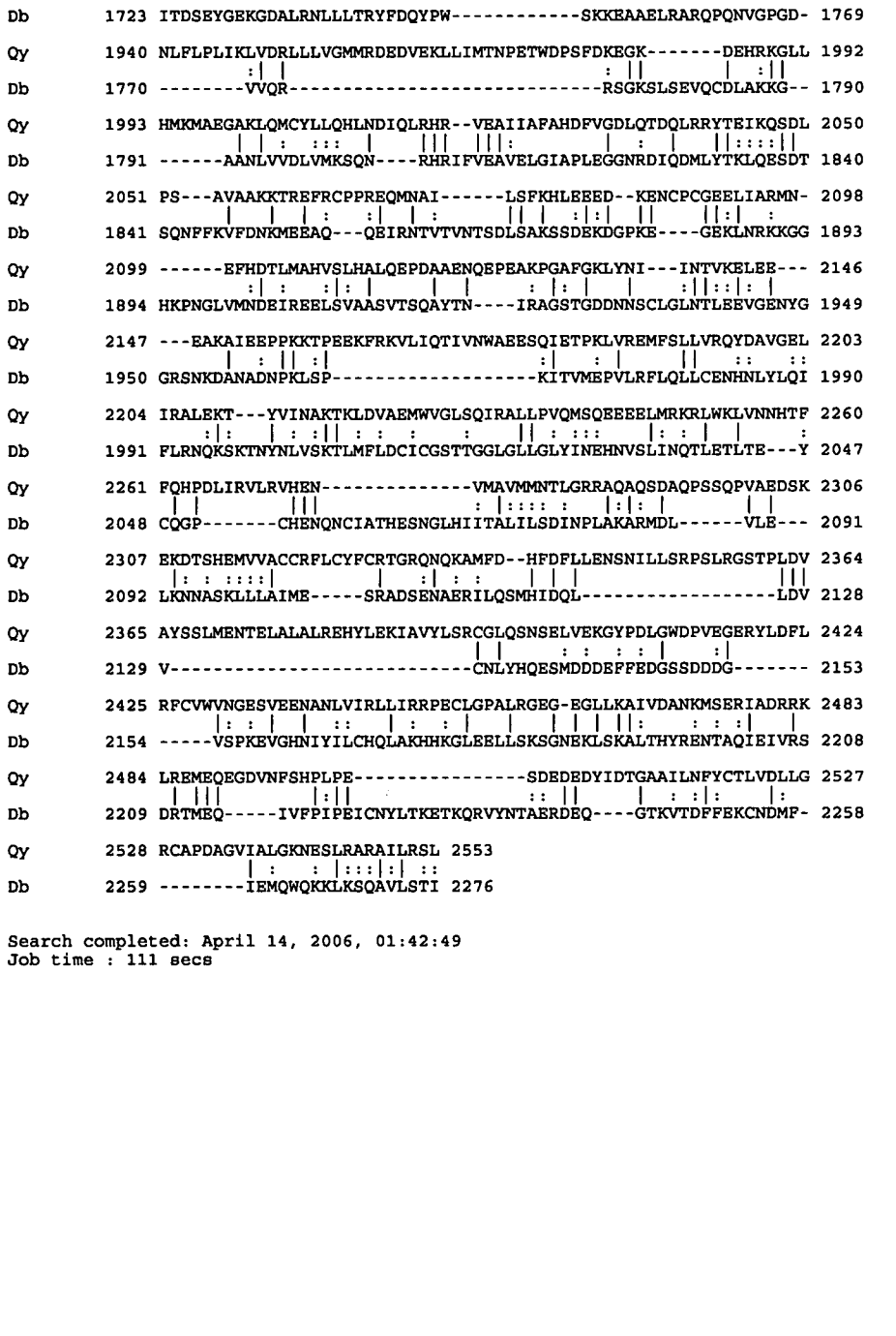
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Qy        844 AGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQRED 903
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Qy        964 QSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHRSPH 1023
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Search completed: April 14, 2006, 01:42:49
Job time : 111 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 13:55:27 ; Search time 14479.5 Seconds
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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	785.8	26.2	15361	4	OCRRR	X15750 Rabbit skel
5	785.8	26.2	15823	4	OCRYAN	X15209 O.cuniculus
6	784.2	26.1	6266	8	AB209425	AB209425 Homo sapi
7	771.8	25.7	15359	6	CS031861	CS031861 Sequence
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23	724.2	24.1	15378	4	PIGRYRN	M91452 Sus scrofa
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36	640.6	21.3	16879	2	AB051576	AB051576 Hemicentr
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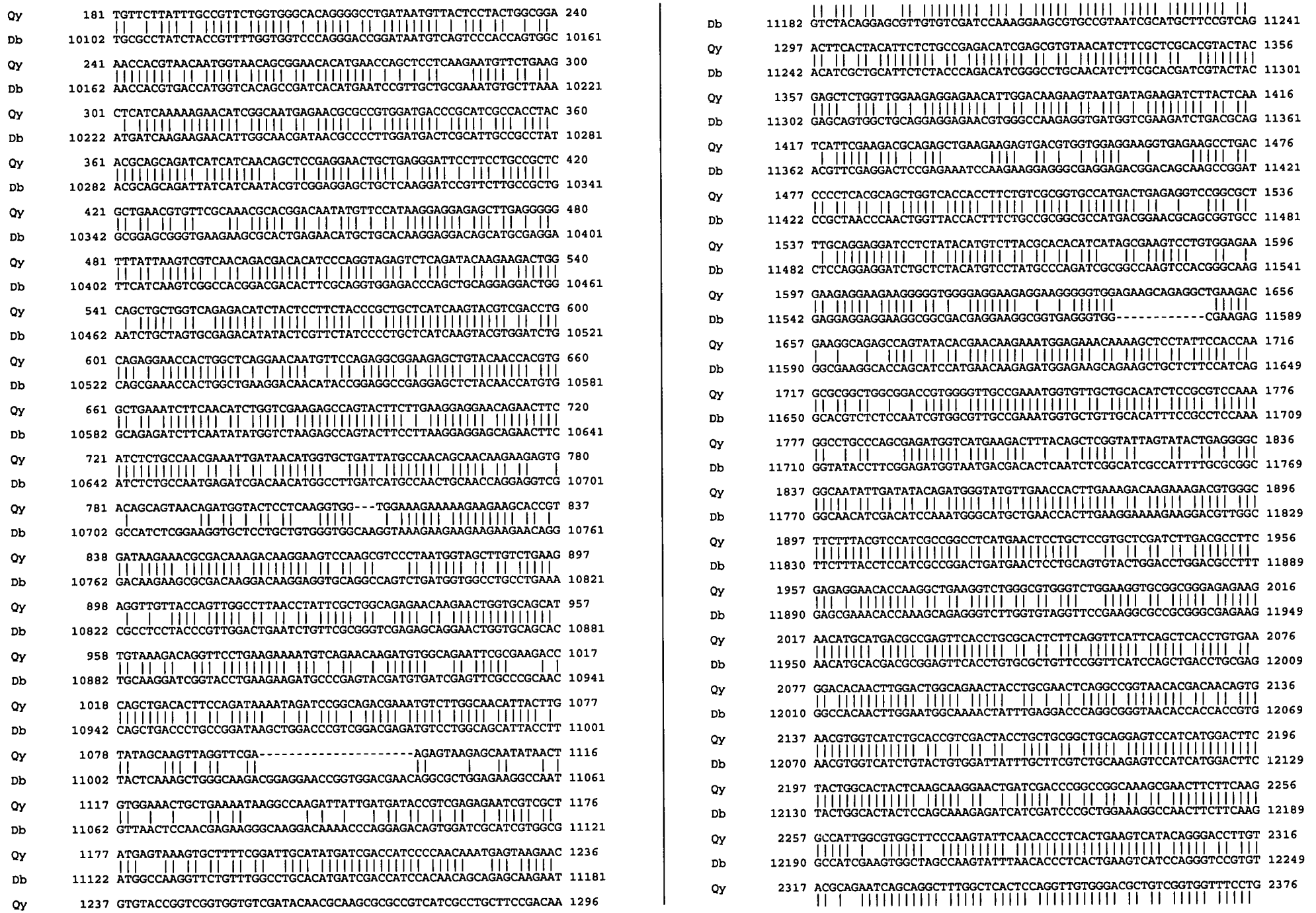
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ACCESSION CQ594804
VERSION CQ594804.1 GI:41651849
KEYWORDS .
SOURCE Drosophila sp.
ORGANISM Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1
AUTHORS Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
TITLE Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof
JOURNAL Patent: WO 0171042-A 22562 27-SEP-2001;
PE Corporation (NY) (US)
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Matches 2236; Conservative 0; Mismatches 753; Indels 36; Gaps 3;

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RESULT 2
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DEFINITION Homarus americanus ryanodine receptor (RyR) mRNA, partial cds.
ACCESSION AF051936
VERSION AF051936.1 GI:2970624
KEYWORDS .
SOURCE Homarus americanus (American lobster)
ORGANISM Homarus americanus
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropidae; Homarus.
REFERENCE 1 (bases 1 to 4916)
AUTHORS Xiong,H., Feng,X., Gao,L., Xu,L., Pasek,D.A., Seok,J.H. and Meissner,G.
TITLE Identification of a two EF-hand Ca2+ binding domain in lobster skeletal muscle ryanodine receptor/Ca2+ release channel
JOURNAL Biochemistry 37 (14), 4804-4814 (1998)
PUBMED 9537997
REFERENCE 2 (bases 1 to 4916)
AUTHORS Xiong,H., Feng,X., Gao,L., Xu,L., Pasek,D.A., Seok,J.H. and Meissner,G.
TITLE Direct Submission
JOURNAL Submitted (02-MAR-1998) Biochemistry & Biophysics, University of North Carolina, Chapel Hill, NC 27599-7260, USA
FEATURES Location/Qualifiers

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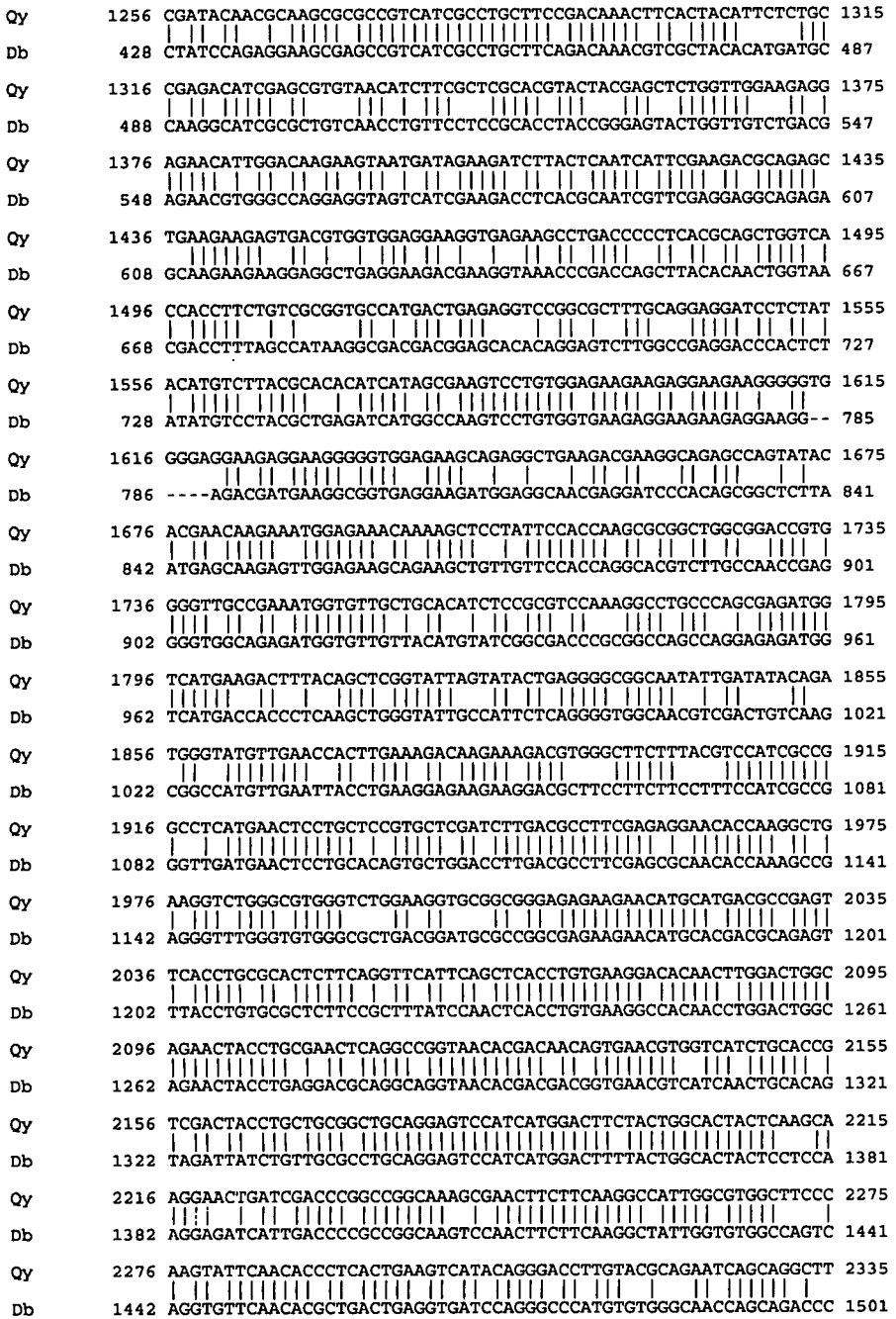
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Qy 1136 AGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAAGTGCTTTTCG 1195
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Db 311 TGGTGCCCACCGTCGACGACACCGTCGATCGCATCGTCGCTATGGCTAAAGTTCTTTATG 370

Qy 1196 GATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGGTCGGTGGTGT 1255
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Db 371 GCCTTCATATCATTGACCACCCGCAGTCCTCC---AAGGAGGTTTGGCGTTCTGTTGTCT 427
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RESULT 3
AF009344
LOCUS AF009344 866 bp mRNA linear INV 17-APR-2000
DEFINITION Heliothis virescens ryanodine receptor (ryr) mRNA, partial cds.
ACCESSION AF009344
VERSION AF009344.1 GI:4102114
KEYWORDS .
SOURCE Heliothis virescens (tobacco budworm)
ORGANISM Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.
REFERENCE 1 (bases 1 to 866)
AUTHORS Puente,E., Suner,M., Evans,A.D., McCaffery,A.R. and Windass,J.D.
TITLE Identification of a polymorphic ryanodine receptor gene from Heliothis virescens (Lepidoptera: noctuidae)
JOURNAL Insect Biochem. Mol. Biol. 30 (4), 335-347 (2000)
PUBMED 10727900
REFERENCE 2 (bases 1 to 866)
AUTHORS Puente,E. and Windass,J.D.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1997) Biologie et Pathologie Digestive, INSERM U151, Institut Louis Bugnard. CHU Rangueil L3, Toulouse 31403 CEDEX 04, France

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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           27.8%;  Score 835.6;  DB 2;  Length 866;
  Best Local Similarity   97.8%;  Pred. No. 2e-173;
  Matches  847;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy       1870 CACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTCATGAACTCC 1929
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Qy       1930 TGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGTCTGGGCGTG 1989
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Db            61 TGCTCAGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGTCTGGGCGTG 120

Qy       1990 GGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACCTGCGCACTC 2049
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Qy       2050 TTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAACTACCTGCGA 2109
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Qy       2110 ACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGACTACCTGCTG 2169
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Qy       2230 CCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACC 2289
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Db        361 CCGGCCGGCAAAGCGAATTTCTTCAAGGCCATTGGCGTAGCTTCCCAAGTATTCAACACC 420

Qy       2290 CTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCTCACTCCAGG 2349
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Db        421 CTCACTGAAGTCATACAGGGACCTTGTACACAGAACCAACAGGCTTTGGCTCACTCCAGG 480

Qy       2350 TTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGACAAGTTGTCG 2409
             || |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        481 TTATGGGACGCTGTCGGTGGTTTCCTGTTCCTGTTCTCCCACATGCAGGACAAGTTGTCG 540

Qy       2410 AAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAGGACATGATC 2469
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Db        541 AAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAGGACATGATC 600

Qy       2470 CCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGCAAGCAAATG 2529
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Qy       2530 GTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATACTTCGACATG 2589
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Db        661 GTGGACACTCTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATACTTCGACATG 720

Qy       2590 TTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGATGCCAATAAC 2649
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Db        721 TTCCTCAAGCTGAAGGACCTGACTTCCAGCGCTAGCTTCCAGGAGATAGATGCCAATAAC 780

Qy       2650 GACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAGAGTTATACT 2709
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Db        781 GACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAGAGTTATACT 840

Qy       2710 CCCGAAGAAATCGAGTTCCTCCTAGC 2735
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Db        841 CCCGAAGAAATCGAGTTCCTCCTAGC 866


RESULT 4
OCRRR
LOCUS       OCRRR                  15361 bp    mRNA    linear   MAM 10-MAR-2001
DEFINITION  Rabbit skeletal muscle mRNA for ryanodine receptor.
ACCESSION   X15750
VERSION     X15750.1  GI:1709
KEYWORDS    calcium binding protein; channel protein; receptor; ryanodine
            receptor.
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
            Leporidae; Oryctolagus.
REFERENCE   1  (bases 1 to 15361)
  AUTHORS   Takeshima,H., Nishimura,S., Matsumoto,T., Ishida,H., Kangawa,K.,
            Minamino,N., Matsuo,H., Ueda,M., Hanaoka,M., Hirose,T. and Numa,S.
  TITLE     Primary structure and expression from complementary DNA of skeletal
            muscle ryanodine receptor
  JOURNAL   Nature 339 (6224), 439-445 (1989)
   PUBMED   2725677
REFERENCE   2  (bases 1 to 15361)
  AUTHORS   Takeshima,H., Nishimura,S., Nishi,M., Ikeda,M. and Sugimoto,T.
  TITLE     A brain-specific transcript from the 3'-terminal region of the
            skeletal muscle ryanodine receptor gene
  JOURNAL   FEBS Lett. 322 (2), 105-110 (1993)
   PUBMED   8097730
REFERENCE   3  (bases 1 to 15361)
  AUTHORS   Numa,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-1989) Numa S., Kyoto University, Dept of Medical
            Chemistry and Molecular Genetics, Faculty of Medicine, Yoshida
            Sakyo-ku, Kyoto 606, Japan
COMMENT     *source: pRR72, pRR203, pRR308, pRR359, pRR451, pRR616. see X15749
            for ryanodine receptor gene 5' end; X15749 and X15750 seqs  are
            shown as a compiled one in [1]
            Data kindly reviewed (27-AUG-1989) by Numa S.
FEATURES             Location/Qualifiers
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                     /clone="pRR705, pRR256, pRR229,"
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     CDS             132. .15245
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ORIGIN

  Query Match             26.2%;  Score 785.8;  DB 4;  Length 15361;
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Qy         98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157
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Qy        158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217
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Qy        218 ATAATGTTACTCCTACT-----------GGCGGAAACCACGTAACAATGGTAACAGCGG 265
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Qy        266 AACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATG 325
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Db      10240 GCAAGGTGGTGGCCGAGGAGGAGCAGCTGCGG---------CTGGAGGCCAAGGCCGAGG 10290

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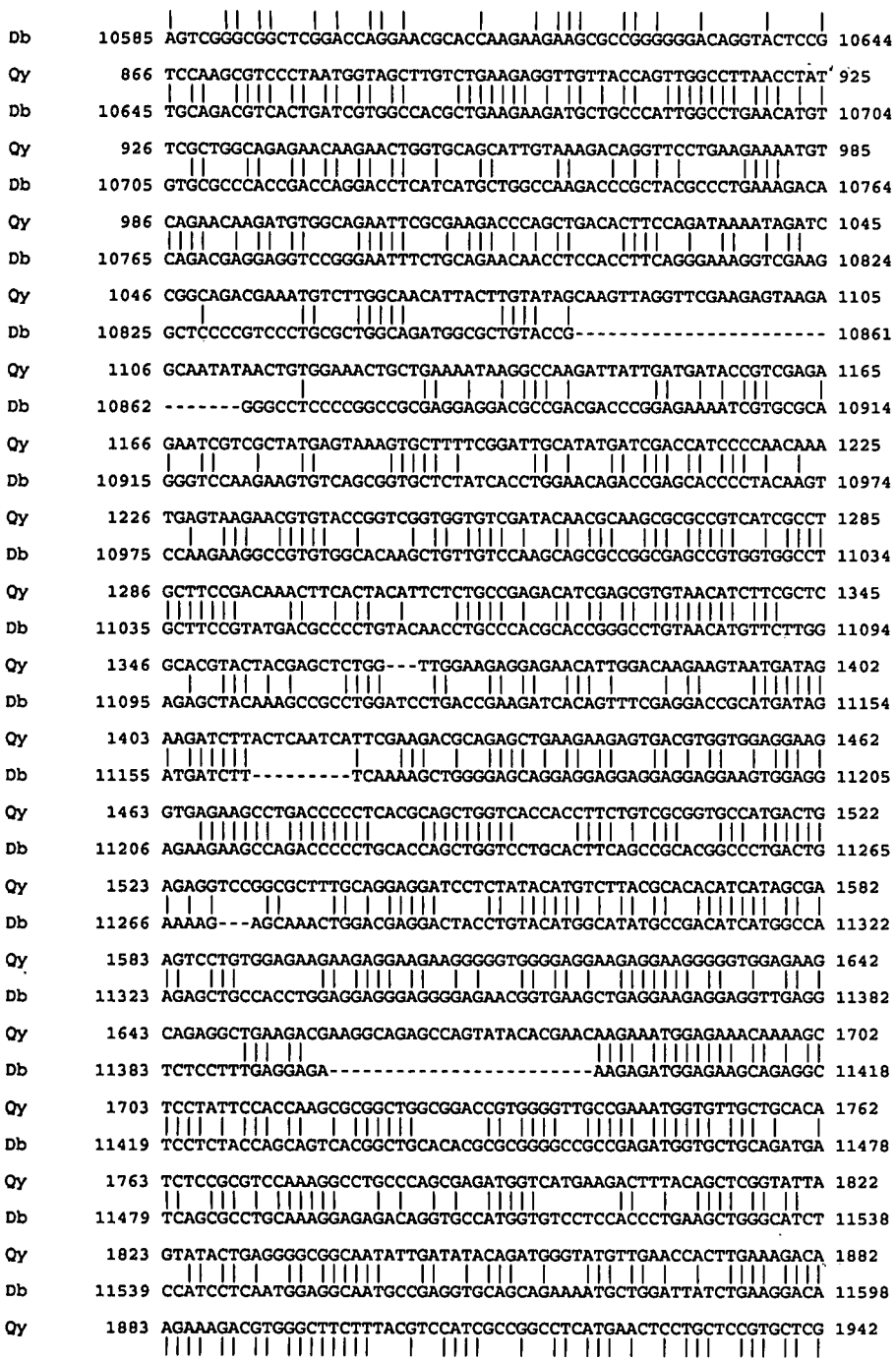
Qy        566 CCTTCTACCCGCTGCTCATCAAGTACGTCGACCTGCAGAGGAACCACTGGCTCAGGAACA 625
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Qy        686 AGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTCATCTCTGCCAACGAAATTGATAACA 745
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Qy        806 AAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGATAAGAAACGCGACAAAGACAAGGAAG 865
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DEFINITION  O.cuniculus mRNA for skeletal muscle ryanodine receptor.
ACCESSION   X15209
VERSION     X15209.1  GI:1713
KEYWORDS    ryanodine receptor.
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
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REFERENCE   1  (bases 1 to 15823)
  AUTHORS   Takeshima,H., Nishimura,S., Matsumoto,T., Ishida,H., Kangawa,K.,
            Minamino,N., Matsuo,H., Ueda,M., Hanaoka,M., Hirose,T. and Numa,S.
  TITLE     Primary structure and expression from complementary DNA of skeletal
            muscle ryanodine receptor
  JOURNAL   Nature 339 (6224), 439-445 (1989)
   PUBMED   2725677
REFERENCE   2  (bases 1 to 15823)
  AUTHORS   Numa,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-1989) Numa S., Kyoto University, Dept of Medical
            Chemistry and Molecular Genetics, Faculty of Medicine, Yoshida,
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ORIGIN

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Db      11287 GCTCCCCGTCCCTGCGCTGGCAGATGGCGCTGTACCG---------------------- 11323

Qy       1106 GCAATATAACTGTGGAAACTGCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGA 1165
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Qy       1166 GAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAA 1225
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Qy       1226 TGAGTAAGAACGTGTACCGGTCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCT 1285
                |  |||  |||||  |     | || |||| |  || |||  ||| |||||  | ||||
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Qy       1286 GCTTCCGACAAACTTCACTACATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTC 1345
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Qy       1583 AGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAG 1642
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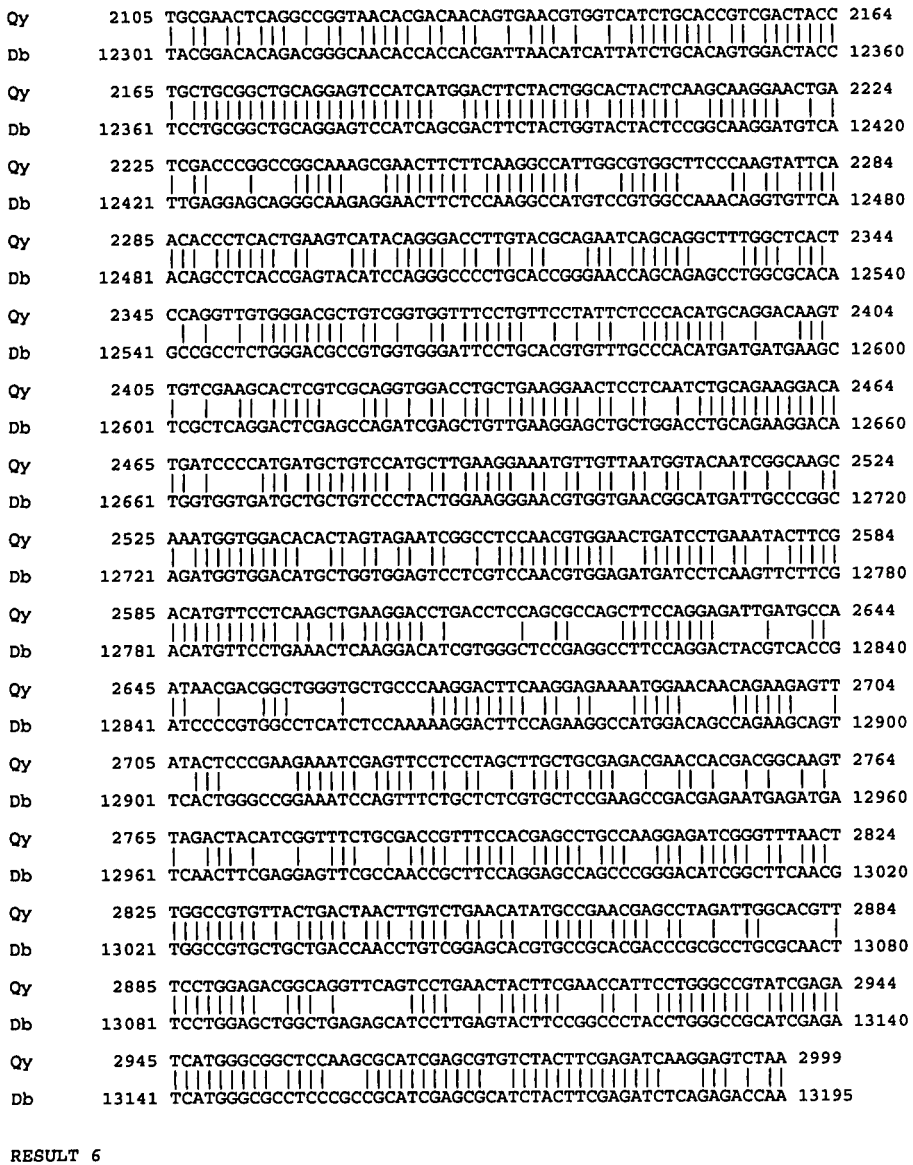
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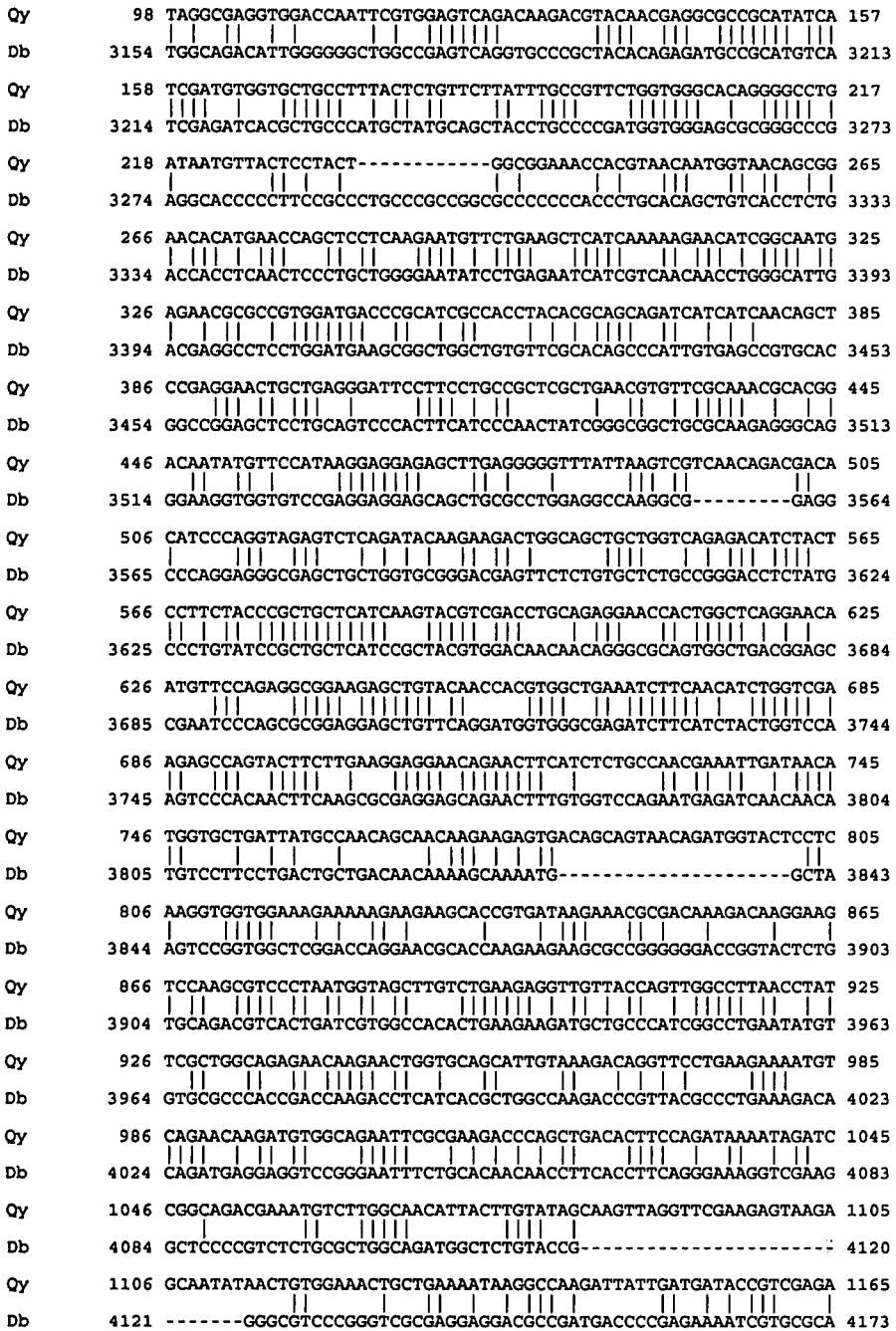
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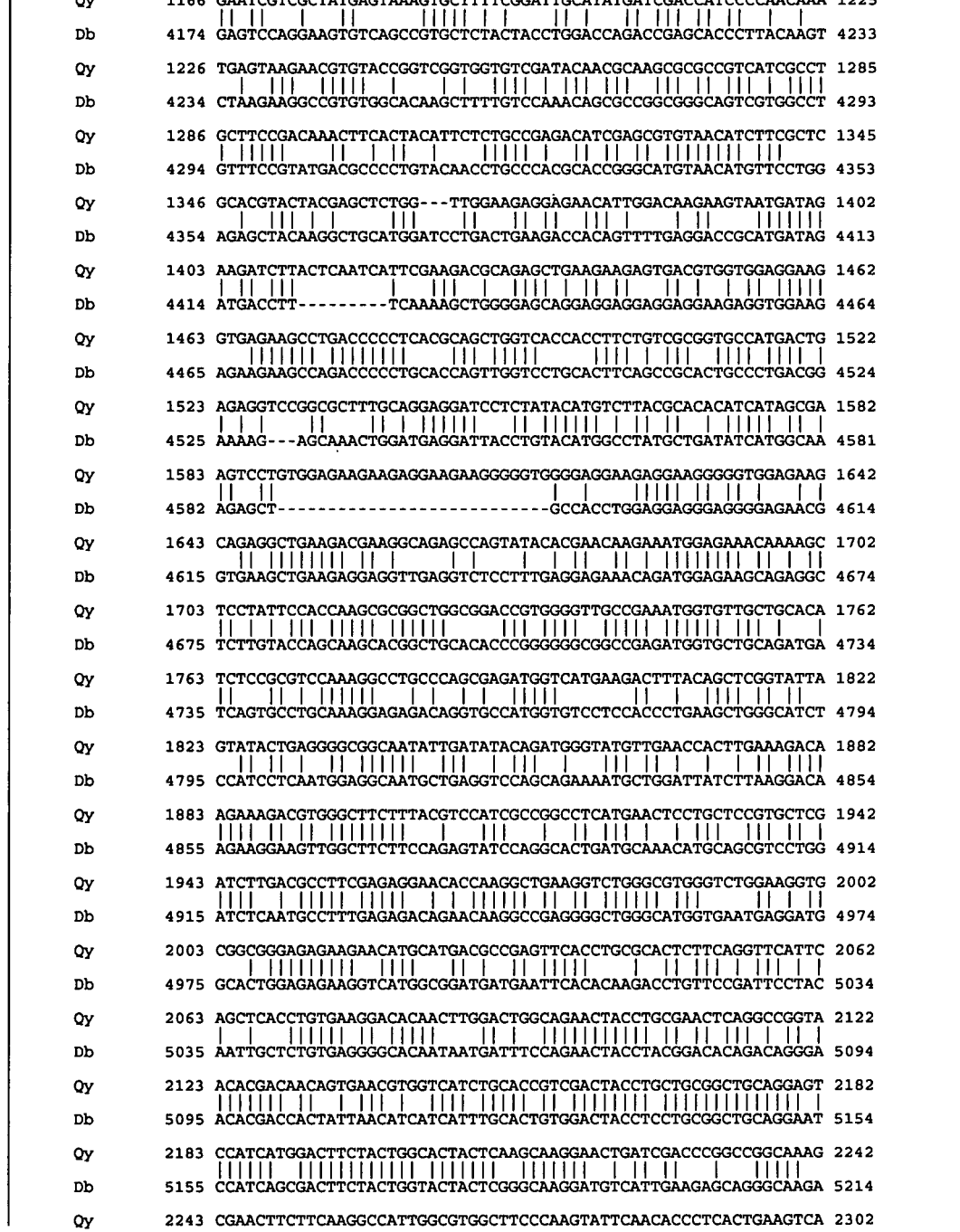
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ACCESSION   AB209425
VERSION     AB209425.1  GI:62088429
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REFERENCE   1
  AUTHORS   Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A., Yokoyama,S.,
            Ohara,O., Nagase,T. and F.Kikuno,R.
  TITLE     None Title
  JOURNAL   Published Only in Database (2005)
REFERENCE   2  (bases 1 to 6266)
  AUTHORS   Totoki,Y., Toyoda,A., Takeda,T., Sakaki,Y., Tanaka,A., Yokoyama,S.,
            Ohara,O., Nagase,T. and F.Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute,
            Department of Human Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
            Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://protein.gsc.riken.go.jp/, Tel:81-438-52-3930,
            Fax:81-438-52-3931)
COMMENT     This work was supported in part by the National Project on Protein
            Structural and Functional Analysis , Ministry of Education, Culture
            , Sports, Science and Technology of Japan. Totoki Y, Toyoda A,
            Takeda T, Sakaki Y, Tanaka A, Yokoyama S. RIKEN Genomic Sciences
            Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan.
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VERSION     CS031861.1  GI:60731692
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  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
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  JOURNAL   Patent: WO 2005016962-A 1367 24-FEB-2005;
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ORIGIN

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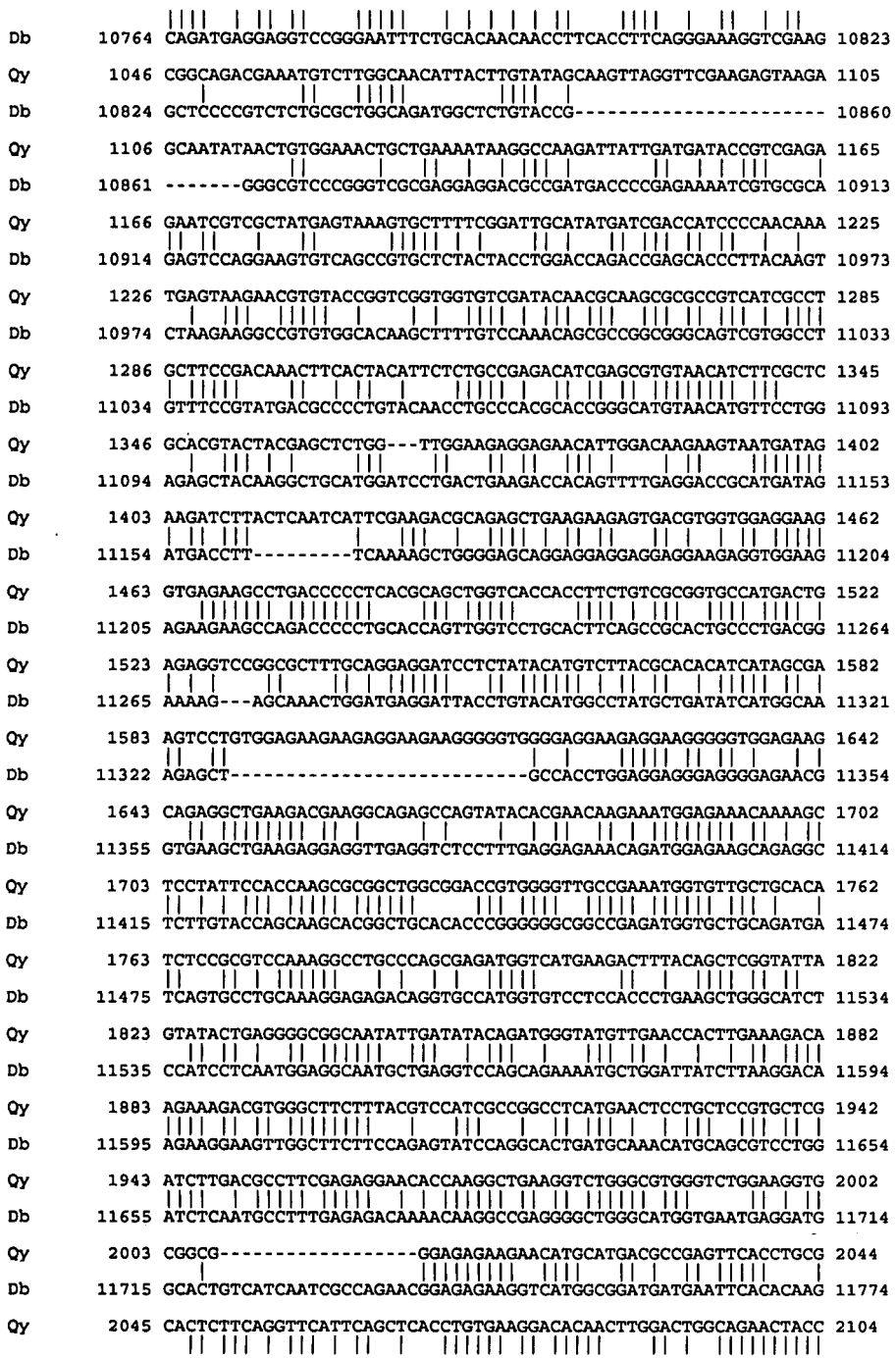
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DEFINITION Sequence 5291 from Patent WO2005016962.
ACCESSION CS035785
VERSION CS035785.1 GI:60733700
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ORGANISM Homo sapiens
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REFERENCE 1
  AUTHORS Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE   Compositions and methods for the treatment of immune related
          diseases
  JOURNAL Patent: WO 2005016962-A 5291 24-FEB-2005;
          Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .15359
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  Query Match             25.7%;  Score 771.8;  DB 6;  Length 15359;
  Best Local Similarity   56.5%;  Pred. No. 2.3e-159;
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Db       9819 TGGGGCTCCCCAACAGTGTGGAGGAGATGTGTCCCGACATCCCGGTGCTGGAGCGGCTCA 9878

Qy         98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157
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Qy        386 CCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGG 445
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Qy        446 ACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACA 505
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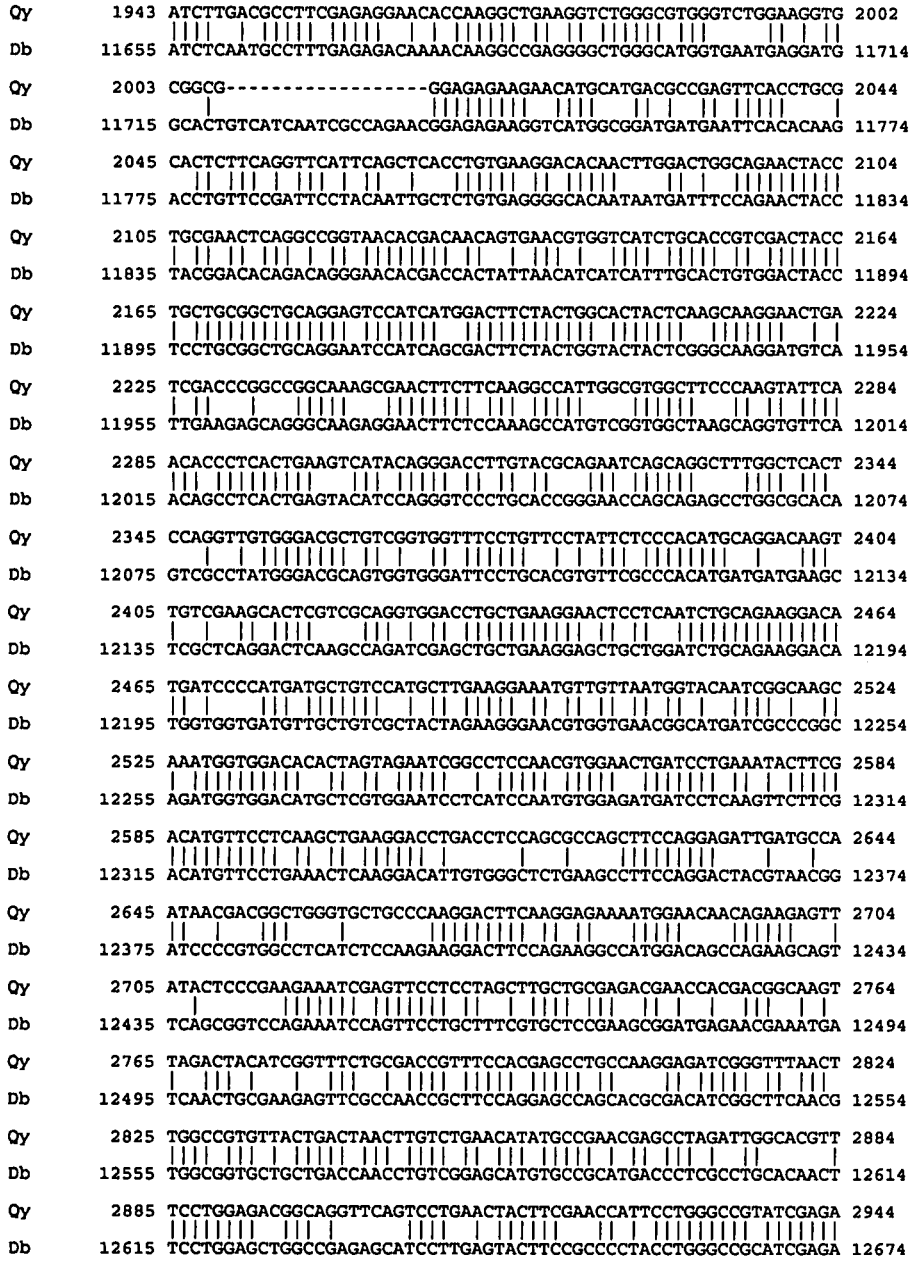
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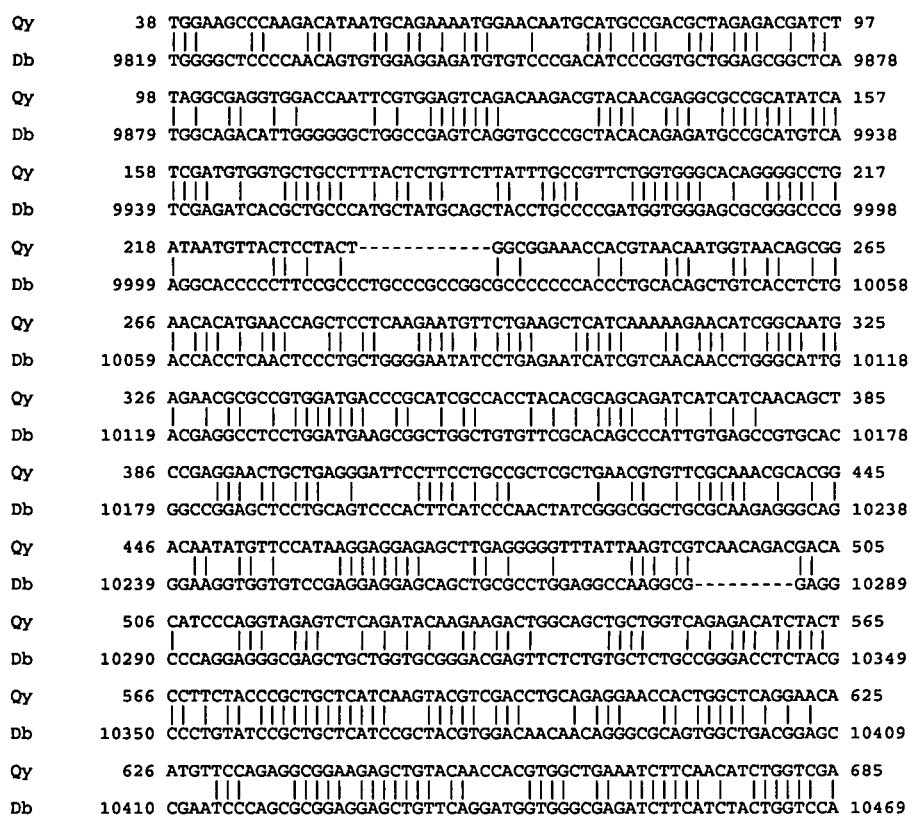
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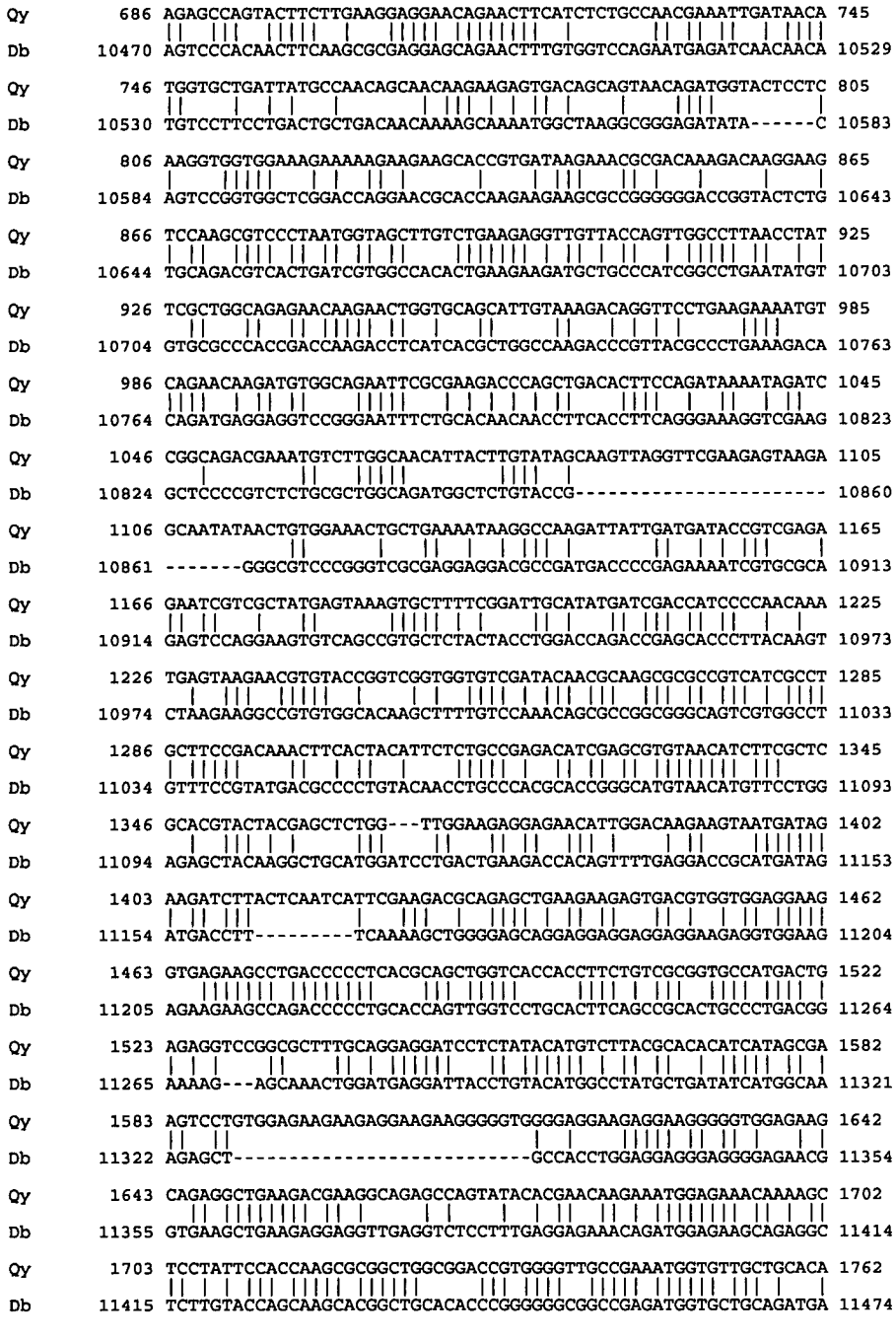
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ACCESSION   CS040813
VERSION     CS040813.1  GI:61848457
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005019258-A 1367 03-MAR-2005;
            Genentech, Inc. (US)
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ORIGIN

  Query Match             25.7%;  Score 771.8;  DB 6;  Length 15359;
  Best Local Similarity   56.5%;  Pred. No. 2.3e-159;
  Matches 1691;  Conservative    0;  Mismatches 1187;  Indels  117;  Gaps    9;
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VERSION     CS044737.1  GI:61851323
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REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,P.M., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005019258-A 5291 03-MAR-2005;
            Genentech, Inc. (US)
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ORIGIN

  Query Match             25.7%;  Score 771.8;  DB 6;  Length 15359;
  Best Local Similarity   56.5%;  Pred. No. 2.3e-159;
  Matches 1691;  Conservative    0;  Mismatches 1187;  Indels  117;  Gaps    9;

Qy         38 TGGAAGCCCAAGACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGATCT 97

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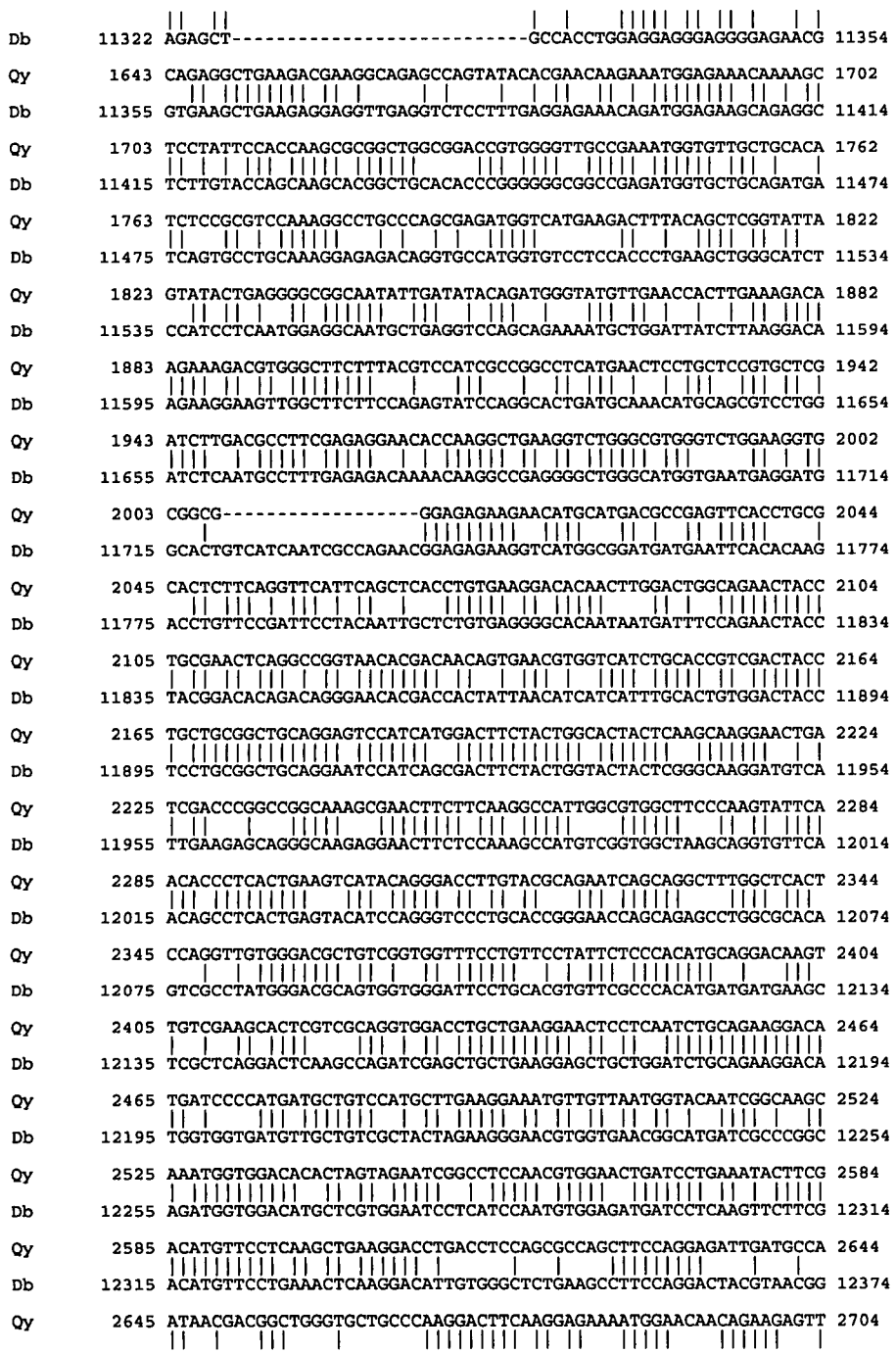
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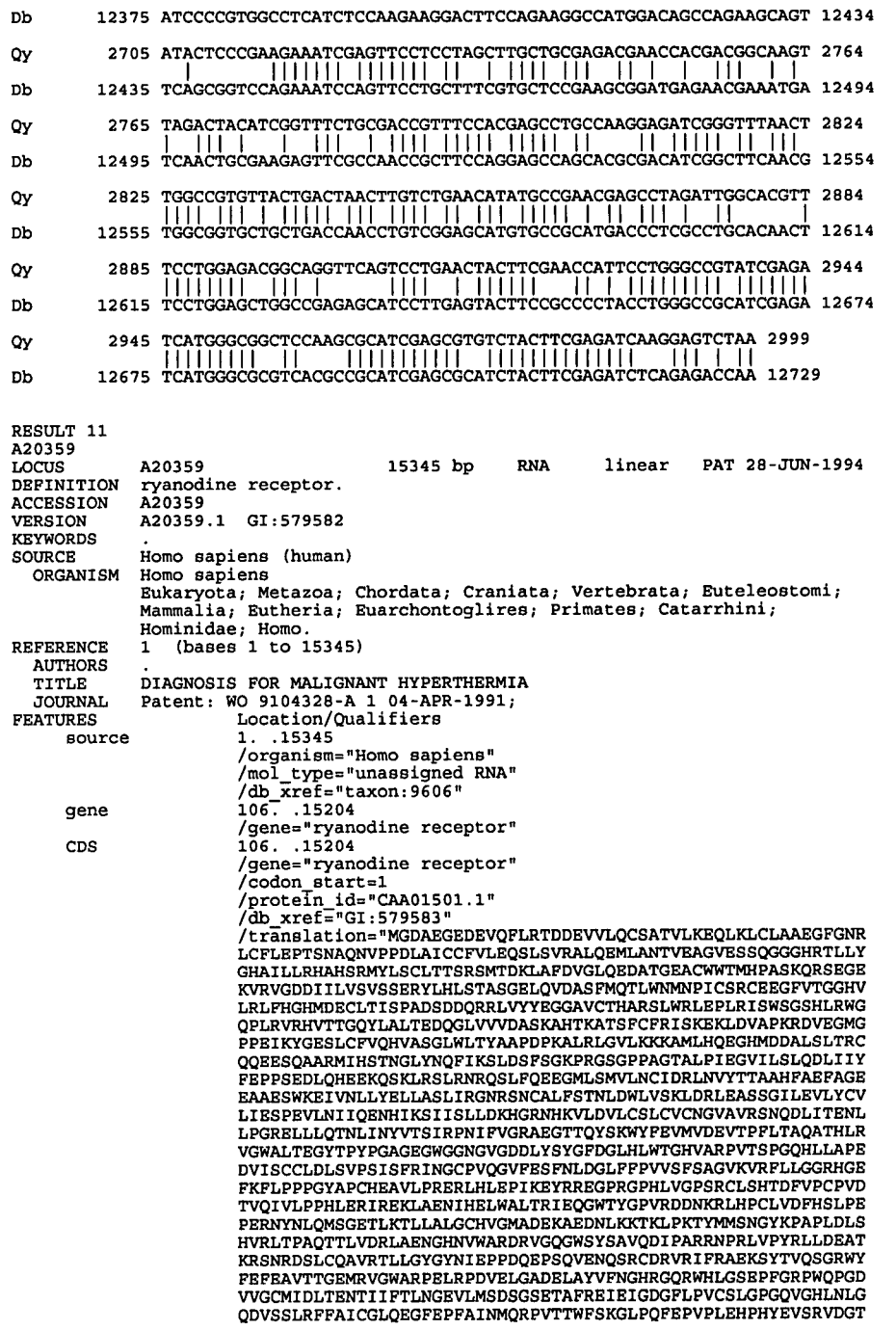
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ACCESSION   A20359
VERSION     A20359.1  GI:579582
KEYWORDS    .
SOURCE      Homo sapiens (human)
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ORIGIN

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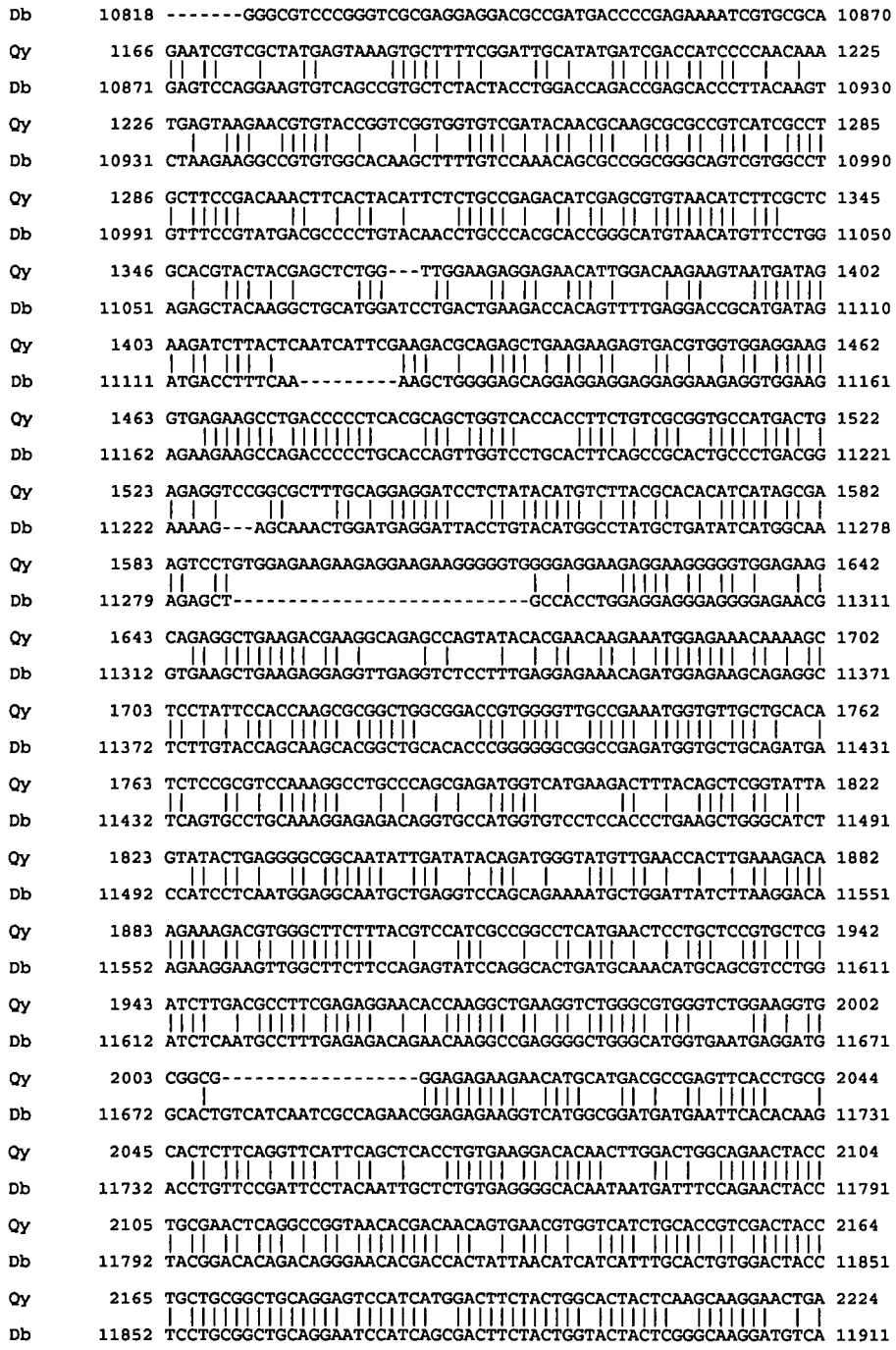
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ACCESSION   J05200
VERSION     J05200.1  GI:337721
KEYWORDS    ryanodine receptor; skeletal muscle sarcoplasmic reticulum Ca+2
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REFERENCE   1  (bases 1 to 15346)
  AUTHORS   Zorzato,F., Fujii,J., Otsu,K., Phillips,M., Green,N.M., Lai,F.A.,
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  TITLE     Molecular cloning of cDNA encoding human and rabbit forms of the
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  JOURNAL   J. Biol. Chem. 265 (4), 2244-2256 (1990)
   PUBMED   2298749
COMMENT     Original source text: Human (adult) muscle, cDNA to mRNA, and DNA.
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ORIGIN      648 bp upstream of SalI site; chromosome 19 proximal long arm.
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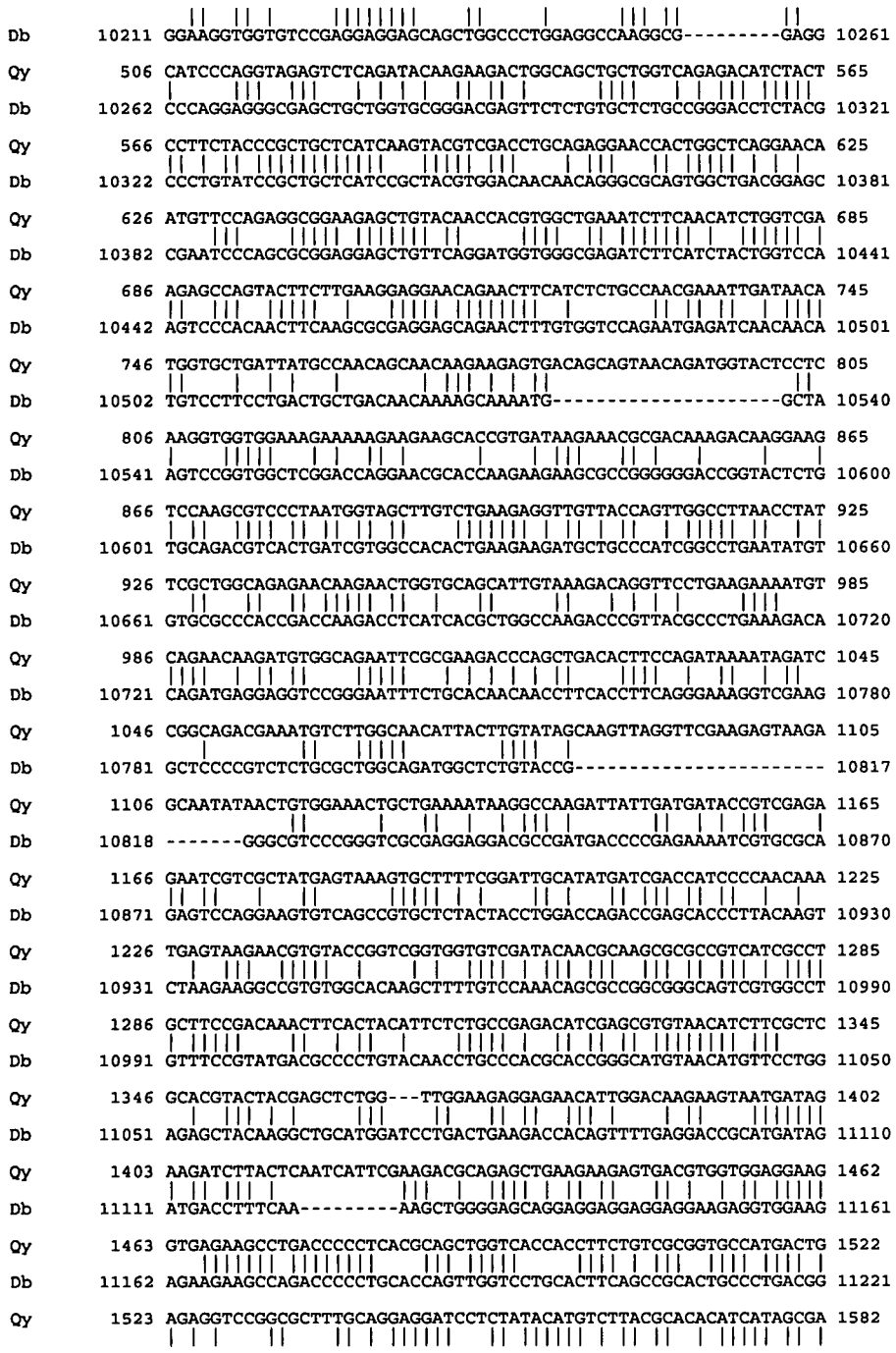
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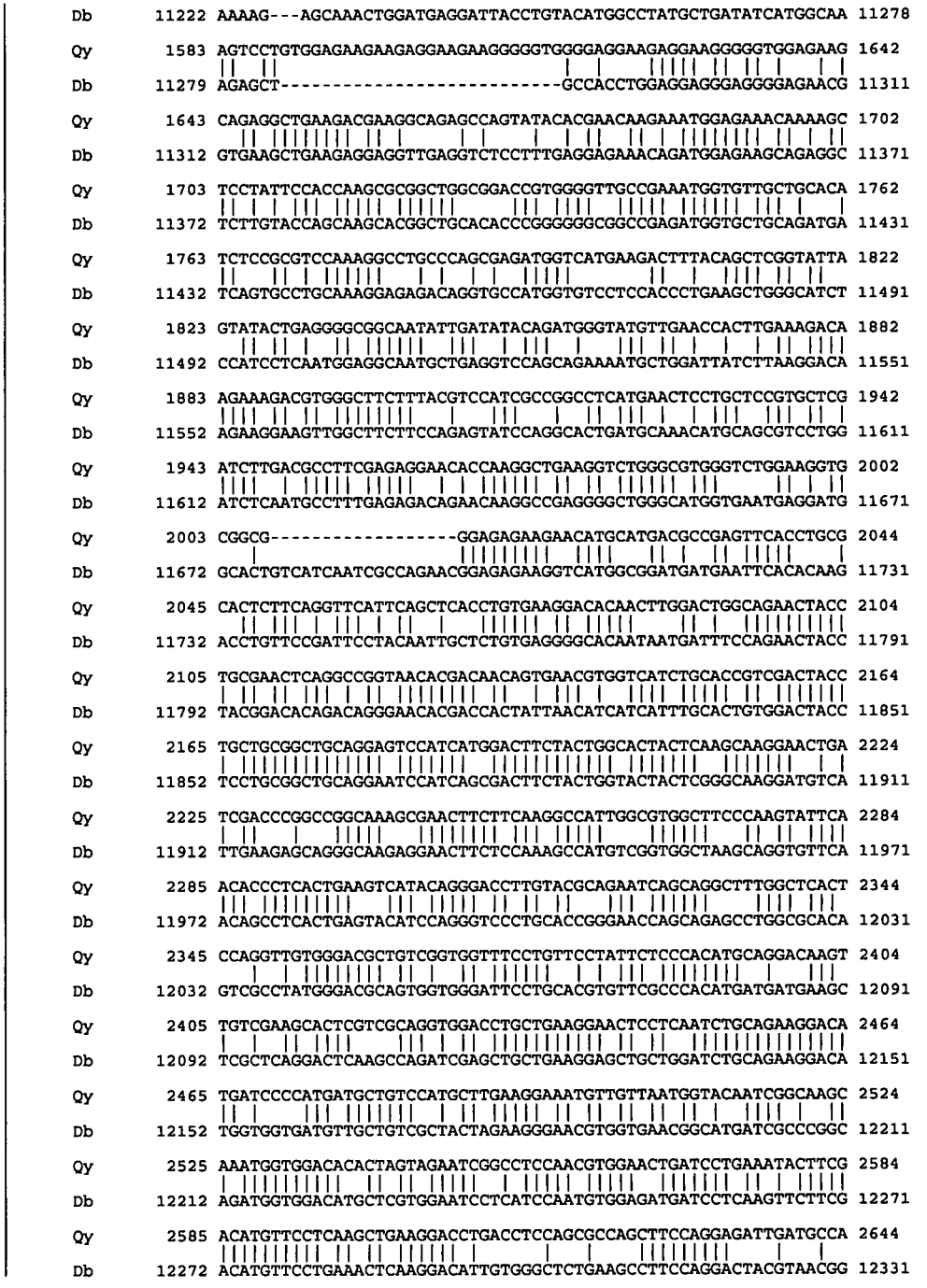
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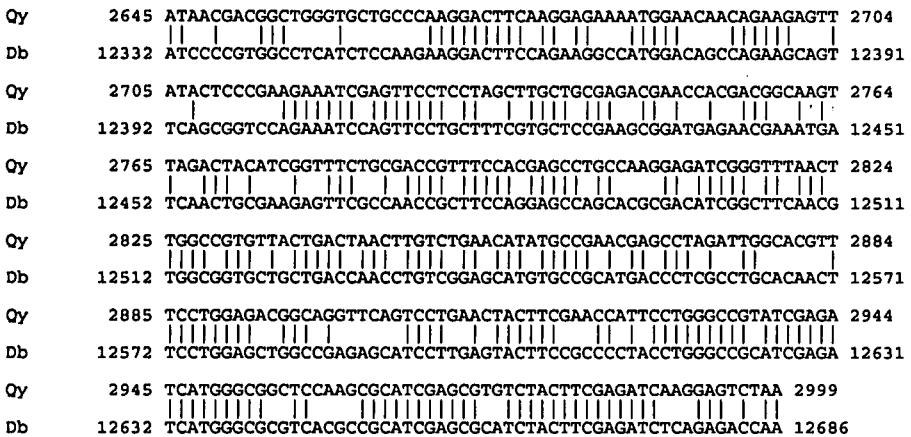
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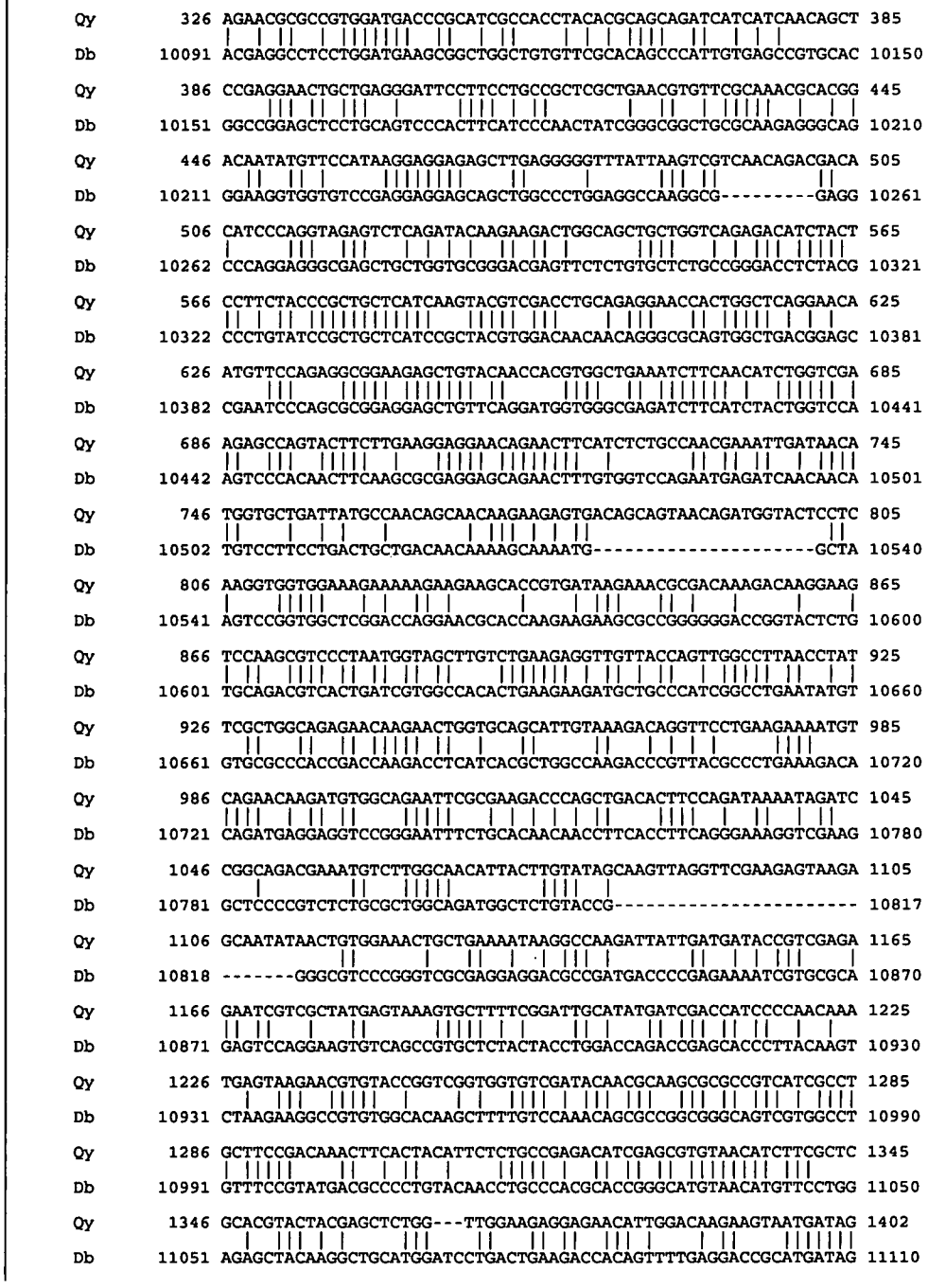

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ACCESSION CS071082
VERSION CS071082.1 GI:63088486
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Sornasse,T., Seilhamer,J.J. and Watson,G.A.
TITLE Tissue specific genes of diagnostic import
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ORIGIN

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VERSION     AF009345.1  GI:4102116
KEYWORDS    .
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REFERENCE   1  (bases 1 to 1722)
  AUTHORS   Puente,E., Suner,M., Evans,A.D., McCaffery,A.R. and Windass,J.D.
  TITLE     Identification of a polymorphic ryanodine receptor gene from
            Heliothis virescens (Lepidoptera: noctuidae)
  JOURNAL   Insect Biochem. Mol. Biol. 30 (4), 335-347 (2000)
   PUBMED   10727900
REFERENCE   2  (bases 1 to 1722)
  AUTHORS   Puente,E. and Windass,J.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1997) Biologie et Pathologie Digestive, INSERM
            U151, Institut Louis Bugnard. CHU Rangueil L3, Toulouse 31403 CEDEX
            04, France
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ORIGIN

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RESULT 15
AY268935
LOCUS       AY268935               15358 bp    mRNA    linear   ROD 06-MAY-2003
DEFINITION  Mus musculus ryanodine receptor (Ryr1) mRNA, complete cds.
ACCESSION   AY268935
VERSION     AY268935.1  GI:30387854
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 15358)
  AUTHORS   Kraev,A., Kraev,N. and MacLennan,D.H.
  TITLE     Complete transcript sequence and strain-specific polymorphisms of
            the Ryr1 gene of the house mouse
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 15358)
  AUTHORS   Kraev,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-APR-2003) Mt. Sinai Hospital, Samuel Lunenfeld
            Research Institute, 600 University Avenue, Toronto, Ontario M5G
            1X5, Canada
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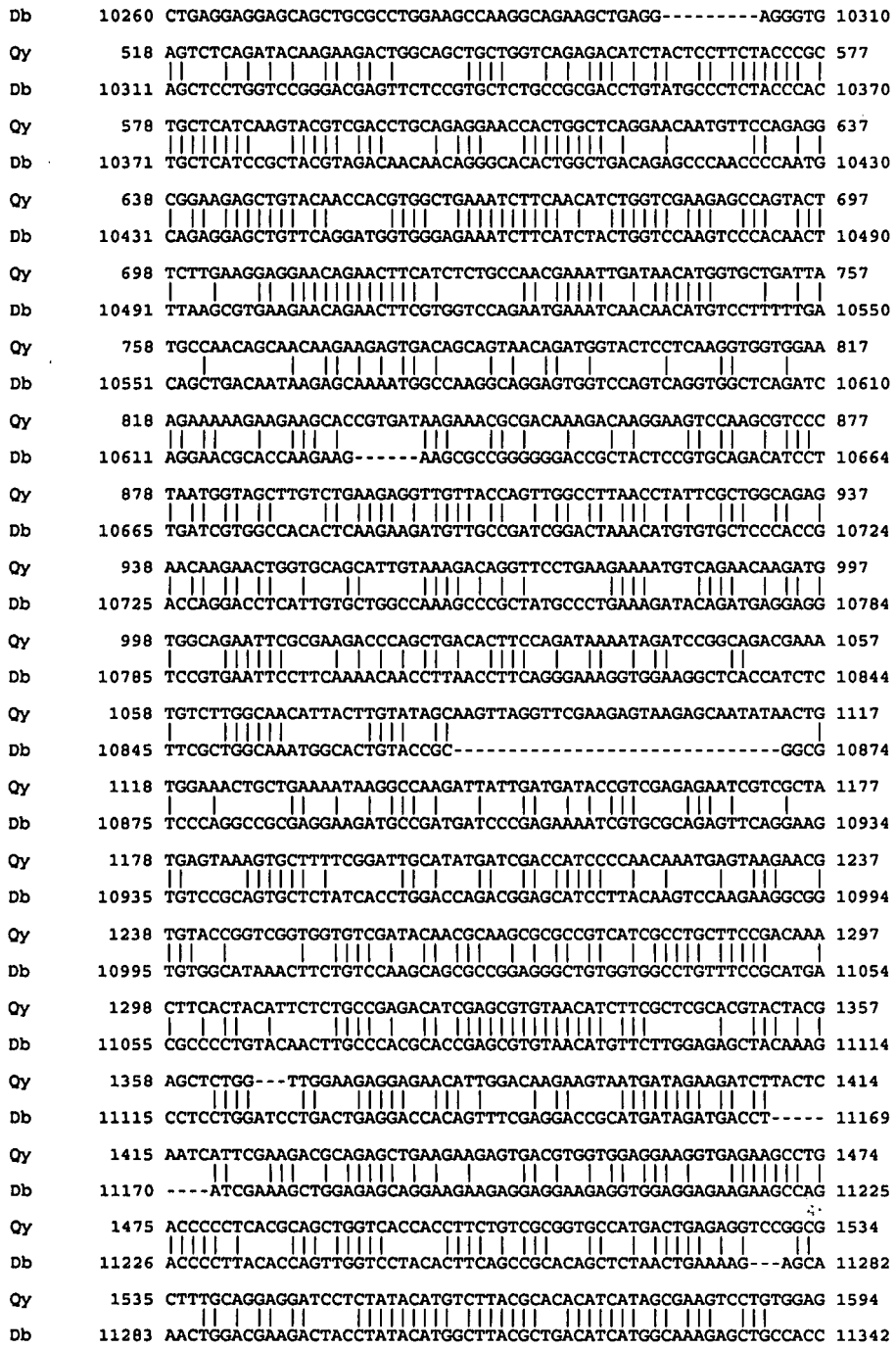
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Db 10935 TGTCCGCAGTGCTCTATCACCTGGACCAGACGGAGCATCCTTACAAGTCCAAGAAGGCGG 10994
Qy 1238 TGTACCGGTCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAA 1297
Db 10995 TGTGGCATAAACTTCTGTCCAAGCAGCGCCGGAGGGCTGTGGTGGCCTGTTTCCGCATGA 11054
Qy 1298 CTTCACTACATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACG 1357
Db 11055 CGCCCCTGTACAACTTGCCCACGCACCGAGCGTGTAACATGTTCTTGGAGAGCTACAAAG 11114
Qy 1358 AGCTCTGG---TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTC 1414
Db 11115 CCTCCTGGATCCTGACTGAGGACCACAGTTTCGAGGACCGCATGATAGATGACCT----- 11169
Qy 1415 AATCATTCGAAGACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTG 1474
Db 11170 ----ATCGAAAGCTGGAGAGCAGGAAGAAGAGGAGGAAGAGGTGGAGGAGAAGAAGCCAG 11225
Qy 1475 ACCCCCTCACGCAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCG 1534
Db 11226 ACCCCTTACACCAGTTGGTCCTACACTTCAGCCGCACAGCTCTAACTGAAAAG---AGCA 11282
Qy 1535 CTTTGCAGGAGGATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAG 1594
Db 11283 AACTGGACGAAGACTACCTATACATGGCTTACGCTGACATCATGGCAAAGAGCTGCCACC 11342
Qy 1595 AAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAG 1654
Db 11343 TGGA----------GGAGGGCGGGGAAAATGGCGAAGAAGGAGGCGAAGAAG 11384
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Qy 2177 AGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAACTGATCGACCCGGCCG 2236
Db 11925 AGGAATCCATCAGTGACTTCTACTGGTATTACTCGGGCAAGGATGTCATCGAGGAACAGG 11984
Qy 2237 GCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTCACTG 2296
Db 11985 GAAAGAGAAACTTCTCCAAAGCCATGTCGGTAGCTAAACAAGTGTTCAACAGCCTCACCG 12044
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Qy       2717 AAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGCAAGTTAGACTACATCG 2776
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Qy       2957 CCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAA 2999
              |     |||||  ||  ||   ||||  ||  ||||||    |||  |  ||
Db      12705 CGCGTCGCATAGAACGGATCTATTTTGAGATCTCAGAGACCAA 12747
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Search completed: April 15, 2006, 01:14:40
Job time : 14505.5 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 14, 2006, 01:43:03 ; Search time 292 Seconds
(without alignments)
4292.767 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Perfect score: 15748
Sequence: 1 MAEAEGGASEQDDVSFLRTE.....RLADNAHDIWAKKKKEELVT 3000

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15748	100.0	5128	4	US-10-668-767-128	Sequence 128, App
2	15693.5	99.7	5134	4	US-10-668-767-130	Sequence 130, App
3	15655.5	99.4	5142	4	US-10-668-767-144	Sequence 144, App
4	15550.5	98.7	5142	4	US-10-668-767-2	Sequence 2, Appli
5	15475	98.3	5100	4	US-10-668-767-146	Sequence 146, App
6	12738	80.9	5127	4	US-10-668-767-8	Sequence 8, Appli
7	12516.5	79.5	5127	4	US-10-668-767-122	Sequence 122, App
8	12489.5	79.3	5113	4	US-10-668-767-121	Sequence 121, App
9	12473.5	79.2	5127	4	US-10-668-767-120	Sequence 120, App
10	12460.5	79.1	5109	4	US-10-668-767-10	Sequence 10, Appl
11	12445	79.0	5104	4	US-10-668-767-6	Sequence 6, Appli
12	12384	78.6	5107	6	US-11-097-143-22563	Sequence 22563, A
13	12354	78.4	5112	4	US-10-668-767-125	Sequence 125, App
14	12338	78.3	5126	4	US-10-668-767-56	Sequence 56, Appl
15	12338	78.3	5126	4	US-10-668-767-124	Sequence 124, App
16	12327	78.3	5101	4	US-10-668-767-4	Sequence 4, Appli
17	12311	78.2	5112	4	US-10-668-767-126	Sequence 126, App
18	12295	78.1	5126	4	US-10-668-767-123	Sequence 123, App
19	12178.5	77.3	4868	4	US-10-668-767-57	Sequence 57, Appl
20	7214	45.8	5071	4	US-10-668-767-58	Sequence 58, Appl
21	6986.5	44.4	5317	4	US-10-668-767-59	Sequence 59, Appl
22	6828	43.4	5107	4	US-10-369-493-6377	Sequence 6377, Ap
23	6778	43.0	4968	4	US-10-668-767-61	Sequence 61, Appl
24	6769	43.0	4767	4	US-10-276-774-1902	Sequence 1902, Ap
25	6769	43.0	4967	4	US-10-668-767-62	Sequence 62, Appl
26	6758	42.9	4967	4	US-10-668-767-60	Sequence 60, Appl
27	6566.5	41.7	3647	4	US-10-408-765A-2436	Sequence 2436, Ap
28	6443	40.9	5038	5	US-10-723-860-1310	Sequence 1310, Ap
29	6443	40.9	5038	5	US-10-756-149-5039	Sequence 5039, Ap
30	6443	40.9	5081	5	US-10-450-763-35328	Sequence 35328, A
31	6442.5	40.9	5032	4	US-10-408-765A-26	Sequence 26, Appl
32	6440	40.9	5081	4	US-10-276-774-1850	Sequence 1850, Ap
33	6434.5	40.9	4870	4	US-10-764-425-144	Sequence 144, App
34	6356	40.4	4899	5	US-10-450-763-42673	Sequence 42673, A
35	6356	40.4	4934	5	US-10-450-763-53705	Sequence 53705, A
36	722.5	4.6	616	5	US-10-450-763-53704	Sequence 53704, A
37	712	4.5	1232	5	US-10-450-763-34060	Sequence 34060, A
38	698.5	4.4	599	5	US-10-450-763-53702	Sequence 53702, A
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40	390	2.5	204	4	US-10-029-386-32508	Sequence 32508, A
41	328	2.1	65	4	US-10-668-767-72	Sequence 72, Appl
42	327.5	2.1	2684	4	US-10-367-094-127	Sequence 127, App
43	323.5	2.1	2677	4	US-10-367-094-124	Sequence 124, App
44	322.5	2.0	2701	4	US-10-408-765A-2130	Sequence 2130, Ap
45	311	2.0	59	4	US-10-668-767-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-10-668-767-128
; Sequence 128, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 5128
; TYPE: PRT
; ORGANISM: Heliothis virescens
; FEATURE:
; OTHER INFORMATION: pXL-Hv7
US-10-668-767-128

Query Match 100.0%; Score 15748; DB 4; Length 5128;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
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Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
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Db        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
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Qy       241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db       241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300

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Qy       361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
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Db       841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900

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Db       901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960

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Qy      1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db      1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080

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Qy      1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320
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Qy      1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800
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Qy      1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860
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Qy      2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160
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Qy      2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220
Db      2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220

Qy      2221 VAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280
Db      2221 VAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280

Qy      2281 MNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRPLCYFCRTGRQNQKAMFDHF 2340
Db      2281 MNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRPLCYFCRTGRQNQKAMFDHF 2340

Qy      2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400
Db      2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400

Qy      2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460
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Db       2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460

Qy       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520

Qy       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580

Qy       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640

Qy       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700

Qy       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760

Qy       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820

Qy       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880

Qy       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940

Qy       2941 KSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 KSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000
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RESULT 2
US-10-668-767-130
; Sequence 130, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 5134
; TYPE: PRT
; ORGANISM: Heliothis virescens
; FEATURE:
; OTHER INFORMATION: pXL-Hv2
US-10-668-767-130

Query Match 99.7%; Score 15693.5; DB 4; Length 5134;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2992; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

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Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSSQDKPAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KSYETKKEGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        661 SAVYRKWYFEVTMDHIEKTTHMIPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
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Db       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200

Qy       1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260

Qy       1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320

Qy       1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380

Qy       1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440

Qy       1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500

Qy       1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560

Qy       1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620

Qy       1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680

Qy       1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740

Qy       1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILELIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800

Qy       1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860

Qy       1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFVMQALA 1920
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db       1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVVREFVMQALA 1920

Qy       1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980

Qy       1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040

Qy       2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100

Qy       2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160

Qy       2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220

Qy       2221 VAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 VAGMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280

Qy       2281 MNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340
             ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db       2281 MNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340

Qy       2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400

Qy       2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460

Qy       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520

Qy       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580

Qy       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640

Qy       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700

Qy       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760

Qy       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820

Qy       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880

Qy       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940

Qy       2941 KSGGRPPEIV-TDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELV 2999
             |||||||||| |||||||:|||||||||||||||||||||||||||||||||||||||||||
Db       2941 KSGGRPPEIVQTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELV 3000

Qy       3000 T 3000
              |
Db       3001 T 3001
```

RESULT 3
US-10-668-767-144
; Sequence 144, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA

```
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 144
;   LENGTH: 5142
;   TYPE: PRT
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   OTHER INFORMATION: pXL-Hv3
US-10-668-767-144

  Query Match            99.4%;  Score 15655.5;  DB 4;  Length 5142;
  Best Local Similarity  99.3%;  Pred. No. 0;
  Matches 2988;  Conservative    5;  Mismatches    7;  Indels    9;  Gaps    2;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLNSDMYL 115
              ||||||||||||||||||||||||||||     ||||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKENLGKGTGSGHRTLLYGNAILLRHLNSDMYL 120

Qy        116 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 180

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 240

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 300

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QNELYLVSREEATTASCAFCLRQEKGDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 360

Qy        356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 420

Qy        416 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 475
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 480

Qy        476 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DLFQEEGILNLILEAIVKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 540

Qy        536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 595
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 600

Qy        596 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 660

Qy        656 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 720

Qy        716 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 775
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 780

Qy        776 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db        781 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRHAAPEGYSPLVESLLPQQILSLEPCFYF 840

Qy        836 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 900

Qy        896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 960

Qy        956 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1015
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        961 RLPNEPFMQSNGYKPAPLDLGAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1020

Qy       1016 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1080

Qy       1076 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1140

Qy       1136 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1200

Qy       1196 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1255
              ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db       1201 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMERDVTHWYTKDQPIFENT 1260

Qy       1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1320

Qy       1316 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1380

Qy       1376 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1440

Qy       1436 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1500

Qy       1496 PSRTNLYGSQVGLN----MATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
              ||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db       1501 PSRTNLYGSQVGLNSNAQMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1560

Qy       1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1620

Qy       1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1680

Qy       1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1740

Qy       1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
              ||||||||||||||||||||||||||||||||||||||||||:|||| ||||||||||||
Db       1741 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCMDILELIEMDKLLSFHSHTLTLYAA 1800

Qy       1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1860

Qy       1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1861 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVV 1920

Qy       1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1980

Qy       1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 PETWDPSFDKGGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2040

Qy       2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2100

Qy       2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2151
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2160

Qy       2152 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2220

Qy       2212 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2280

Qy       2272 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQ 2331
             ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db       2281 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQ 2340

Qy       2332 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2400

Qy       2392 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2460

Qy       2452 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2520

Qy       2512 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2580

Qy       2572 PAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDR 2631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 PAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDR 2640

Qy       2632 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2700

Qy       2692 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2760

Qy       2752 GAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLS 2811
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLS 2820

Qy       2812 KNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2871
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 KNYDGEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2880

Qy       2872 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2940

Qy       2932 NRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 2991
             ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db       2941 NRSSMRRQSKSGGRPPEIVTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 3000

Qy       2992 KKKKEELVT 3000
             |||||||||
Db       3001 KKKKEELVT 3009


RESULT 4
US-10-668-767-2
; Sequence 2, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 5142
;   TYPE: PRT
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1755)..(1755)
;   OTHER INFORMATION: Xaa = Ser
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4250)..(4250)
;   OTHER INFORMATION: Xaa = Thr
US-10-668-767-2

  Query Match            98.7%;  Score 15550.5;  DB 4;  Length 5142;
  Best Local Similarity  98.6%;  Pred. No. 0;
  Matches 2966;  Conservative   12;  Mismatches   22;  Indels    9;  Gaps    2;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              |||||||||||||| ||||||||:|||||||||||||| ||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSILRTEDMVCMSCTATGERVCLAAEGLGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLNSDMYL 115
              |||||||||||||||||||||||||||      |||||||:|||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKENLGKGTGSGYRTLLYGNAILLRHLNSDMYL 120

Qy        116 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        121 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVAIERY 180

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 240

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WTKDGGQNIVVYKGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 300

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QNELYLVSREEPTTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 360

Qy        356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415
              |||||||||||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db        361 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDLSRSQEEESMTARVIRKCSSLFTK 420
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Qy     416 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 475
Db     421 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLTNYFAQPDEDMEHEEKQNKFRALRNRQ 480

Qy     476 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 535
Db     481 DLFQEEGILNLILEAIDKINVVTSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 540

Qy     536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 595
Db     541 TNCAQFANSNRFNWLFSRLGSQASGEGTGMLDVLHCILIDSPEALNMMRDEHIKVIISLL 600

Qy     596 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 655
Db     601 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 660

Qy     656 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 715
Db     661 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 720

Qy     716 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 775
Db     721 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 780

Qy     776 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 835
Db     781 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 840

Qy     836 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895
Db     841 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 900

Qy     896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955
Db     901 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 960

Qy     956 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1015
Db     961 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVGQLAENTHNLWARERIQQGWTYGLNED 1020

Qy    1016 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1075
Db    1021 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1080

Qy    1076 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1135
Db    1081 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1140

Qy    1136 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1195
Db    1141 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1200

Qy    1196 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1255
Db    1201 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1260

Qy    1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1315
Db    1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1320

Qy    1316 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1375
Db    1321 RRWVEIKDRQRILMKEAVEAQMSAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1380

Qy    1376 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1435
Db    1381 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1440

Qy    1436 PFKPFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495
Db    1441 PFKPFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1500

Qy    1496 PSRTNLYGSQVGLN----MATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db    1501 PSRTNLYGSQVGLNSNAQMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1560

Qy    1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db    1561 GVRIYPGQDPTHMYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1620

Qy    1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db    1621 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1680

Qy    1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db    1681 SVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1740

Qy    1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db    1741 LQVHALKLSGIRGWXMLCEDAVSMLALHIPEEDRCIDILELIEMDKLLSFHSHTLTLYAA 1800

Qy    1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db    1801 LCYQSNYRAAHALCSHADQKQLLYAIQSQYMSGPLRQGFYDLLTALHLESHATTMEACKN 1860

Qy    1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
Db    1861 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVV 1920

Qy    1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
Db    1921 REFVMQALAEAVETNQVHNWDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1980

Qy    1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
Db    1981 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEATIAFAHDFV 2040

Qy    2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
Db    2041 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNVILSFKHLEEEDKENCPCGE 2100

Qy    2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2151
Db    2101 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2160

Qy    2152 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2211
Db    2161 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2220

Qy    2212 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2271
Db    2221 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2280

Qy    2272 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQ 2331
Db    2281 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQ 2340

Qy    2332 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2391
Db    2341 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2400

Qy    2392 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2451
Db    2401 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2460

Qy    2452 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2511
Db    2461 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2520

Qy    2512 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2571
Db    2521 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2580

Qy    2572 PAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDR 2631
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Db       2581 PAAGEERPKSDMPSGLIPGHKQSVGLFLGRVYGIETQELFYKLLEEAFLPDLRAATMLDR 2640

Qy       2632 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2691

Db       2641 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2700

Qy       2692 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2751

Db       2701 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2760

Qy       2752 GAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLS 2811

Db       2761 GAGQGAFGASSDEEKRLTMMLFSSIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYTLS 2820

Qy       2812 KNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2871

Db       2821 KNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2880

Qy       2872 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2931

Db       2881 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2940

Qy       2932 NRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 2991

Db       2941 NRSSMGRQSKSGGRPPEIVTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 3000

Qy       2992 KKKKEELVT 3000

Db       3001 KKKKEELVT 3009
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RESULT 5
US-10-668-767-146
; Sequence 146, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 5100
; TYPE: PRT
; ORGANISM: Heliothis virescens
; FEATURE:
; OTHER INFORMATION: pXL-Hv6
US-10-668-767-146

Query Match 98.3%; Score 15475; DB 4; Length 5100;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 2958; Conservative 4; Mismatches 5; Indels 38; Gaps 3;

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Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLNSDMYL 115

Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKENLGKGTGSGHRTLLYGNAILLRHLNSDMYL 120

Qy        116 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175

Db        121 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 180

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235

Db        181 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 240

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295

Db        241 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 300

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355

Db        301 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 360

Qy        356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415

Db        361 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 420

Qy        416 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 475

Db        421 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 480

Qy        476 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 535

Db        481 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 540

Qy        536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 595

Db        541 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 600

Qy        596 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 655

Db        601 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 660

Qy        656 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 715

Db        661 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 720

Qy        716 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 775

Db        721 YSYGLDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 780

Qy        776 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 835

Db        781 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 840

Qy        836 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895

Db        841 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 900

Qy        896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955

Db        901 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 960

Qy        956 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1015

Db        961 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1020

Qy       1016 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1075

Db       1021 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1080

Qy       1076 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1135

Db       1081 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1140

Qy       1136 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1195

Db       1141 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1200
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Qy       1196 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1260

Qy       1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1320

Qy       1316 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1375
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1380

Qy       1376 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1435
             |||||||||||          ||||||||||||||||||||||||||||||||||||||||
Db       1381 SRPPRKGSMTR----------GQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1428

Qy       1436 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495
             ||||||||||||||||||||||||||||||||||||||||||||||:|| :
Db       1429 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQSNAQ------- 1481

Qy       1496 PSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRI 1555
                          ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1482 --------------MATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRI 1527

Qy       1556 YPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADE 1615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1528 YPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIIIDDYDRVVENVNRQSCYMVRADE 1587

Qy       1616 LYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEA 1675
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1588 LYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEA 1647

Qy       1676 TSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVH 1735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1648 TSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVH 1707

Qy       1736 ALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQ 1795
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1708 ALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILELIEMDKLLSFHSHTLTLYAALCYQ 1767

Qy       1796 SNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVI 1855
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1768 SNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVI 1827

Qy       1856 PLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFV 1915
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1828 PLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVVREFV 1887

Qy       1916 MQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW 1975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1888 MQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW 1947

Qy       1976 DPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQ 2035
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Db       1948 DPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQ 2007

Qy       2036 TDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIA 2095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2008 TDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIA 2067

Qy       2096 RMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPP 2155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2068 RMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPP 2127

Qy       2156 KKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINA 2215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2128 KKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINA 2187

Qy       2216 KTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHEN 2275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 KTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHEN 2247

Qy       2276 VMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2335
             |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db       2248 VMAVMMNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2307

Qy       2336 MFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2395
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2308 MFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2367

Qy       2396 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2455
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2368 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2427

Qy       2456 ALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAI 2515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2428 ALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAI 2487

Qy       2516 LNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAG 2575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2488 LNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAG 2547

Qy       2576 EERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGC 2635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2548 EERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGC 2607

Qy       2636 ESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREA 2695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2608 ESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREA 2667

Qy       2696 VSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQ 2755
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2668 VSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQ 2727

Qy       2756 GAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYD 2815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2728 GAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYD 2787

Qy       2816 DEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVY 2875
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2788 DEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVY 2847

Qy       2876 GEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSS 2935
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2848 GEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSS 2907

Qy       2936 MRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKK 2995
             |||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db       2908 MRRQSKSGGRPPEIVTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKK 2967

Qy       2996 EELVT 3000
             |||||
Db       2968 EELVT 2972
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RESULT 6
US-10-668-767-8
; Sequence 8, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 5127
;   TYPE: PRT
;   ORGANISM: Peregrinus maidis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (416)..(416)
;   OTHER INFORMATION: Xaa = Ile
US-10-668-767-8

  Query Match           80.9%;  Score 12738;  DB 4;  Length 5127;
  Best Local Similarity  80.5%;  Pred. No. 0;
  Matches 2446;  Conservative  236;  Mismatches  278;  Indels   78;  Gaps   24;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||::||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADSEGG-SEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              | |||||||||||||||||||||||| |||||||||||||||||||| |||||||| ||
Db         60 STCVFVIEQALSVRALQELVTAAGSEEGKGTGSGHRTLLYGNAILLRHQNSDMYLACSST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:|||||||:|||||||||||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||::|||||||||||||||||||||||||||||||||||||||||||||||||||||||::
Db        180 ENDLSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWSEAP 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||: |||:
Db        240 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHLTTGRYLGVNENNELH 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              |: |:|||||  |||||||||| ||||||||||||||||||:|||||||||:|
Db        300 LIVRDEATTALSAFCLRQEKDDQKVVLEDKDLEVIGAPIIKYGDSTVLVQHSETGLWLTY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||:|||||||||||||||||||||||||||||||:|  ||
Db        360 KSYETKKKGVGKVEEKQAVLHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTQFXRGL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| |||||:| |:||| |||||||||||||||| :|||||||:|||||||||||||
Db        420 ETLQVNRRHSLFCATVNLNEMVMCLEDLINYFAQPADDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              |||||||||||||||||||||    |||||||||::|||||||||||||||||||||||
Db        480 EGILNLILEAIDKINVITSQGFLVS-LAGDESGQSWDIISGYLYQLLAAIIKGNHTNCAQ 538

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        539 FANSNRLNWLFSRLGSQASSEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              |||||||||||||||||||||||||||:|||||||| || |||||:|||||||||| |
Db        599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLPQTQLVDHVASVRPNIFVGRVVG 658

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              ||||:|||||||||||:|||| ||||||||||:|||||||||||||||||||||||||||
Db        659 SAVYQKWYFEVTMDHIEQTTHMTPHLRIGWANTSGYVPYPGGGEKWGGNGVGDDLYSYGF 718

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              ||| ||:||||| |   || ||:|:|||||| :|||||||| | |||  : | | :|| :
Db        719 DGANLWTGGRKTCV-LPHATEPPIKKGDVIGVSLDLTVPIITFSFNGSPIRGCFRDFNYD 777

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              |||||||||| |||||||||:||||:|  || :||||||||||:||::||||||||:|
Db        778 GMFFPVISCSHKLSCRFLLGGDHGRLKYVPPEEFSPLVESLLPQQVLSIDPCFYFGNLNK 837

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
                |:||  |:||||||||||||| :::|| |:| ||||||||||||||||||||:|::

Db        838 CVLSGPWTVEDDTAFVPTPVDTTKVSLPNYIESIRDKLAENIHEMWAMNKIEAGWMFGEK 897

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              |:|: |:|||| |::|||||||| ||||||||||||||::||||:||: :|||||
Db        898 RDDIRKVHPCLIQFDQLPPAEKRYDSQLAVQTLKTILALGYYITMDKPPSRIKTIRLPNE 957

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              |||||||||||||:|::|||||:|||||||||||||||:|||||||||||||||| |
Db        958 PFMQSNGYKPAPLDLTAISLTPKMEELVDQLAENTHNLWAKERIQQGWTYGLNEDSDMLR 1017

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||| |||:|||||||||||||||||||||| ||||||| ||||| |||: :|  ||
Db       1018 SPHLVPYCKVDEAIKKANRDTASETVRTLLVYGYNLDPPTGEAHEALLAEASRLRQTHFR 1077

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
              |||||||||::|||||||||||||||||||| :|  ||  || || ||||||:||||||
Db       1078 TYRAEKNYAVTTGKWYFEFEILTAGPMRVGWARSDCPPGSQLGNDEYSWAFDGFNEEKVY 1137

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200
              |  ||||:|| ||||||||||:| |:|||||||||||||||||:||||||::|||| |
Db       1138 LGTGESFGRQWQVGDVVGVFLDLLDHTMSFSLNGELLMDALGGETSFADVQGESFVPAFT 1197

Qy       1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPPCVNMKRDVTHWYTKDQPIFENTDEMID 1260
              |||||||:|||:|||| ||:|||||||||||||||| | ||:||||| ||||||::  |
Db       1198 LGVGQKAKLTFGQDVTVLKFFTTCGLQEGYEPPCVNMNRAVTYWYTKDHPIFENTEDYAD 1257

Qy       1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320
              :|||||||||||||||||| ||:|||||||||||||||: ||:|:|| :|| |
Db       1258 SRIDVTRIPAGSDTPPCLKISHNLFESMEKANWEFLRLSLPVICHSSFIEESEKLKRWQE 1317

Qy       1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLH--YEDN--------QEELPSSK 1370
              |: ||  |: || :   |||::|||:|| :|:|||||  | ::         :  |::|
Db       1318 IRIRQHRLLVEA-DQTTPAHMEQIMKSGLSMSDIKGLHRGYSEDAVEADEMMMQSTPTTK 1376

Qy       1371 MK-RLPSRPPRKGSMTRGVTIQNYNNLQPGQVNG------MHRSTSEAEMAKYDLGAQGL 1423
              | | ||||||||::|        |     :||      |:|||| :: :|:   |
Db       1377 SKMRQPSRPPRKGSLSR--------NEDMPMINGSLEQSKMNRSTSELDLNRYNADLQN- 1427

Qy       1424 TPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPN-----P 1478
                |||| |||||||:||  ||  |::|  |:|:|:|:| | |   |  :  | :    |
Db       1428 DKDDKK-KRGRSPFRFFSRKREASNER--SKKAKSPEPNSMMEADRGQMGRSQHHMMRTP 1484

Qy       1479 QIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIP 1538
              :||:  : :       | |:|:              |||| : |: |  |:||||||
Db       1485 TVKVTAPDMKVIPPTI-PERSNM--------------PKQMTGAPLSGSGIESVGNEIP 1528

Qy       1539 DAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDR 1598
              | |||||||||||||:|||||||:|||||||  : :|||||  | :|   |:: |
Db       1529 DGECLKLINEYFYGVRIFPGQDPTHVYVGWVTTQYHFFANEFNQSKVRKVTVHTLDEFSR 1588

Qy       1599 VVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFK 1658
              | |:|:|||||||:|||:|||  ::: |||||||||| || :|| :|||||||:|| |
Db       1589 VNESVDRQSCYMVRSDELFNEVTNDSSGKGASQGMFIGCFVDAATGYISFTCEGKETSHK 1648

Qy       1659 FKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQC 1718
              |||||||||||||||||||||||||||||::|:|||||||  |::|| ||||||||||
Db       1649 FKMEPETKLFPAIFVEATSKEILQIELGRTSTTLPLSAAVLQNSERHVNPQFPPRLKVQC 1708

Qy       1719 LKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKL 1778
              |||||||||| |||||||||||||||||||| :|||||||||||| ||||| |||:||
Db       1709 LKPHQWARVPNVSLQVHALKLSDIRGWSMLCEDPMSMLALHIPEEDRSIDILELIEMEKL 1768

Qy       1779 LSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALH 1838
              ||||:||||||||:|||||||| ||:|||:|||||||:| |||||||||||||||||||
Db       1769 LSFHAHTLTLYAALCFQSNYRAAHTLCSHVDEKQLLYAIRSDYMSGPLRQGFYDLLIALH 1828

Qy       1839 LESHATTMEACKNEFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIA------ 1892
              ||||| ||| |||||:||:| ||| :||:|:| ||||||:|||| |
Db       1829 LESHAYTMEVCKNEFIIPIGQELKDVYEDPEMCHSLRSLKTESVLPTMKMTDKADEPSPS 1888

Qy       1893 ESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRL 1952
              | :  | :|||| |||:| |:||| || |||: ||:|||||||||||| ||||:||||||
Db       1889 EVVDNIRSLYSPQFPLDVVRDFVMAALDEAVQINQLHNRDPVGGSNENYFLPLLKLVDRL 1948
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Qy       1953 LLVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLN 2012
Db       1949 LLVGMLRDGDVMKLLIMFSPETWDTAFEKDGKDEHRKGLLTMKMAEGAKLQMCYLLHHLY 2008

Qy       2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNA 2072
Db       2009 DIQLRHRVEAIISFSVDFVGDLQSDQLRRYIEIKQSDLPSAIAAKKTREFRCPPREQMNA 2068

Qy       2073 ILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAE-NQEPEAKPGAF 2131
Db       2069 ILGFKNLEEGDIENCPCGDELRERLNSFHEKLMHKVSLLALQEPSEEEASAEEVKKPNAL 2128

Qy       2132 GKLYNIINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFS 2191
Db       2129 NRLYNFINAVKELEETPQIEEEPEKKTPEEIFRKVLISTIVKWAEETQIESPKLVREMFS 2188

Qy       2192 LLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRL 2251
Db       2189 LLVRQYDTVGELIRALGKTYVINSKTKDDAALMWVGLSQIRALLPVQMSQEEEGLMRERL 2248

Qy       2252 WKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTS 2311
Db       2249 WKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAPQAGQEGEPVAKEKDTS 2308

Qy       2312 HEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLME 2371
Db       2309 HEMVVACCRFLCYFCRTSRQNQKAMFDHFAFLLENSNILLSRPSLRGSTPLDVAYSSLME 2368

Qy       2372 NTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVN 2431
Db       2369 NTELALALREHYLEKIAIYLSRCGLQSNSELIEKGYPDLGWDPVEGERYLDFLRFCVWVN 2428

Qy       2432 GESVEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEG 2491
Db       2429 GESVEENANLVIRLLIRRPGCLGPALRGEGEGLLRAIVDANKMSERIADRRKVMD-EPEG 2487

Qy       2492 D---VNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARA 2548
Db       2488 TTMVMHFEHPLPESDDDEDYIDTGAAILAFYCTLVDLLGRCAPDSSVIAQGKNESLRARA 2547

Qy       2549 ILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQ 2608
Db       2548 ILRSLVPLEDLQGVLSLKFTLQNPAAGEERPKSDMPSGLIPGHKQSVVLFLERVYGIETQ 2607

Qy       2609 ELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENY 2668
Db       2608 ELFPRLLEEAFLPDLRAATMLDRNDGSESDMALAMNRYIGNSILPLLITHSKFYNEADNY 2667

Qy       2669 ASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSE 2728
Db       2668 ASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSSMQPSMLLKLLRKLTVDVSKLTE 2727

Qy       2729 YTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPE 2788
Db       2728 YTTVALRLLTLHYDRCAKYYGSTG-GQGLYGSSSDEEKRLTMMLFSNIFDSLSKMDYDPE 2786

Qy       2789 LFGKALPCLIAIGCALPPDYSLSKNYDDEFYG-KEQAAGDLDNPQYDPQPINTSSVALNN 2847
Db       2787 LFGKALPCLTAIGCALPPDYSLSKNYDDELYGARDSQAGPSDGP-YNPQPINTHSVVLNN 2845

Qy       2848 DLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDY-----EKER 2902
Db       2846 DLNTIVQKFSEHYHDAWASRKLENGWTYGDQWSDSQKTHPRLKPYNMLNDYVEPSIERER 2905

Qy       2903 YKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPH 2962
Db       2906 YKEPVRESIKALLAIGWTVEHSEADVPLTSRGSIRRQSK-----PNAMVDSSTPFNYHPN 2960

Qy       2963 PVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000
Db       2961 PIDMTNLTLGREMQNMAERLAENAHDIWAKKKKEELIT 2998
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RESULT 7
US-10-668-767-122
; Sequence 122, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
;   LENGTH: 5127
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: gi 17352469
US-10-668-767-122

  Query Match             79.5%;  Score 12516.5;  DB 4;  Length 5127;
  Best Local Similarity   78.8%;  Pred. No. 0;
  Matches 2387;  Conservative  263;  Mismatches  312;  Indels   67;  Gaps   21;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

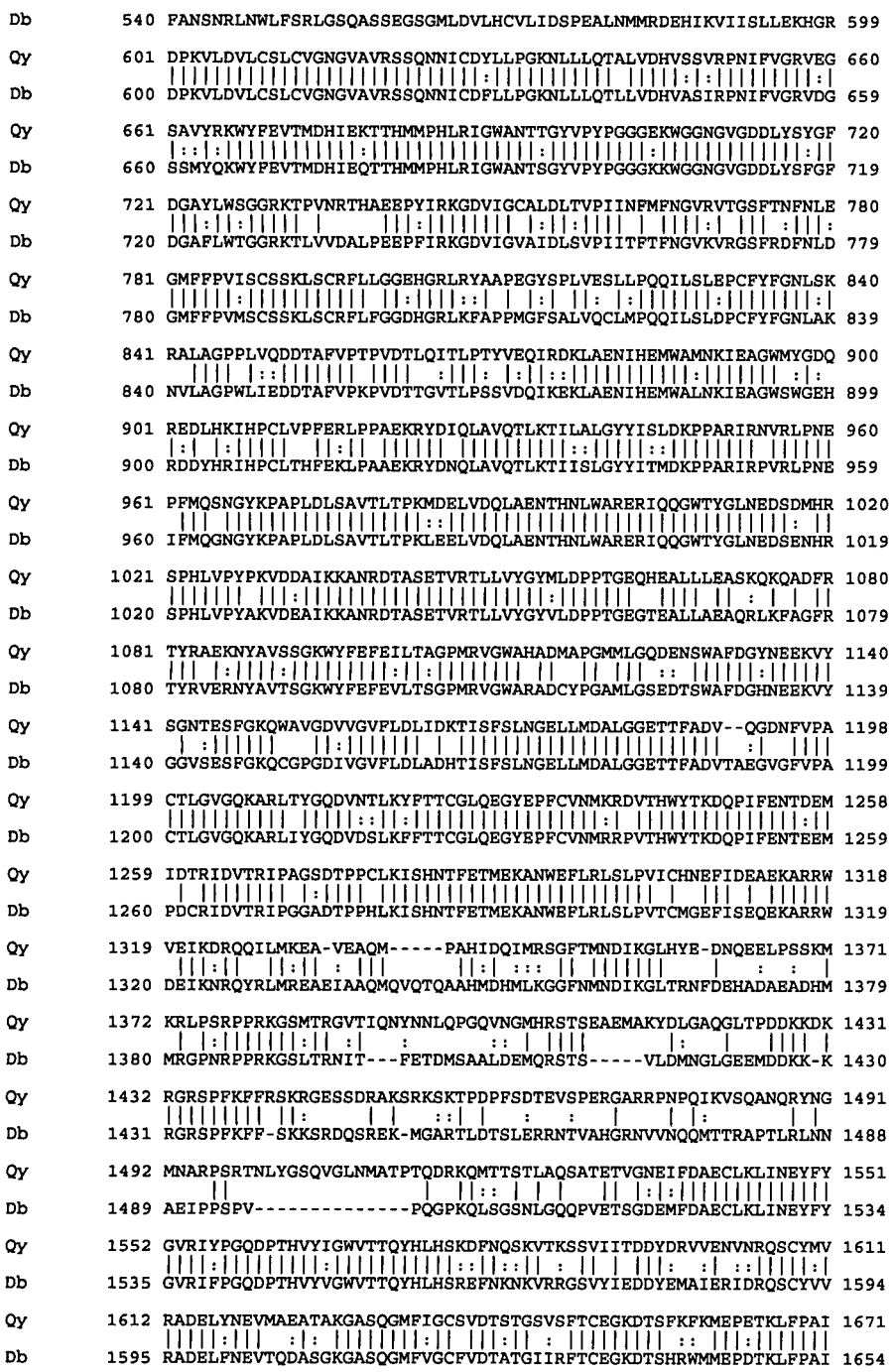
Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
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Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db        480 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
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Db 540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599
Qy 601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db 600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659
Qy 661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db 660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719
Qy 721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db 720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779
Qy 781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db 780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db 960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNEEKVY 1139
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db 1140 GGVSESFGKQCGPGDIVGVFLDLADHTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1199
Qy 1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db 1200 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1259
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db 1260 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1319
Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1431 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1488
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1489 AEIPPSPV----------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1534
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1535 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1594
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1655 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1714
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1715 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1774
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDI----------AESITE 1897
Db 1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPD 1894
Qy 1898 ISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957
Db 1895 IDQLYSPKFPLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1954
Qy 1958 MRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017
Db 1955 LTDEDVQRLLVMIDPETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLR 2014
Qy 2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db 2015 HRVESIIAFSHDFVGDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFK 2074
Qy 2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYN 2136
Db 2075 NLEPDDQDNCTCGLELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYN 2134
Qy 2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196
Db 2135 FINTVKELEEGPKEVEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQ 2194
Qy 2197 YDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2256
Db 2195 YDTVGELVRALEKTYVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2254
Qy 2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEM 2314
Db 2255 NATFFQHPDLIRILRVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEM 2313
Qy 2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374
Db 2314 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTE 2373
Qy 2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434
Db 2374 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2433
Qy 2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493
Db 2434 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2492
Qy 2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551
Db 2493 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILR 2552
Qy 2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611
Db 2553 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2612
Qy 2612 YKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASL 2671
Db 2613 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2672
Qy 2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731
Db 2673 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2732

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Qy       2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791
Db       2733 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2791

Qy       2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851
Db       2792 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2849

Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
Db       2850 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2909

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969
Db       2910 KGLLAIGWTVEHSEVEVALNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2964

Qy       2970 TLSREMQNMAERLADNAHDIWAKKKKEEL 2998
Db       2965 TLSREMQNMAERLAENSHDIWAKKKNEEL 2993


RESULT 8
US-10-668-767-121
; Sequence 121, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
;   LENGTH: 5113
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: gi 17352467
US-10-668-767-121

  Query Match             79.3%;  Score 12489.5;  DB 4;  Length 5113;
  Best Local Similarity   78.8%;  Pred. No. 0;
  Matches 2376;  Conservative  271;  Mismatches  315;  Indels   53;  Gaps   20;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAAIIKGNHTNCAQ 540
Db        480 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db        660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db        720 DGAFLWTGGRKTLVVDALPEEPPIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db        780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db        840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db        900 RDDYHRIHPCLTHPEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db        960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db       1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db       1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMH 1139

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db       1140 AGSIEHFGVRYEAGDVIGCFIDVKEQTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1199

Qy       1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db       1200 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1259

Qy       1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db       1260 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1319

Qy       1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db       1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379
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Qy       1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db       1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430

Qy       1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db       1431 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1488

Qy       1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db       1489 AEIPPSPV--------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1534

Qy       1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db       1535 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1594

Qy       1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db       1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654

Qy       1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db       1655 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1714

Qy       1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db       1715 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1774

Qy       1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db       1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834

Qy       1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
Db       1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITEPIPDIDQLYSPKFPLEVV 1894

Qy       1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
Db       1895 RQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGVLTDEDVQRLLVMID 1954

Qy       1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
Db       1955 PETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLRHRVESIIAFSHDFV 2014

Qy       2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
Db       2015 GDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFKNLEPDDQDNCTCGL 2074

Qy       2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYNIINTVKELEEEAKA 2150
Db       2075 ELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYNFINTVKELEEGPKE 2134

Qy       2151 IEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKT 2210
Db       2135 VEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQYDTVGELVRALEKT 2194

Qy       2211 YVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVL 2270
Db       2195 YVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNATFFQHPDLIRIL 2254

Qy       2271 RVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEMVVACCRFLCYFCRT 2328
Db       2255 RVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRT 2313

Qy       2329 GRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2388
Db       2314 GRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2373

Qy       2389 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIR 2448
Db       2374 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGESVEENANLVIRLLIR 2433

Qy       2449 RPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDED 2505
Db       2434 RPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEED 2492

Qy       2506 EDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL 2565
Db       2493 EDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILRSLVPLEDLQGVLSL 2552

Qy       2566 RFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRA 2625
Db       2553 KFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRT 2612

Qy       2626 ATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKN 2685
Db       2613 ATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASLLDATLHTVYRLSKN 2672

Qy       2686 RMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745
Db       2673 RMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHPDRCA 2732

Qy       2746 KYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALP 2805
Db       2733 KYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALP 2791

Qy       2806 PDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWA 2865
Db       2792 PDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWA 2849

Qy       2866 SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE 2925
Db       2850 SRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSE 2909

Qy       2926 VDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNLTLSREMQNMAERLA 2983
Db       2910 VEVALNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNLTLSREMQNMAERLA 2964

Qy       2984 DNAHDIWAKKKKEEL 2998
Db       2965 ENSHDIWAKKKNEEL 2979
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RESULT 9
US-10-668-767-120
; Sequence 120, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 5127
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: gi 17352465
US-10-668-767-120

Query Match 79.2%; Score 12473.5; DB 4; Length 5127;
Best Local Similarity 78.4%; Pred. No. 0;

Matches 2376; Conservative 272; Mismatches 314; Indels 67; Gaps 21;

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Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGRGA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db        480 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db        660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db        720 DGAFLWTGGRKTLVVDALPEEPPIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db        780 GMFPPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db        840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db        900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db        960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db       1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db       1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMH 1139

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db       1140 AGSIEHFGVRYEAGDVIGCFIDVKEQTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1199

Qy       1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db       1200 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1259

Qy       1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db       1260 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1319

Qy       1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db       1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379

Qy       1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db       1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430

Qy       1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db       1431 RGRSPFKFP-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1488

Qy       1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db       1489 AEIPPSPV--------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1534

Qy       1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db       1535 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1594

Qy       1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db       1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654

Qy       1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db       1655 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1714

Qy       1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db       1715 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1774

Qy       1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db       1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834

Qy       1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDI----------AESITE 1897
Db       1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPD 1894

Qy       1898 ISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957
Db       1895 IDQLYSPKFPLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1954

Qy       1958 MRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017
Db       1955 LTDEDVQRLLVMIDPETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLR 2014

Qy       2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db       2015 HRVESIIAFSHDFVGDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFK 2074

Qy       2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYN 2136
Db       2075 NLEPDDQDNCTCGLELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYN 2134
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Qy       2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196
Db       2135 FINTVKELEEGPKEVEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQ 2194

Qy       2197 YDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2256
Db       2195 YDTVGELVRALEKTYVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2254

Qy       2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEM 2314
Db       2255 NATFFQHPDLIRILRVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEM 2313

Qy       2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374
Db       2314 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTE 2373

Qy       2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434
Db       2374 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2433

Qy       2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493
Db       2434 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2492

Qy       2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551
Db       2493 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILR 2552

Qy       2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611
Db       2553 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2612

Qy       2612 YKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASL 2671
Db       2613 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2672

Qy       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731
Db       2673 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2732

Qy       2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791
Db       2733 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2791

Qy       2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851
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Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
Db       2850 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2909

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969
Db       2910 KGLLAIGWTVEHSEVEVALNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2964

Qy       2970 TLSREMQNMAERLADNAHDIWAKKKKEEL 2998
Db       2965 TLSREMQNMAERLAENSHDIWAKKKNEEL 2993
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RESULT 10
US-10-668-767-10
; Sequence 10, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
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;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 5109
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-10-668-767-10

  Query Match             79.1%;  Score 12460.5;  DB 4;  Length 5109;
  Best Local Similarity   78.7%;  Pred. No. 0;
  Matches 2371;  Conservative  273;  Mismatches  316;  Indels   53;  Gaps   20;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDGLIPVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
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Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
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Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVVISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGKEKWGGNGVGDDLYSYGF 720
Db        660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db        720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
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Db 780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFPGNLAK 839
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
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Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
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Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
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Qy 1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
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Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
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Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
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Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
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Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
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Db 1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQPPPRLKVQCLKPHQWARVPNQS 1731
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Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
Db 1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITEPIPDIDQLYSPKFPLEVV 1894
Qy 1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
Db 1895 RQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGVLTDEDVQRLLVMID 1954
Qy 1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
Db 1955 PETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMRYLLHHLYDTQLRHRVESIIAFSHDFV 2014
Qy 2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
Db 2015 GDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFKNLEPDDQDNCTCGL 2074
Qy 2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYNIINTVKELEEEAKA 2150
Db 2075 ELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYNFINTVKELEEGPKE 2134
Qy 2151 IEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKT 2210
Db 2135 VEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQYDTVGELVRALEKT 2194
Qy 2211 YVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVL 2270
Db 2195 YVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNATFFQHPDLIRIL 2254
Qy 2271 RVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEMVVACCRFLCYFCRT 2328
Db 2255 RVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRT 2313
Qy 2329 GRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2388
Db 2314 GRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2373
Qy 2389 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIR 2448
Db 2374 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYPDFLRYCVWVNGESVEENANLVIRLLIR 2433
Qy 2449 RPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDED 2505
Db 2434 RPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEED 2492
Qy 2506 EDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL 2565
Db 2493 EDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILRSLVPLEDLQGVLSL 2552
Qy 2566 RFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRA 2625
Db 2553 KFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRT 2612
Qy 2626 ATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKN 2685
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Qy 2686 RMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745
Db 2673 RMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHFDRCA 2732
Qy 2746 KYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALP 2805
Db 2733 KYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALP 2791
Qy 2806 PDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWA 2865
Db 2792 PDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWA 2849
Qy 2866 SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE 2925
Db 2850 SRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSE 2909
Qy 2926 VDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADN 2985
Db 2910 VEVPLNHRGSTRRQSK-----PQI--NEGSPFNYNPHPVDMSNLTLSREMQNMAERLAEN 2962

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Qy       2986 AHDIWAKKKKEEL 2998
              :||||||||| |||
Db       2963 SHDIWAKKKNEEL 2975


RESULT 11
US-10-668-767-6
; Sequence 6, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 5104
;   TYPE: PRT
;   ORGANISM: Periplaneta americana
US-10-668-767-6

  Query Match             79.0%;  Score 12445;  DB 4;  Length 5104;
  Best Local Similarity   78.3%;  Pred. No. 0;
  Matches 2383;  Conservative  266;  Mismatches  294;  Indels  100;  Gaps   32;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||::| |:||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db          1 MADSE-GSSEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCYLENIADKNIPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGK-GTGSGHRTLLYGNAILLRHLNSDMYLACLS 119
              ||||||||||||||||||||  |: || |||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTATSSQEGKGGTGSGHRTLLYGNAILLRHQNSDMYLACLS 119

Qy        120 TSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTT 179
              |||| |||:||||||:|||||||||:|||||||||||||||||||||||||||||||||||
Db        120 TSSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTA 179

Qy        180 KENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKD 239
              ||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db        180 KENELSVVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWSNV 239

Qy        240 GGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNEL 299
              |||||:|||||||||||||||||||||||||||||||||||||||||:||||||||: |||
Db        240 SGQNIVIYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHLTTGRYLGVNENNEL 299

Qy        300 YLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLS 359
              :|| |||||||| | |||||||| :|||||||||||||||||||:||||:|||||:
Db        300 HLVCREEATTASSTFFLRQEKDDQKIILEDKDLEVIGAPIIKYGDSTVLVQHSDTGLWLT 359

Qy        360 YKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFING 419
              ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||:||:|
Db        360 YKSYETKKKGVGKVEEKQAVLHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTQFISG 419

Qy        420 LETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQ 479
              || || ||| |:| : ||| |||||||||||||:||||||||:||||||||||||
Db        420 LENLQSNRRSSLFCSFVNLNEMVMCLEDLINYFAQPEEDMEHEEKQNRFRALRNRQDLFQ 479

Qy        480 EEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCA 539
              |||||||||||||:|:||||||:   ||||||||||::|||||||||||||||||||||
Db        480 EEGILNLILEAIDKVNIITSQGFMVS-LAGDESGQSWDVISGYLYQLLAAIIKGNHTNCA 538

Qy        540 QFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHG 599
              ||||:|||||||||||||| |||||||||||||||||||||:|||||||||||||||||
Db        539 QFANTNRLNWLFSRLGSQASSEGTGMLDVLHCVLIDSPEALNMMKDEHIKVIISLLEKHG 598

Qy        600 RDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVE 659
              |||||||||||||||||||||||||||||||:|||||||||| ||||||:||||||||| |
Db        599 RDPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASVRPNIFVGHVS 658

Qy        660 GSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYG 719
              |||||||||:|| :||:|:|||: ||:||||||| |||||||||||||||||||||:|
Db        659 GSAVYRKWYYEVAIDHVEQTTHLNPHIRIGWANTAGYVPYPGGGEKWGGNGVGDDLYSFG 718

Qy        720 FDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNL 779
              |||:|||:||||: |    :|   |:|||||||||||:||| |  ||  | |:| :|||
Db        719 FDGSYLWTGGRKSEV-MPGSEISNIKKGDVIGCALDLTIPIITFTLNGQLVQGAFRDFNL 777

Qy        780 EGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLS 839
              :||||||||||: |||||||:||||::  |: :||| |||||||||:::|||||||||
Db        778 DGMFFPVISCSSKVGCRFLLGGDHGRLKFTPPDEFSPLFESLLPQQILTIDPCFYFGNLS 837

Qy        840 KRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGD 899
              |  | ||  |:||||||| |||| :|||:|:| |:|||||||||||||||||| |||
Db        838 KCVLTGPWYVEDDTAFVPNPVDTSMVTLPSYIENIKDKLAENIHEMWAMNKIEAGWQYGD 897

Qy        900 QREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPN 959
              :| |  | ||||: |::|||||||| |||||||||::||||:||:| ||:||: |||||
Db        898 KRNDTRKYHPCLIQFDKLPPAEKRYDSQLAVQTLKTVIALGYHISIDNPPSRIKTVRLPN 957

Qy        960 EPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMH 1019
              |||||||||||||||||: |: ||:||:|||||||||||||:|||||||||||:  |
Db        958 EPFMQSNGYKPAPLDLSAINLSGKMEELIDQLAENTHNLWAKERIQQGWTYGLNEELQML 1017

Qy       1020 RSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEA-LLLEASKQKQAD 1078
              |||||||| |||||||||||||||||||||||||| ||||||| :|| || : :  :
Db       1018 RSPHLVPYSKVDDAIKKANRDTASETVRTLLVYGYNLDPPTGETNEATLLTDENTNRYLT 1077

Qy       1079 FRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEK 1138
              |||||||| |||:|||||||||||| ||||||||    :||  :| ||||||||||||||
Db       1078 FRTYRAEKTYAVASGKWYFEFEILTNGPMRVGWARFTCSPGYQIGSDENSWAFDGYNEEK 1137

Qy       1139 VYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPA 1198
              :| |  ||||:|| ||||||||||:| |||||||||||| |||||||::|||: ||||
Db       1138 IYMGTAESFGRQWQVGDVVGVFLDLMDHTISFSLNGELLMDTLGGETTFSEVQGEGFVPA 1197

Qy       1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
              |||:||||:||:|||||:|||||||||||||||||||| ||:||||||||||||:
Db       1198 FTLGLGQKAKLTFGQDVNSLKYFTTCGLQEGYEPFCVNMKRPVTYWYTKDQPIFENTDD- 1256

Qy       1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
                : |||||||||||||||||||||||||:|||||||||||||   |||| || |||
Db       1257 FSSVIDVTRIPAGSDTPPCLKISHNTFETMERANWEFLRLSLPVICLPNFIDEQEKQRRW 1316

Qy       1319 VEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLH--YED----NQEELPSS--- 1369
              ||: ||  |: :: |   ||||:|||:|||:|:|||||  | |    | | :|::
Db       1317 QEIRIRQHRLLSQS-EHATPAHIEQIMKSGFSMSDIKGLHRGYSDDPVENDEMMPNTAPL 1375

Qy       1370 ----KMKRLPSRPPRKGSMTR--GVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDL---GA 1420
                  | :  | |||||||::|   :||:|      |::|   ||:||     |:
Db       1376 PPRGKNQPPPPRPPRKGSLSRHDDLTIEN-----DGKLN---RSSSELNFNIYNQQNGNG 1427

Qy       1421 QGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPN--- 1477
              | :  |||| |||||||:||  |:   ||  |  ::|||||  :  |      | |||
Db       1428 QDINKDDKK-KRGRSPFRFFSRKKEGPSDNPK--RAKTPDPARNV-VRSRNAAHRPNTLN 1483

Qy       1478 ----PQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPT-QDR---KQMTTSTLAQSA 1529
                  |||:|                    ||: | : |  ||    :  : | : :
Db       1484 ERITPQIRV--------------------SQMDLKLVPPAIPDRPGGPKAMSFTPSSAG 1522

Qy       1530 TETVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSS 1589
              | ||||||| ||||||||:|||||:|||||||:||||||:|||||:| | ||:
Db       1523 IEFVGNEIFDLECLKLINEYYYGVRIFPGQDPTHVYVGWVTTQFHLHSKDFSQNHVRKST 1582
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Qy       1590 VIITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFT 1649
Db       1583 VTIVDEHNRILESIDRQSCYMVRSDELYNEVTNDSSGKGASQGMAIGCFIDIATGVMSFT 1642

Qy       1650 CEGKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQ 1709
Db       1643 CEGKETSFKFKMEPDIKLFPAIFVEASSKEILQIELGRTSTTLPLSAAVLQNSERHVLPQ 1702

Qy       1710 FPPRLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDI 1769
Db       1703 FPPRLKVQCLRPHQWARVPNDSLHIHTLKLSDIRGWSILCEDPVSMIALHIPEEDRCIDI 1762

Qy       1770 LEPIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQG 1829
Db       1763 LELIEMEKLLSFHAHTLTLYAAVCYQANYRAAHILCTHVNQKQLLYAICSEYMSGPLRQG 1822

Qy       1830 FYDLLIALHLESHATTMEACKNEFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMT 1889
Db       1823 FYDLLIALHLESHATTMEVCKNEYIIPLGHELTALYDDPQMGHSLRSLQTESVRPQMKMT 1882

Qy       1890 DIAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLV 1949
Db       1883 EISDVIDNVRNLYSPYFPLQVVREYVMAALEEAVLVNQVHNRDPIGGSNENLFLPLLKLV 1942

Qy       1950 DRLLLVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQ 2009
Db       1943 DRLLLVGMLRDEDVEKLLIMINPETWDPEFQKDGPDEHRKGLLHMKMAEGAKLQMCYLLH 2002

Qy       2010 HLNDIQLRHRVEAIIAPAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQ 2069
Db       2003 HLCDIQLRHRVESIISFSYQFVNDIQIDQLRRYNEIKQSDLPSAVAAKKTREFRCPPREQ 2062

Qy       2070 MNAILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAE------NQE 2123
Db       2063 MNAILGFKNLDSDDKENCLIGDELRERMNEFNEKLMKQILLVALQESEDDKLDLNNINRE 2122

Qy       2124 PEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETP 2183
Db       2123 -----GKIKQFYNFINAVKD-EANENGLNEHEKKIPEEIFRKVLITTIVSWAEETQIETP 2176

Qy       2184 KLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEE 2243
Db       2177 KLVREMFSLLVRQYDSVGELIRALEKTYVINFKTKEDVAQMWVGLSQIRSLLPVQMSQEE 2236

Qy       2244 EELMRKRLWKLVNNHTPFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPV-A 2302
Db       2237 EELMRERLWKLVNNHTPFQHPDLIRVLRMHENVMAVMMNTLGRRAQAQS--QPGGTTVTG 2294

Qy       2303 EDS----KEKDTSHEMVVACCRPLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRG 2358
Db       2295 QDGEIVPKEKDTSHEMVVACCRPLCYFCRTSRQNQKAMFDHFSFLLENSNILLSRPSLRG 2354

Qy       2359 STPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGE 2418
Db       2355 STPLDVAYSSLMENTELALALREHYLEKIAIYLSRCGLQSNSELIEKGYPDLGWDPVEGE 2414

Qy       2419 RYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERI 2478
Db       2415 RYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGEGEGLLRAIIDANKMSERI 2474

Qy       2479 ADRRK-LREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIA 2537
Db       2475 AERRKFLEESGNQENIQLDHPLPESEDDEDYIDTGAAILNFYCTLVDLLGRCAPDSSVIA 2534

Qy       2538 LGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGL 2597
Db       2535 LGKNESLRARAILRSLVPLEDLHGVLSLRFTLQNPAAGQDRPKSDMPSGLIPGHKQSVVL 2594

Qy       2598 FLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIK 2657
Db       2595 FLERVYGIEMQELFFTLLEEAFLPDLRTATMLDRNDGLESDMALAMNRYIGNSVLPLLIG 2654

Qy       2658 HAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLR 2717
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Db       2655 HSKFYSESDNYANLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPSMLLKLLR 2714

Qy       2718 KLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAPGASSDEEKRLTMMLFSNIF 2777
Db       2715 KLTVDVSNLSEYTTVALRLLTLHYDRCAKYYGSTG-GQGIYGASSDEEKRLTMMLFSNIF 2773

Qy       2778 DSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG-KEQAAGDLDNPQYDPQ 2836
Db       2774 DSLSKMDYDPELFGKALPCLSAIGCALPPDYSLSKNYDDEWYGSKQNIQGPSDGP-YNPQ 2832

Qy       2837 PINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLN 2896
Db       2833 PINTNSIVLDNDLNSIVHKFSEHYHDAWANRKLENGWVYGEQFNDVNKSHPRLKPYMMLS 2892

Qy       2897 DYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATP 2956
Db       2893 EYEKELYKEPVRESLKALLAIGWSIEHSENDAPLNNRGSVRRQSKS--------NENVTP 2944

Qy       2957 FDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELV 2999
Db       2945 FDYHPNPIDMTNLTLTREMQNMAERLAENSHDIWAKKKKEEVM 2987
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RESULT 12
US-11-097-143-22563 con. of 09/614,150, filing date: 07/11/2000.
; Sequence 22563, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 22563
; LENGTH: 5107
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-22563

Query Match 78.6%; Score 12384; DB 6; Length 5107;
Best Local Similarity 78.3%; Pred. No. 0;
Matches 2356; Conservative 272; Mismatches 314; Indels 66; Gaps 20;

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Qy         22 MVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDLSQCVFVIEQALSVRALQELVT 81
Db          1 MVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDLSQCVFVIEQALSVRALQELVT 60

Qy         82 AAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLSTSSSQDKLAFDVGLQQHSQGEA 141
Db         61 AAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLSTSSSNDKLSFDVGLQEHSQGEA 120
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```
Db       2256 AVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2314

Qy       2336 MFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2395
             |||||||||:|:||||:||||||||||||||||||||||||||||||||||||||||||||
Db       2315 MFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2374

Qy       2396 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2455
             ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db       2375 LQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGESVEENANLVIRLLIRRPECLGP 2434

Qy       2456 ALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDEDEDYIDTG 2512
             ||||||||| :|||:||:|||||:|| |::: | || :   ||:||||| :|||||||||
Db       2435 ALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEEDEDYIDTG 2493

Qy       2513 AAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRPTLNNP 2572
             |||||||||||||||||| ||  |||||||||||||||||||||||:|||:
Db       2494 AAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILRSLVPLEDLQGVLSLKFTLSQT 2553

Qy       2573 AAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRN 2632
             | |||:|||||||||:| :|||: |||||||||| |:|||:|||:|||||| ||:||::
Db       2554 APGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRTATILDKS 2613

Qy       2633 DGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQ 2692
             || |||||:|||||||||||||: |||||||||||||||||||||||||||||||||||||
Db       2614 DGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASLLDATLHTVYRLSKNRMLTKGQ 2673

Qy       2693 REAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTG 2752
             |||||||||||| |||:|||||||||||||||||||||||||::|||||||||
Db       2674 REAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHFDRCAKYYGST- 2732

Qy       2753 AGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSK 2812
              |||::|||||||||||||:|||||||||| |||:|||||||||||||||||||||||||
Db       2733 QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALPPDYSLSK 2792

Qy       2813 NYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENG 2872
             | |:::||::  |   | ||| | ||:|::| |:||||::|||||||||||||::| |
Db       2793 NTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWASRRLEGG 2850

Qy       2873 WVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNN 2932
             | ||:  ||: : ||||||||||::||:|||::|||| || ||||||:||||||::  |:
Db       2851 WTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSEVEVALNH 2910

Qy       2933 RSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIW 2990
             | | |||||     |:|    :  :||:||||||||:||||||||||||||:|:||||
Db       2911 RGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNLTLSREMQNMAERLAENSHDIW 2965

Qy       2991 AKKKKEEL 2998
              |||| |||
Db       2966 AKKKNEEL 2973
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RESULT 13
US-10-668-767-125
; Sequence 125, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
;  LENGTH: 5112
;  TYPE: PRT
;  ORGANISM: Drosophila melanogaster
;  FEATURE:
;  OTHER INFORMATION: gi 2160477
US-10-668-767-125

  Query Match            78.4%;  Score 12354;  DB 4;  Length 5112;
  Best Local Similarity  78.2%;  Pred. No. 0;
  Matches 2359;  Conservative  265;  Mismatches  337;  Indels   54;  Gaps   21;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
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Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:||||||:|||||||||:||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||||| ||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |   |||||:|:||||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFSW-QEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||||||||||||||| |||||||||:|||||||||||:|| |
Db        359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 418

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| |||||:||  ||| |||||||||||||:||::|||||||||:|||||||||||||
Db        419 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 478

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||:|||||||||||:|||||||| |||||:||||::|| ||||||||||||||||||||
Db        479 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 538

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              |||||||||||||||||| ||:|||||||||||||||||||||||||||||||||||||
Db        539 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              |||||||||||||||||||||||||||:|||||||||| ||||||:|:||||||||:|
Db        599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 658

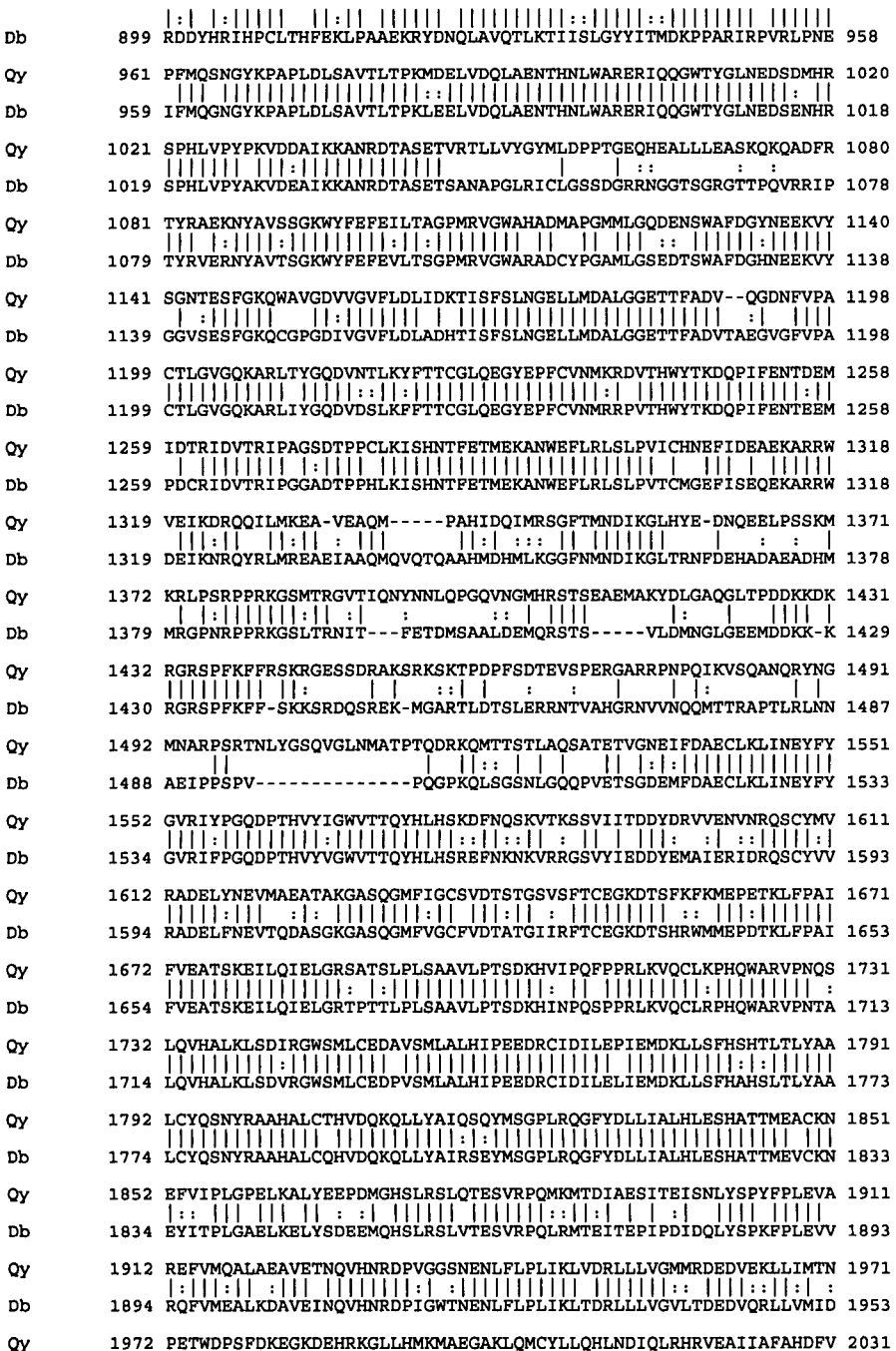
Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              |::|:|||||||||||:|||||||||||||:|||||||||:||||||||||||||:||
Db        659 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 718

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              |||:||:||||| |     |||:|||||||:||:|||| | ||||:| ||| :|||:
Db        719 DGAFLWTGGRKTLVVDALPEEPPIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 778

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||:|||||||||| ||:||||::| | |:| ||: |:|||||:|||||||:|
Db        779 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 838

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              |||| |::||||||| ||||  :|||: |:||::|||||||||||:||||||| :|:
Db        839 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 898

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
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RESULT 14
US-10-668-767-56

; Sequence 56, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 5126
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-668-767-56

Query Match 78.3%; Score 12338; DB 4; Length 5126;
Best Local Similarity 77.9%; Pred. No. 0;
Matches 2359; Conservative 266; Mismatches 336; Indels 68; Gaps 22;

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Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:||||||:||||||||||:||||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
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Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||||| ||||||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |   |||||:|:||||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFSW-QEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
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Db        359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 418

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
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Db        419 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 478

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
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Db        479 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 538

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
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Db        539 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              |||||||||||||||||||||||||:|||||||||| |||||:|:|||||||||:|
Db        599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 658

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              |::|:|||||||||||||:|||||||||||||||:|||||||||:|||||||||||:||
Db        659 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 718

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
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Db        719 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 778

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||:|||||||||| ||:||||::| | |:| ||: |:|||||:|||||||:|
Db        779 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 838

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              |||| |::|||||| |||| :|||: |:||::|||||||||:||||||| :|:
Db        839 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 898

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              |:| |:|||||  ||:|| |||||| ||||||||||::|||||::|||||||| ||||||
Db        899 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 958

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              ||| ||||||||||||||||::|||||||||||||||||||||||||||||||||: ||
Db        959 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1018

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||| |||:|||||||||||||          |   | ::       : :
Db       1019 SPHLVPYAKVDEAIKKANRDTASETSANAPGLRICLGSSDGRRNGGTSGRGTTPQVRRIP 1078

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
              ||| |:|||:|||||||||:||:|||||||| ||  || ||| :: |||||:||||||
Db       1079 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNEEKVY 1138

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
              | :|||||   ||:||||||| | |||||||||||||||||||||||| :|  ||||
Db       1139 GGVSESFGKQCGPGDIVGVFLDLADHTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1198

Qy       1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPPCVNMKRDVTHWYTKDQPIFENTDEM 1258
              |||||||||| |||||::||:|||||||||||||||||:| |||||||||||||:||
Db       1199 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPPCVNMRRPVTHWYTKDQPIFENTEEM 1258

Qy       1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
              | |||||||| |:|||| |||||||||||||||||||||||||| |  ||| | ||||||
Db       1259 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1318

Qy       1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
              |||:||  ||:|| : |||       ||:| ::: || |||||||     |  :  |
Db       1319 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1378

Qy       1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
              | |:|||||:|| :|  :       :: | ||||       |:   |  |||| |
Db       1379 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1429

Qy       1432 RGRSPFKFPRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
              ||||||||| ||:     | |  ::| |  :  :   |  | |:      | |
Db       1430 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1487

Qy       1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
              ||                |  ||:: | | |   || |:|:|||||||||||||
Db       1488 AEIPPSPV-------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1533

Qy       1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
              ||||:|||||||:|||||||::||::|| : || | |||:  :| ::|||||:|
Db       1534 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1593

Qy       1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
              |||||:|||  :|: ||||||||:|| |||:|| : |||||||| :: |||:|||||||
Db       1594 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1653

Qy       1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
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Db       1654 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1713
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Qy       1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
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Db       1714 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1773

Qy       1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
             |||||||||||||| |||||||||||:|:|||||||||||||||||||||||||||||| |||
Db       1774 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1833

Qy       1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDI--------------AESITE 1897
             |:: ||| ||| || : :| |||||| |||||||::||:|              :| | :
Db       1834 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPD 1893

Qy       1898 ISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957
             |  |||| ||||| |:|||:|| :||| |||||||:| :||||||||||| |||||||:
Db       1894 IDQLYSPKFPLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1953

Qy       1958 MRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017
             : ||||::||:| :||||| :|::|||||||||| |||||||||||||| || | |||
Db       1954 LTDEDVQRLLVMIDPETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLR 2013

Qy       2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
             ||||:||||:||||||||||||| |||||||||||||||:|||||||||| || ||
Db       2014 HRVESIIAFSHDFVGDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFK 2073

Qy       2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYN 2136
             :|| :|:::|| || ||  |: :|||:||  |||:|||||  |     | | |   |:||
Db       2074 NLEPDDQDNCTCGLELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYN 2133

Qy       2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196
              |||||||| | :||| |||||| ||||||:|||:|||||||| ||||||||||:||
Db       2134 FINTVKELEEGPKEVEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQ 2193

Qy       2197 YDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2256
             || ||||:|||||||||| : : |||||||||||||||||||||||||||||||||||||
Db       2194 YDTVGELVRALEKTYVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2253

Qy       2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEM 2314
             | |||||||||:|||||||||||||:|||||||||| |:   |||   ||||||||||
Db       2254 NATFFQHPDLIRILRVHENVMAVMMNTIGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEM 2312

Qy       2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374
             |||||||||||||||||||||||||||||:|:||||:|||||||||||||||||||||||
Db       2313 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTE 2372

Qy       2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434
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Db       2373 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2432

Qy       2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493
             |||||||||||||||||||||||||||||| :|||:||:|||||:|| |::: | || :
Db       2433 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2491

Qy       2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551
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Db       2492 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARASLR 2551

Qy       2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611
             |||||||||||||:|||:  | |||:|||||||||:| :|||: |||||||||| |:||
Db       2552 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2611

Qy       2612 YKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASL 2671
             |:|||:||||||| ||:||::|| |||||:||||||||||||: ||||||||||
Db       2612 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2671

Qy       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731
             |||||||||||||||||||||||||||||||| |||:|||||||||||||||||||||||
Db       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2731

Qy       2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791
             |||||||||::|||||||||  |||::|||||||||||:|||||||||| |||:|||||
Db       2732 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2790

Qy       2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851
             |||||||||||||||||||||||||||||||| |:::||::  |   | ||| | ||:|::| |:||||:
Db       2791 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2848

Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
             :|||||||||||||::| || ||:  ||: : |||||||||::||:|||::|||| |
Db       2849 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2908

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969
             | ||||||:||||||::| |:| | |||||     |:|    :  :||:||||||||:||
Db       2909 KGLLAIGWTVEHSEVEVPLNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2963

Qy       2970 TLSREMQNMAERLADNAHDIWAKKKKEEL 2998
             |||||||||||||:|:|||||||| |||
Db       2964 TLSREMQNMAERLAENSHDIWAKKKNEEL 2992


RESULT 15
US-10-668-767-124
; Sequence 124, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
;   LENGTH: 5126
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: gi 2160476
US-10-668-767-124

  Query Match             78.3%;  Score 12338;  DB 4;  Length 5126;
  Best Local Similarity   77.9%;  Pred. No. 0;
  Matches 2359;  Conservative  266;  Mismatches  336;  Indels   68;  Gaps   22;

Qy         1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
             ||||||| |||||||||||||| |||||||||||||||||||||||||||||:||||
Db         1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

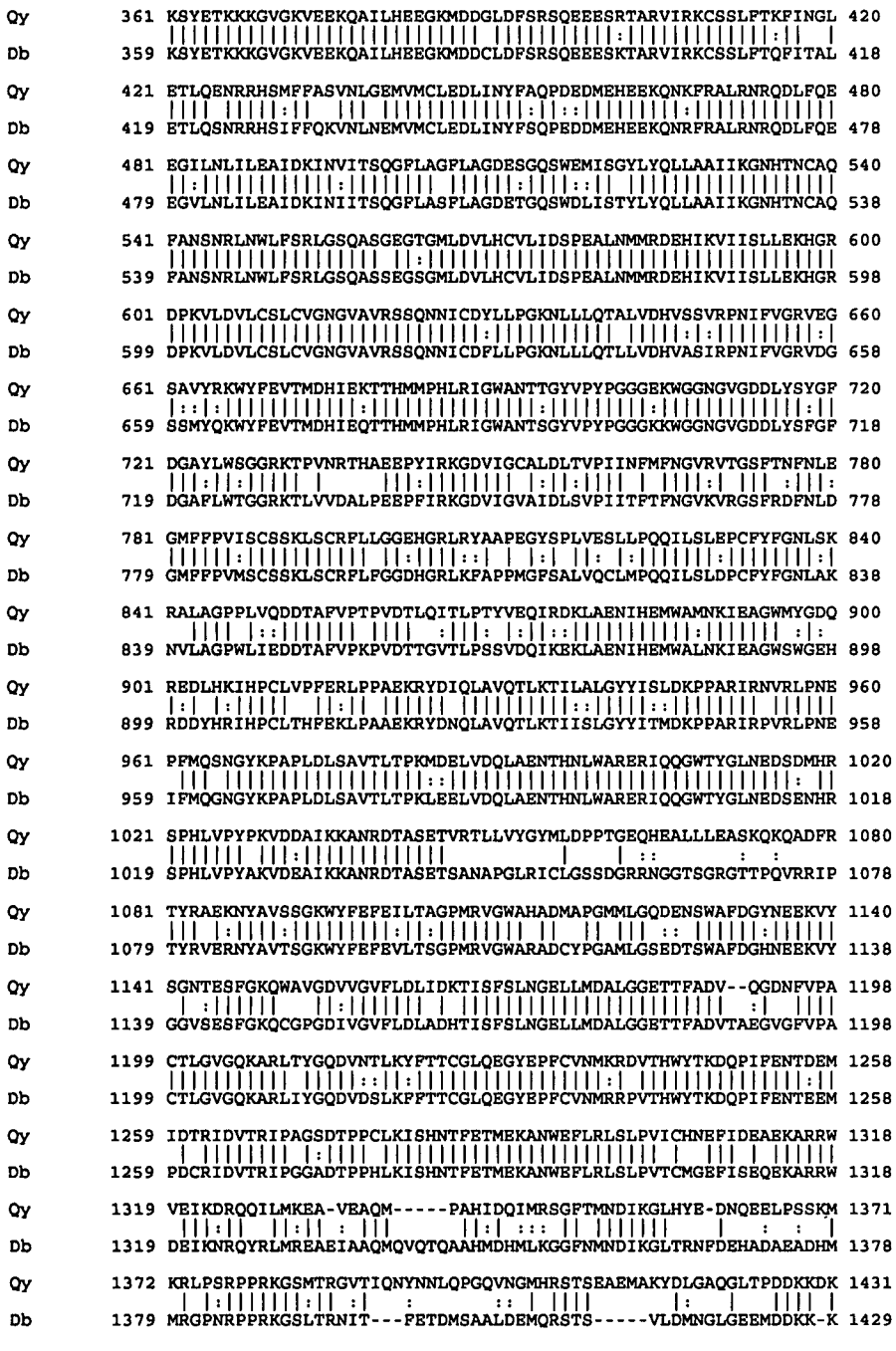
Qy        61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy       121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
             ||| |||:||||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db       120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy       181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
             ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db       180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy       241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
             |||||:|||| ||:|||||||||||||| |||||||||||||||||||||||| |||
Db       240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy       301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
             || :|||: |:  |   |||||:|:|||||||||:|||||||:|||||| || |||||
Db       300 LVKKEEASIATTTFSW-QEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358
```


Qy 361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db 359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 418
Qy 421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db 419 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 478
Qy 481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db 479 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 538
Qy 541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db 539 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598
Qy 601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db 599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 658
Qy 661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db 659 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 718
Qy 721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db 719 DGAFLWTGGRKTLVVDALPEEPPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 778
Qy 781 GMFPPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db 779 GMFPPVMSCSSKLSCRFLPGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 838
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 839 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 898
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 899 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 958
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db 959 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1018
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1019 SPHLVPYAKVDEAIKKANRDTASETSANAPGLRICLGSSDGRRNGGTSGRGTTPQVRRIP 1078
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1079 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNEEKVY 1138
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db 1139 GGVSESFGKQCGPGDIVGVFLDLADHTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1198
Qy 1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db 1199 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1258
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db 1259 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1318
Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGPTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1319 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1378
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1379 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1429
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1430 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1487
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1488 AEIPPSPV----------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1533
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1534 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1593
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1594 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1653
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1654 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1713
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1714 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1773
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1774 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1833
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDI----------AESITE 1897
Db 1834 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPD 1893
Qy 1898 ISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957
Db 1894 IDQLYSPKFPLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1953
Qy 1958 MRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017
Db 1954 LTDEDVQRLLVMIDPETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLR 2013
Qy 2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db 2014 HRVESIIAFSHDFVGDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFK 2073
Qy 2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYN 2136
Db 2074 NLEPDDQDNCTCGLELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYN 2133
Qy 2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196
Db 2134 FINTVKELEEGPKEVEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQ 2193
Qy 2197 YDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2256
Db 2194 YDTVGELVRALEKTYVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2253
Qy 2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEM 2314
Db 2254 NATFFQHPDLIRILRVHENVMAVMMNTIGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEM 2312
Qy 2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374
Db 2313 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTE 2372
Qy 2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434
Db 2373 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2432
Qy 2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493
Db 2433 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2491
Qy 2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551

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Db       2492 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARASLR 2551

Qy       2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611

Db       2552 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2611

Qy       2612 YKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASL 2671

Db       2612 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2671

Qy       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731

Db       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2731

Qy       2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791

Db       2732 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2790

Qy       2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851

Db       2791 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2848

Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911

Db       2849 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2908

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969

Db       2909 KGLLAIGWTVEHSEVEVPLNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2963

Qy       2970 TLSREMQNMAERLADNAHDIWAKKKKEEL 2998

Db       2964 TLSREMQNMAERLAENSHDIWAKKKNEEL 2992


Search completed: April 14, 2006, 01:48:46
Job time : 307 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 14, 2006, 01:28:43 ; Search time 417 Seconds
(without alignments)
5075.743 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Perfect score: 15748
Sequence: 1 MAEAEGGASEQDDVSFLRTE.....RLADNAHDIWAKKKKEELVT 3000

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	12581	79.9	5105	2	Q7PMK5_ANOGA	Q7pmk5 anopheles g
2	12518	79.5	5105	2	Q7PJQ9_ANOGA	Q7pjq9 anopheles g
3	12473.5	79.2	5127	1	RY44_DROME	Q24498 drosophila
4	7214	45.8	5071	2	P91905_CAEEL	P91905 caenorhabdi
5	7078.5	44.9	5207	2	Q60WP5_CAEBR	Q60wp5 caenorhabdi
6	6986.5	44.4	5317	2	Q8TA74_HEMPU	Q8ta74 hemicentrot
7	6828	43.4	5107	2	Q94279_CAEEL	Q94279 caenorhabdi
8	6778	43.0	4968	2	Q29621_RABIT	Q29621 oryctolagus
9	6770.5	43.0	4969	1	RYR2_RABIT	P30957 oryctolagus
10	6769	43.0	4967	1	RYR2_HUMAN	Q92736 homo sapien
11	6769	43.0	4967	2	Q546N8_HUMAN	Q546n8 homo sapien
12	6758	42.9	4967	2	Q9ERN6_MOUSE	Q9ern6 mus musculu
13	6566.5	41.7	4965	2	Q5VWP1_HUMAN	Q5vwp1 homo sapien
14	6534.5	41.5	5037	2	Q91313_RANCA	Q91313 rana catesb
15	6453.5	41.0	5035	1	RYR1_PIG	P16960 sus scrofa
16	6453.5	41.0	5035	2	Q29105_PIG	Q29105 sus scrofa
17	6452.5	41.0	5035	2	Q80X16_MOUSE	Q80x16 mus musculu
18	6449.5	41.0	4859	2	Q95201_MUSVI	Q95201 mustela vis
19	6445.5	40.9	5035	2	Q29104_PIG	Q29104 sus scrofa
20	6443	40.9	5038	1	RYR1_HUMAN	P21817 homo sapien
21	6439	40.9	5037	1	RYR1_RABIT	P11716 oryctolagus
22	6438.5	40.9	4859	2	Q7M2T9_9CARN	Q7m2t9 mustela sp.
23	6434.5	40.9	4870	1	RYR3_HUMAN	Q15413 homo sapien
24	6422	40.8	4869	2	Q90985_CHICK	Q90985 gallus gall
25	6415	40.7	4868	2	Q91319_RANCA	Q91319 rana catesb
26	6413	40.7	4872	2	Q9TS33_RABIT	Q9ts33 oryctolagus
27	6275	39.8	5081	2	O13054_MAKNI	O13054 makaira nig
28	6169.5	39.2	4864	2	Q5RGQ4_BRARE	Q5rgq4 brachydanio
29	6146	39.0	3398	1	Q4RLR0_TETNG	Q4rlr0 tetraodon n
30	5964	37.9	4910	2	Q4SFN5_TETNG	Q4sfn5 tetraodon n
31	5555.5	35.3	4833	2	Q4RNG0_TETNG	Q4rng0 tetraodon n
32	4937	31.4	4251	2	Q4RFS4_TETNG	Q4rfs4 tetraodon n
33	4854	30.8	3383	2	Q4S750_TETNG	Q4s750 tetraodon n
34	2998.5	19.0	1128	2	P79271_PIG	P79271 sus scrofa
35	2800.5	17.8	1020	2	Q80ZZ5_MOUSE	Q80zz5 mus musculu
36	1805	11.5	1135	2	Q4T5B8_TETNG	Q4t5b8 tetraodon n
37	1564.5	9.9	597	2	Q95LG7_CANFA	Q95lg7 canis famil
38	1495	9.5	671	2	Q95LG6_CANFA	Q95lg6 canis famil
39	1379.5	8.8	2583	2	Q4S752_TETNG	Q4s752 tetraodon n
40	1318.5	8.4	763	2	Q4T4U8_TETNG	Q4t4u8 tetraodon n
41	1062.5	6.7	487	2	Q4SYB3_TETNG	Q4syb3 tetraodon n
42	1035	6.6	379	2	Q99JF9_MOUSE	Q99jf9 mus musculu
43	772	4.9	329	2	Q4R606_MACFA	Q4r606 macaca fasc
44	603	3.8	239	2	Q6UC92_MELGA	Q6uc92 meleagris g
45	553.5	3.5	497	2	Q4T7D1_TETNG	Q4t7d1 tetraodon n

ALIGNMENTS

RESULT 1
Q7PMK5_ANOGA
ID Q7PMK5_ANOGA PRELIMINARY; PRT; 5105 AA.
AC Q7PMK5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000019607.
GN ORFNames=ENSANGG00000017118;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008979; EAA13701.3; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005262; F:calcium channel activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR000699; Ca-rel_channel.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003608; MIR.
DR InterPro; IPR003032; Ryanodine_recept.
DR InterPro; IPR001215; Ryanodn_receptor.
DR InterPro; IPR009460; Ryanrecept_TM4-6.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02815; MIR; 1.
DR Pfam; PF06459; RR_TM4-6; 1.
DR Pfam; PF01365; RYDR_ITPR; 2.
DR Pfam; PF02026; RyR; 4.
DR Pfam; PF00622; SPRY; 3.
DR PRINTS; PR00795; RYANODINER.
DR ProDom; PD000012; EF-hand; 1.

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DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50919; MIR; 5.
SQ   SEQUENCE   5105 AA;  577467 MW;  216B209E723AD77A CRC64;

  Query Match           79.9%;  Score 12581;  DB 2;  Length 5105;
  Best Local Similarity   79.2%;  Pred. No. 0;
  Matches 2400;  Conservative  251;  Mismatches  293;  Indels   88;  Gaps   24;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGG-SEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHNNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:|||||:|||||||||:||||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||::|||||||||||||||||||||||||||||||||||||||||||||||||||||: |
Db        180 ENDLSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWSLDS 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              ||||||||||||||||||||||||||||||||||| |||||||:|||||||||: |||
Db        240 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWSHPMRIRHLTTGRYLGVNENNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              |:||::|||:  || || |||||| |||||||:|||||||||||||:|| |:|||:||
Db        300 LMSRDQATTSQTAFVLRLEKDDQKVVLEDKDLEIIGAPIIKYGDSTVIMQHYESGLWVSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFISGL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              ||||||||||:|  :|||||||||||||||||::|||||||||: ||||||||||||
Db        420 ETLQENRRHSIFLQTVNLGEMVMCLEDLINYFAQPEDDMEHEEKQNRLRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||:|||||||||||:|||| ||| |||||||:|||||||||||||||||||||||||||
Db        480 EGVLNLILEAIDKINVISSQGFLASFLASDESGQSWDMISGYLYQLLAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              |||||||||||||||||| ||:|||||||||||||||||||||||||||||||||||||
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              |||||||||||||||||||||||||:|||||||||| |||||:|:||||||||||||||
Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTGLVDHVASIRPNIFVGRVEG 659

Qy        661 SAVYRKWYPEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              ||:|:|||||||||||: ||| |||||||| ||||||||||||||||||||||||:|||
Db        660 SAIYQKWYFEVTMDHIEQMTHMTPHLRIGWANTAGYVPYPGGGEKWGGNGVGDDLFSYGF 719

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              || | || ||:| |       ||:|:||||||| |||:||:| | |||  | | ||:|||:
Db        720 DGVYFWSAGRRTCVVPREVTEPPIKKGDVIGCTLDLSVPVIRFTFNGEPVQGCFTDFNLD 779

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||:|||||||||| ||::|||::  | |:|||: |:| | |||:|||||||:|
Db        780 GMFFPVMSCSSKLSCRFLFGGDNGRLKFNPPPGFSPLVQCLMPHQNLSLDPCFYFGNLNK 839

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              |||| ||:||:|||| ||||  :|||: || |:|||||||||||:|||||| :|::
Db        840 NVLAGPWLVEDDSAFVPKPVDTSIVTLPSSVETIKDKLAENIHEMWALNKIEAGWTWGER 899

Qy        901 REDLHKIHPCLVPPERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              |:|:::|||||  ||:|| |||||| |||||||||||||||:|||||||| :||||:
Db        900 RDDVYRIHPCLTSFEKLPAAEKRYDCQLAVQTLKTILALGYYISMDKPPARIRPIRLPND 959

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              |:|| |||||||||||  |||||:||||||||||||||:|||||||||||||:  |
Db        960 PYMQGNGYKPAPLDLSAAVLTPKMEELVDQLAENTHNLWAKERIQQGWTYGLNEDSENLR 1019

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||| |||:|||||||||||||||||:||| ||||||| :|||  || :|| | :|
Db       1020 SPHLVPYSKVDEAIKKANRDTASETVRTLLIYGYNLDPPTGEANEALAAEALRQKFAAYR 1079

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
              ||| |: |||:|||||||:|||||||||| ||  || ||| |: |||||||||||
Db       1080 TYRVERTYAVTSGKWYFEFEVLTAGPMRVGWARADCNPGTMLGSDDASWAFDGYNEEKVS 1139

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV---QGDNFVP 1197
                | |||||||  ||:||||||:| ||||||||||||||||||||||    |  |||
Db       1140 GGATESFGKQWVPGDIVGVFLDLVDHTISFSLNGELLMDALGGETTFADVNAPDGVGFVP 1199

Qy       1198 ACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDE 1257
              |||:|:|||||: |||||::||:|||||||||||||||||| ||||||||||||||||
Db       1200 ACTIGIGQKARVVYGQDVDSLKWFTTCGLQEGYEPFCVNMKRPVTHWYTKDQPIFENTDE 1259

Qy       1258 MIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARR 1317
              : : :|||||| |:|||||:|||||||||||||||||||||||| | | || | || ||
Db       1260 IPECKIDVTRIPGGADTPPCMKISHNTFETMEKANWEFLRLSLPVTCANTFITEQEKMRR 1319

Qy       1318 WVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKM----KR 1373
              | ||: ||  || | |:   ||| | |||||||||||||   :::   : :|    |
Db       1320 WEEIRIRQHRLMTE-VDHSAPAHFDHIMRSGFTMNDIKGLHRNYSEDAAEADEMMRNGPR 1378

Qy       1374 LPSRPPRKGSMTRGVTIQNYNNLQPG-QVNGMHRSTSEAEMAKY-DLGAQGLTPDDKKDK 1431
              |||   :| ::            || ::||   :||: |:  | |   :|   ||:| |
Db       1379 RPSRHQGRGGLS----------PPGIEING--EATSDGELNAYSDNELEG--GDDRK-K 1422

Qy       1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
              ||||||: |  || :| |: | |::  |:|                |: |  :||:|     |
Db       1423 RGRSPFRLFGKKRDQSKDKLKDRRTPEPEP-----------RKSN--LKVTQ-----RG 1463

Qy       1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
                | | ::|          |  | :|| |          |: |||::||:||:|||||||
Db       1464 QATRMSNSDLRA------QAPLTPERKGM-----GSPQVESFGNEVYDADCLRLINEYFY 1512

Qy       1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
              ||||:|||||||||:|||||||||:|||:|:|:||  ::: : |: :: :| |||||||||
Db       1513 GVRIFPGQDPTHVYVGWVTTQYHVHSKEFSQNKVRHAAIYVEDENEKTIEIVNRQSCYMV 1572

Qy       1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
              |||||:|||  ::: |||||||||:|| |||:||:: ||||||:||  | |||:||||||
Db       1573 RADELFNEVTQDSSGKGASQGMFVGCFVDTATGTIRFTCEGKETSHVFLMEPDTKLFPAI 1632

Qy       1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
              |||||||||||||||: |:|||||||||||||: |||||||||||||||||||||||| :
Db       1633 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQFPPRLKVQCLKPHQWARVPNTA 1692

Qy       1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
              |||||||||||||||||| |||||||||||||||||| ||:|:|| ||:||||||:|
Db       1693 LQVHALKLSDIRGWSMLCEDPVSMLALHIPEEDRCIDILELIEIDRLLQFHAHTLTLYSA 1752

Qy       1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
              |||||||||||||:|||||||||:|||||| |||||||:|||||||||| |||
Db       1753 LCYQSNYRAAHALCSHVDQKQLLYAIQSEYMSGPLRLGFYDLLISLHLESHATTMEVCKN 1812

Qy       1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIA----------------E 1893
              |::|||| ||: || :|:| |||||||| ||||:| ||:||                |
Db       1813 EYIIPLGSELRELYIDPEMCHSLRSLQTLSVRPEMNMTEIAPTPSQSNMPTIVAPDSSSE 1872

Qy       1894 SITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLL 1953
                | | :|||| ||||| ||||| || |||: |||||||:|||||||||||:||||
Db       1873 PIPAIDSLYSPRFPLEVVREFVMSALQEAVQINQVHNRDPIGGSNENLFLPLIKLIDRLL 1932

Qy       1954 LVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLND 2013
              |||:: :|||||||| :|||||||:|||:|||||||| |||||||||||||| || |
Db       1933 LVGVITNEDVEKLLIMIDPETWDPSFEKEGRDEHRKGLLTMKMAEGAKLQMCYLLHHLYD 1992

Qy       2014 IQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAI 2073
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Db       1993 VQLRHRVESIIAFAHNYVGDLQQDQLRRYIEIKQSDLPSAVAAKKTREFRCPPREQMNAI 2052

Qy       2074 LSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAE-NQEPEAKPGAFG 2132

Db       2053 LGYKNLEEDDLENASCGPELRNRLIEFHEKLMGKVSLNALQEPEEPEADKLEEGRPGAMK 2112

Qy       2133 KLYNIINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSL 2192

Db       2113 KLYNFINAVKELEEDPKEPVEEEKKTPEEVFRKVLIKQLVSWAEESQIENPKLVREMFGL 2172

Qy       2193 LVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLW 2252

Db       2173 LVRQYDTIGELIKALNKTYVINSKTKGDVANMWIGLSQIRALLPVQMSQEEEELMRKRLW 2232

Qy       2253 KLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDS--KEKDT 2310

Db       2233 KLVNNHTFFQHPDLIRILRVHENVMAVMMNTLGRRAQAQSDA-PVQTADGEESAPKEKDT 2291

Qy       2311 SHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLM 2370

Db       2292 SHQMVVACCRFLCYFCRTGRMNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLM 2351

Qy       2371 ENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRPCVWV 2430

Db       2352 ENTELALALREHYLEKIAIYLSRCGLQSNSELIERGYPDLGWDPVEGERYLDFLRPCVWV 2411

Qy       2431 NGESVEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQE 2490

Db       2412 NGESVEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERISERRKMQD-EAE 2470

Qy       2491 GDV---NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRAR 2547

Db       2471 GTITGLNFSHPLPEGDDDEDYIDTGAAILCFYCTLVDLLGRCAPDAAVIEQGKNESLRAR 2530

Qy       2548 AILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIET 2607

Db       2531 AILRSLVPLEDLQGVLSLKFTLTNPALGEDRPKSDMPSGLVPGHKQSIVLFLERVYGIET 2590

Qy       2608 QELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAEN 2667

Db       2591 QELFYRLLEDAFLPDLRAATMLDRSDGSESDMALSMNRYIGNSILPLLIKHSKFYNEAEN 2650

Qy       2668 YASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLS 2727

Db       2651 YASLLDATLHTVYRMSKNRMLTKGQREAVSDFLVALTSAMHPAMLLKLLRKLTIDVSKLS 2710

Qy       2728 EYTTVALRLLTLHYERCAKYYGSTGAGQGA-FGASSDEEKRLTMMLFSNIFDSLSKMDYE 2786

Db       2711 EYTTVALRLLTLHYERCAKYYGTTGGGQASQFGASSDEEKRLTMLLFSNIFDSLSNMDYD 2770

Qy       2787 PELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALN 2846

Db       2771 PELFGKALPCLIAIGCALPPDYSLSKNSDDDLYGKPTGGGP-DQPHYNPQPIDTTAVQLT 2829

Qy       2847 NDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEP 2906

Db       2830 NDLNQIVQKFSEHYHDAWASRKLENGWTYGDQWSDANKTHPRLKPYNTLSEYERERYREP 2889

Qy       2907 VRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDM 2966

Db       2890 VRESLKALLALHWRIEHSEGDVPLSNRGSMRRQSKPN---LELQGDTGSPFNYNPHPVDM 2946

Qy       2967 TNLTLSREMQNMAERLADNAHDIWAKKKKEEL 2998

Db       2947 TNLTLSREMQNMAERLAENSHDIWAKKKNEEL 2978


RESULT 2
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ID   Q7PJQ9_ANOGA PRELIMINARY;      PRT;  5105 AA.
AC   Q7PJQ9;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000023306.
GN   ORFNames=ENSANGG00000017118;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008979; EAA43660.2; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005262; F:calcium channel activity; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR   GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50919; MIR; 5.
SQ   SEQUENCE   5105 AA;  577811 MW;  75604F82F3AB3692 CRC64;

  Query Match           79.5%;  Score 12518;  DB 2;  Length 5105;
  Best Local Similarity   78.7%;  Pred. No. 0;
  Matches 2385;  Conservative  262;  Mismatches  297;  Indels   88;  Gaps   24;

Qy         1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Db         1 MAEAEGG-SEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 59

Qy        61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

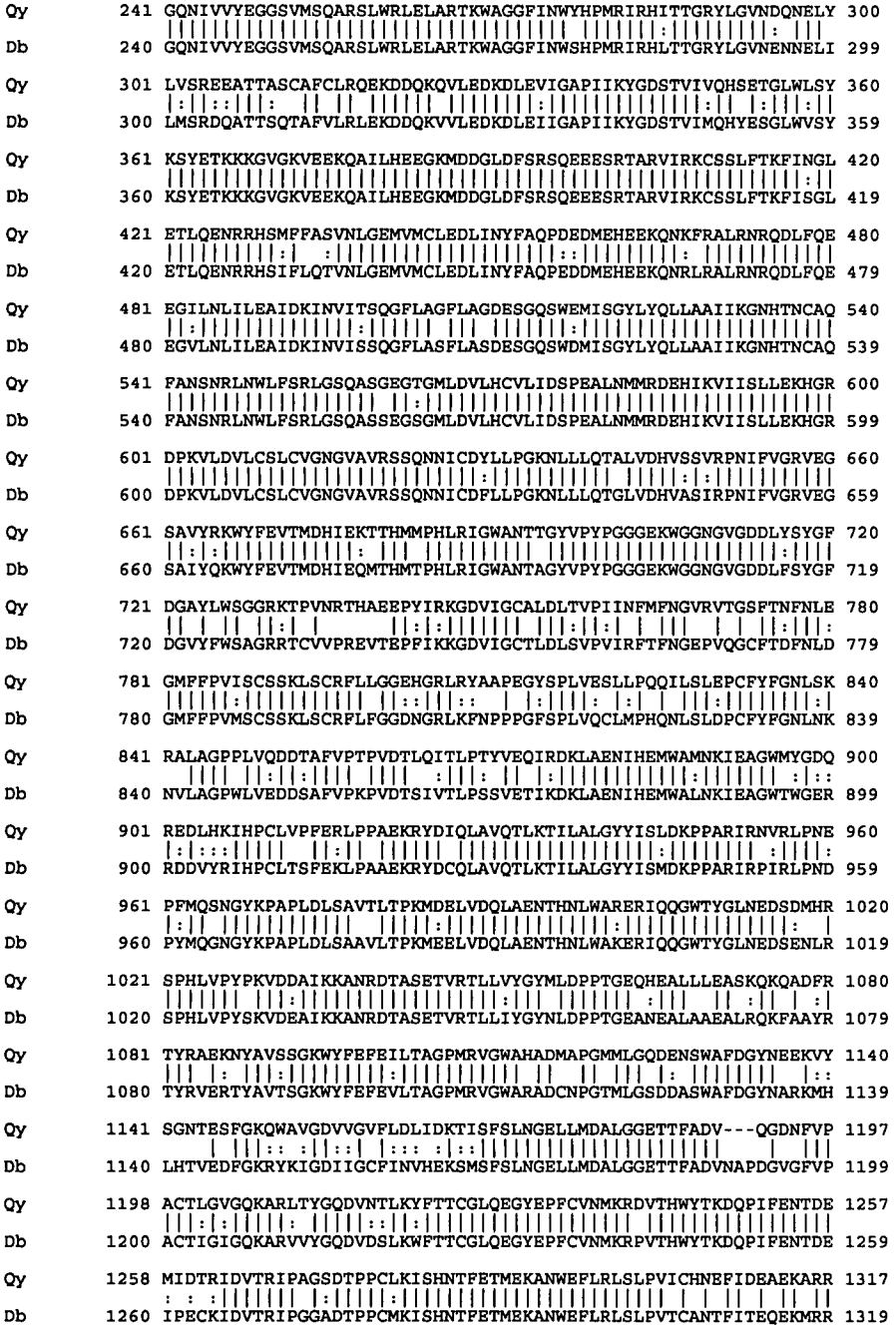
Db        60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHNNSDMYLACLST 119

Qy       121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Db       120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy       181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240

Db       180 ENDLSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWSLDS 239
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Qy 241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db 240 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWSHPMRIRHLTTGRYLGVNENNELI 299
Qy 301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db 300 LMSRDQATTSQTAFVLRLEKDDQKVVLEDKDLEIIGAPIIKYGDSTVIMQHYESGLWVSY 359
Qy 361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db 360 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFISGL 419
Qy 421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db 420 ETLQENRRHSIFLQTVNLGEMVMCLEDLINYFAQPEDDMEHEEKQNRLRALRNRQDLFQE 479
Qy 481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db 480 EGVLNLILEAIDKINVISSQGFLASFLASDESGQSWDMISGYLYQLLAAIIKGNHTNCAQ 539
Qy 541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db 540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599
Qy 601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db 600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTGLVDHVASIRPNIFVGRVEG 659
Qy 661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db 660 SAIYQKWYFEVTMDHIEQMTHMTPHLRIGWANTAGYVPYPGGGEKWGGNGVGDDLFSYGF 719
Qy 721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db 720 DGVYFWSAGRRTCVVPREVTEPPIKKGDVIGCTLDLSVPVIRFTFNGEPVQGCFTDFNLD 779
Qy 781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db 780 GMFFPVMSCSSKLSCRFLFGGDNGRLKFNPPPGFSPLVQCLMPHQNLSLDPCFYFGNLNK 839
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 840 NVLAGPWLVEDDSAFVPKPVDTSIVTLPSSVETIKDKLAENIHEMWALNKIEAGWTWGER 899
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 900 RDDVYRIHPCLTSFEKLPAAEKRYDCQLAVQTLKTILALGYYISMDKPPARIRPIRLPND 959
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db 960 PYMQGNGYKPAPLDLSAAVLTPKMEELVDQLAENTHNLWAKERIQQGWTYGLNEDSENLR 1019
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1020 SPHLVPYSKVDEAIKKANRDTASETVRTLLIYGYNLDPPTGEANEALAAEALRQKFAAYR 1079
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1080 TYRVERTYAVTSGKWYFEFEVLTAGPMRVGWARADCNPGTMLGSDDASWAFDGYNARKMH 1139
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV---QGDNFVP 1197
Db 1140 LHTVEDFGKRYKIGDIIGCFINVHEKSMSFSLNGELLMDALGGETTFADVNAPDGVGFVP 1199
Qy 1198 ACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDE 1257
Db 1200 ACTIGIGQKARVVYGQDVDSLKWFTTCGLQEGYEPFCVNMKRPVTHWYTKDQPIFENTDE 1259
Qy 1258 MIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARR 1317
Db 1260 IPECKIDVTRIPGGADTPPCMKISHNTFETMEKANWEFLRLSLPVTCANTFITEQEKMRR 1319
Qy 1318 WVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKM----KR 1373
Db 1320 WEEIRIRQHRLMTE-VDHSAPAHFDHIMRSGFTMNDIKGLHRNYSEDAAEADEMMRNGPR 1378
Qy 1374 LPSRPPRKGSMTRGVTIQNYNNLQPG-QVNGMHRSTSEAEMAKY-DLGAQGLTPDDKKDK 1431
Db 1379 RPSRHQGRGGLS----------PPGIEING--EATSDGELNAYSDNELEG--GDDRK-K 1422
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1423 RGRSPFRLFGKKRDQSKDKLKDRRTPEPEP----------RKSN--LKVTQ-----RG 1463
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1464 QATRMSNSDLRA------QAPLTPERKGM-----GSPQVESFGNEVYDADCLRLINEYFY 1512
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1513 GVRIFPGQDPTHVYVGWVTTQYHVHSKEFSQNKVRHAAIYVEDENEKTIEIVNRQSCYMV 1572
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1573 RADELFNEVTQDSSGKGASQGMFVGCFVDTATGTIRFTCEGKETSHVFLMEPDTKLFPAI 1632
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1633 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQFPPRLKVQCLKPHQWARVPNTA 1692
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1693 LQVHALKLSDIRGWSMLCEDPVSMLALHIPEEDRCIDILELIEIDRLLQFHAHTLTLYSA 1752
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1753 LCYQSNYRAAHALCSHVDQKQLLYAIQSEYMSGPLRLGFYDLLISLHLESHATTMEVCKN 1812
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIA----------------E 1893
Db 1813 EYIIPLGSELRELYIDPEMCHSLRSLQTLSVRPEMNMTEIAPTPSQSNMPTIVAPDSSSE 1872
Qy 1894 SITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLL 1953
Db 1873 PIPAIDSLYSPRFPLEVVREFVMSALQEAVQINQVHNRDPIGGSNENLFLPLIKLIDRLL 1932
Qy 1954 LVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLND 2013
Db 1933 LVGVITNEDVEKLLIMIDPETWDPSFEKEGRDEHRKGLLTMKMAEGAKLQMCYLLHHLYD 1992
Qy 2014 IQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAI 2073
Db 1993 VQLRHRVESIIAFAHNYVGDLQQDQLRRYIEIKQSDLPSAVAAKKTREFRCPPREQMNAI 2052
Qy 2074 LSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAE-NQEPEAKPGAFG 2132
Db 2053 LGYKNLEEDDLENASCGPELRNRLIEFHEKLMGKVSLNALQEPEEPEADKLEEGRPGAMK 2112
Qy 2133 KLYNIINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSL 2192
Db 2113 KLYNFINAVKELEEDPKEPVEEEKKTPEEVFRKVLIKQLVSWAEESQIENPKLVREMFGL 2172
Qy 2193 LVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLW 2252
Db 2173 LVRQYDTIGELIKALNKTYVINSKTKGDVANMWIGLSQIRALLPVQMSQEEEELMRKRLW 2232
Qy 2253 KLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDS--KEKDT 2310
Db 2233 KLVNNHTFFQHPDLIRILRVHENVMAVMMNTLGRRAQAQSDA-PVQTADGEESAPKEKDT 2291
Qy 2311 SHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLM 2370
Db 2292 SHQMVVACCRFLCYFCRTGRMNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLM 2351
Qy 2371 ENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWV 2430

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                    |||||||||||||||||:|||||||||||||:|:|||||||||||||||||||||||||
Db       2352 ENTELALALREHYLEKIAIYLSRCGLQSNSELIERGYPDLGWDPVEGERYLDFLRFCVWV 2411

Qy       2431 NGESVEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQE 2490
                    |||||||||||||||||||||||||||||||||||||||||||||||::|||::: | |
Db       2412 NGESVEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERISERRKMQD-EAE 2470

Qy       2491 GDV---NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRAR 2547
                |  :   |||||||| |:|||||||||||| |||||||||||||||| ||  |||||||||
Db       2471 GTITGLNFSHPLPEGDDDEDYIDTGAAILCFYCTLVDLLGRCAPDAAVIEQGKNESLRAR 2530

Qy       2548 AILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIET 2607
                    |||||||||||||||||:||| ||| ||:||||||||||:||||||: ||||||||||
Db       2531 AILRSLVPLEDLQGVLSLKFTLTNPALGEDRPKSDMPSGLVPGHKQSIVLFLERVYGIET 2590

Qy       2608 QELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAEN 2667
                    |||||:|||:|||||||||||||||:|| |||||||||||||||||||||||: |||||||
Db       2591 QELFYRLLEDAFLPDLRAATMLDRSDGSESDMALSMNRYIGNSILPLLIKHSKFYNEAEN 2650

Qy       2668 YASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLS 2727
                    |||||||||||||:|||||||||||||||||||||||||| |:||||||||||:||||||
Db       2651 YASLLDATLHTVYRMSKNRMLTKGQREAVSDFLVALTSAMHPAMLLKLLRKLTIDVSKLS 2710

Qy       2728 EYTTVALRLLTLHYERCAKYYGSTGAGQGA-FGASSDEEKRLTMMLFSNIFDSLSKMDYE 2786
                    |||||||||||||||||||:|| || : |||||||||||||:|||||||||| |||:
Db       2711 EYTTVALRLLTLHYERCAKYYGTTGGGQASQFGASSDEEKRLTMLLFSNIFDSLSNMDYD 2770

Qy       2787 PELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALN 2846
                    |||||||||||||||||||||||||||||| ||: |||    |  | | |:||||:|::| | |
Db       2771 PELFGKALPCLIAIGCALPPDYSLSKNSDDDLYGKPTGGGP-DQPHYNPQPIDTTAVQLT 2829

Qy       2847 NDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEP 2906
                    |||| |||||||||||||||:|||| ||: |||: |||||||||| |::||:|||:||
Db       2830 NDLNQIVQKFSEHYHDAWASRKLENGWTYGDQWSDANKTHPRLKPYNTLSEYERERYREP 2889

Qy       2907 VRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDM 2966
                    ||||||||||: | :|||| |:| :|| |||||||      |:  |: :||:||||||||
Db       2890 VRESLKALLALHWRIEHSEGDVPLSNRGSMRRQSKPN---LELQGDTGSPFNYNPHPVDM 2946

Qy       2967 TNLTLSREMQNMAERLADNAHDIWAKKKKEEL 2998
                    |||||||||||||||:|:|||||||| |||
Db       2947 TNLTLSREMQNMAERLAENSHDIWAKKKNEEL 2978


RESULT 3
RY44_DROME
ID   RY44_DROME     STANDARD;      PRT;  5127 AA.
AC   Q24498; Q24321; Q24499; Q24500; Q24501; Q8MKS3; Q8MKS4; Q8MKS5;
AC   Q9V4Y7;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ryanodine receptor 44F.
GN   Name=Rya-r44F; Synonyms=dry, RyR; ORFNames=CG10844;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS A; B; C AND D), FUNCTION, TISSUE
RP   SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX   MEDLINE=94102409; PubMed=8276118; DOI=10.1016/0014-5793(94)80634-9;
RA   Takeshima H., Nishi M., Iwabe N., Miyata T., Hosoya T., Masai I.,
RA   Hotta Y.;
RT   "Isolation and characterization of a gene for a ryanodine
RT   receptor/calcium release channel in Drosophila melanogaster.";
RL   FEBS Lett. 337:81-87(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [3]
RP   GENOME REANNOTATION, AND ALTERNATIVE SPLICING.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 4619-5127, DEVELOPMENTAL STAGE, AND TISSUE
RP   SPECIFICITY.
RC   TISSUE=Brain;
RX   MEDLINE=93202018; PubMed=1338312;
RA   Hasan G., Rosbash M.;
RT   "Drosophila homologs of two mammalian intracellular Ca(2+)-release
RT   channels: identification and expression patterns of the inositol
RT   1,4,5-triphosphate and the ryanodine receptor genes.";
RL   Development 116:967-975(1992).
RN   [5]
RP   FUNCTION, AND TISSUE SPECIFICITY.
RX   MEDLINE=20283930; PubMed=10811919; DOI=10.1073/pnas.110145997;
RA   Sullivan K.M.C., Scott K., Zuker C.S., Rubin G.M.;
RT   "The ryanodine receptor is essential for larval development in
RT   Drosophila melanogaster.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:5942-5947(2000).
CC   -!- FUNCTION: Communication between transverse-tubules and
CC       sarcoplasmic reticulum. Contraction of muscle is triggered by
CC       release of calcium ions from SR following depolarization of T-
CC       tubules (By similarity).
CC   -!- FUNCTION: Intracellular calcium channel that is required for
CC       proper muscle function during embryonic development and may be
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CC       essential for excitation-contraction coupling in larval body wall
CC       muscles.
CC   -!- SUBUNIT: Homotetramer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=Q24498-2; Sequence=Displayed;
CC       Name=B;
CC         IsoId=Q24498-3; Sequence=VSP_050196;
CC       Name=C;
CC         IsoId=Q24498-4; Sequence=VSP_050195;
CC       Name=D;
CC         IsoId=Q24498-5; Sequence=VSP_050195, VSP_050196;
CC   -!- TISSUE SPECIFICITY: During embryonic stages 9-10, expression is
CC       seen in mesoderm of all segments in progenitors of the cephalic
CC       and somatic muscles. Adults exhibit high expression in tubular
CC       'jump' muscles of thorax and leg, and lower expression in the
CC       brain, ventral ganglion, head muscles and proboscis muscles.
CC   -!- DEVELOPMENTAL STAGE: Abundant in 6-12 hours embryos, reduced
CC       expression in second and third instar larval stages and adults.
CC   -!- MISCELLANEOUS: The calcium release channel is modulated by calcium
CC       ions, magnesium ions, ATP and calmodulin (By similarity).
CC   -!- MISCELLANEOUS: The calcium release channel activity resides in the
CC       C-terminal region while the remaining part of the protein
CC       constitutes the 'foot' structure spanning the junctional gap
CC       between the SR and the T-tubule. It is possible that the foot
CC       structure interacts with the cytoplasmic region of the
CC       dihydropyridine receptor (By similarity).
CC   -!- MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Ca-
CC       release channel in junctional SR and modulates its activity (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the ryanodine receptor family.
CC   -!- SIMILARITY: Contains 5 MIR domains.
CC   -!- SIMILARITY: Contains 3 SPRY domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; D17389; BAA04212.1; -; Genomic_DNA.
DR   EMBL; D17389; BAA41469.1; -; Genomic_DNA.
DR   EMBL; D17389; BAA41470.1; -; Genomic_DNA.
DR   EMBL; D17389; BAA41471.1; -; Genomic_DNA.
DR   EMBL; AE003835; AAF59036.2; -; Genomic_DNA.
DR   EMBL; AE003835; AAM71082.1; -; Genomic_DNA.
DR   EMBL; AE003835; AAM71083.1; -; Genomic_DNA.
DR   EMBL; AE003835; AAM71084.1; -; Genomic_DNA.
DR   EMBL; Z18536; CAA79221.1; -; mRNA.
DR   Ensembl; CG10844; Drosophila melanogaster.
DR   FlyBase; FBgn0011286; Rya-r44F.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; TAS.
DR   GO; GO:0006816; P:calcium ion transport; TAS.
DR   GO; GO:0006936; P:muscle contraction; IMP.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   PANTHER; PTHR13715:SF1; Ryanodn_receptor; 10.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   PROSITE; PS50919; MIR; 5.
KW   Alternative splicing; Calcium; Calcium channel; Calcium transport;
KW   Developmental protein; Glycoprotein; Ion transport; Ionic channel;
KW   Phosphorylation; Receptor; Repeat; Transmembrane; Transport.
FT   TOPO_DOM      1   3232       Cytoplasmic.
FT   TRANSMEM   3233   3253       M' (Potential).
FT   TRANSMEM   3301   3321       M'' (Potential).
FT   TRANSMEM   3376   3396       M1 (Potential).
FT   TRANSMEM   3963   3983       M2 (Potential).
FT   TRANSMEM   4452   4472       M3 (Potential).
FT   TRANSMEM   4651   4671       M4 (Potential).
FT   TRANSMEM   4683   4703       M5 (Potential).
FT   TRANSMEM   4742   4762       M5 (Potential).
FT   TRANSMEM   4885   4905       M5 (Potential).
FT   TRANSMEM   4924   4944       M8 (Potential).
FT   TRANSMEM   4963   4983       M9 (Potential).
FT   TRANSMEM   5004   5024       M10 (Potential).
FT   DOMAIN       94    148       MIR 1.
FT   DOMAIN      155    200       MIR 2.
FT   DOMAIN      210    264       MIR 3.
FT   DOMAIN      270    328       MIR 4.
FT   DOMAIN      336    394       MIR 5.
FT   DOMAIN      663    802       SPRY 1.
FT   REPEAT      845    956       1.

  Query Match             79.2%;  Score 12473.5;  DB 1;  Length 5127;
  Best Local Similarity   78.4%;  Pred. No. 0;
  Matches 2376;  Conservative  272;  Mismatches  314;  Indels   67;  Gaps   21;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||| |||||||||||||||| |||||||||||||||||||||||||||||:||||
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:||||||:|||||||||:||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||||| |||||||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |||||||||:|:||||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||||||||||||||||| |||||||||:|||||||||:||  |
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| |||||:|| ||| |||||||||||||:||::|||||||||:|||||||||||||
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||:|||||||||||:|||||||| |||||:||||::|| ||||||||||||||||||||
Db        480 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              |||||||||||||||||| ||:|||||||||||||||||||||||||||||||||||||
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
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```
Qy       2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851
             ||||||||||||||||||||||| |:::||::  |   | ||| | ||:|::| |:||||:
Db       2792 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2849

Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
              :|||||||||||||||::| || ||:  ||: : |||||||||::||:|||::|||| |
Db       2850 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2909

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969
              | ||||||:||||||::  |:| | |||||     |:|    :  :||:||||||||:|| 
Db       2910 KGLLAIGWTVEHSEVEVALNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2964

Qy       2970 TLSREMQNMAERLADNAHDIWAKKKKEEL 2998
              |||||||||||||:|:|||||||| |||
Db       2965 TLSREMQNMAERLAENSHDIWAKKKNEEL 2993
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RESULT 4
P91905_CAEEL
ID P91905_CAEEL PRELIMINARY; PRT; 5071 AA.
AC P91905;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ryanodine receptor.
GN Name=ryr-1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Bristol N2;
RX MEDLINE=97280790; PubMed=9135117; DOI=10.1006/jmbi.1997.0910;
RA Sakube Y., Ando H., Kagawa H.;
RT "An abnormal ketamine response in mutants defective in the ryanodine
RT receptor gene ryr-1 (unc-68) of Caenorhabditis elegans.";
RL J. Mol. Biol. 267:849-864(1997).
DR EMBL; D45899; BAA08309.1; -; Genomic_DNA.
DR HSSP; P09860; 1DTL.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005262; F:calcium channel activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoxygenase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000699; Ca-rel_channel.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002202; HMG-CoA_red.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR003608; MIR.
DR InterPro; IPR003032; Ryanodine_recept.
DR InterPro; IPR001215; Ryanodn_receptor.
DR InterPro; IPR009460; Ryanrecept_TM4-6.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00036; efhand; 2.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF02815; MIR; 1.
DR Pfam; PF06459; RR_TM4-6; 1.
DR Pfam; PF01365; RYDR_ITPR; 2.
DR Pfam; PF02026; RyR; 4.
DR Pfam; PF00622; SPRY; 3.
DR PRINTS; PR00795; RYANODINER.
DR SMART; SM00054; EFh; 2.
DR SMART; SM00472; MIR; 4.
DR SMART; SM00449; SPRY; 3.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00066; HMG_COA_REDUCTASE_1; UNKNOWN_1.
DR PROSITE; PS50919; MIR; 5.
KW Receptor.
SQ SEQUENCE 5071 AA; 576357 MW; 145EF32288613324 CRC64;

 Query Match 45.8%; Score 7214; DB 2; Length 5071;
 Best Local Similarity 47.2%; Pred. No. 0;
 Matches 1462; Conservative 539; Mismatches 881; Indels 218; Gaps 51;

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Qy          5 EGGASEQDDVSFLRTEDMVCLSCTAT--------GERVCLAAEGFGNRHCFLENIADKNI 56
              | |  |||||||||| |:|||| |:          |||||  |||||| | |||::||:| 
Db          6 EQGGGEQDDVSFLRTGDIVCLSCVASHNRDGVLGSERVCLCTEGFGNRMCTLENVSDKDI 65

Qy         57 PPDLSQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLA 116
              |||:: |:  |: |||:|||||:::|           ||:|||||:|: |:|: |:|||| 
Db         66 PPDIAMCMLYIDNALSMRALQEMMSADSDHKSASGAGGHKTLLYGHAVQLKHVQSEMYLA 125

Qy        117 CLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYL 176
              |||: || |||||||||:|: ::|||||||:|||||||||||||||||||:||||||||||| 
Db        126 CLSSCSSNDKLAFDVGVQETNEGEACWWTIHPASKQRSEGEKVRVGDDVILVSVATERYL 185

Qy        177 HTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTW 236
              |         :: |||| | |::|   :|  | : :|::|| |||| ||| |||||||  | 
Db        186 HMAYSKGYMVI-ASFHQTLWNIQSVSSGSMRTRNMGFLFGNDVLRLFHGNDECLTIPENW 244

Qy        237 TKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQ 296
              ::    |:|:|||||: ::|||||||:|| | || |  : |    ||:|||:|||||| | 
Db        245 SEHPQHNMVIYEGGAAVTQARSLWRVELIRMKWHGALVGWEQVFRIKHITSGRYLGVLD- 303

Qy        297 NELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGL 356
              | : |  :|:|      || : | || :||:|::|: | :|   |:||::   :|| :| | 
Db        304 NSVQLYHKEKADFDLTAFVMCQNKDPKKQMLDEKEEEGMGNATIRYGETNAFIQHVKTQL 363

Qy        357 WLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKF 416
              ||||:: |  |||:|||||:|:  ::| |||   |  : ||||::|||||||||:  || 
Db        364 WLSYQTTEVTKKGLGKVEEKKAVALKDGHMDDCYTFFMALEEESKSARVIRKCSSVLNKF 423

Qy        417 INGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQD 476
              : |:: ||     |  :  |:| |::  :|||| |||||::: : |||||  ||||:||| 
Db        424 LKGIDALQLEGNQSTDWTRVDLNEVLKLMEDLIEYFAQPNDEQDFEEKQNHLRALRSRQD 483

Qy        477 LFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHT 536
              ||||||:|:|:|: ||| : : :     || | |:|:   || || ||| |:||:|||| 
Db        484 LFQEEGVLNMILDTIDKFSQMEALPDFAG-LIGEETHVKWEQISTYLYLLVAAMIKGNHY 542

Qy        537 NCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLE 596
              ||||||:: ||:||| || :  | |  |:||||:||| :|||||||: : ||: :|||| 
Db        543 NCAQFASAQRLDWLFGRLSNPQSAE--GILDVLYCVLTESPEALNMINEGHIRSVISLLE 600

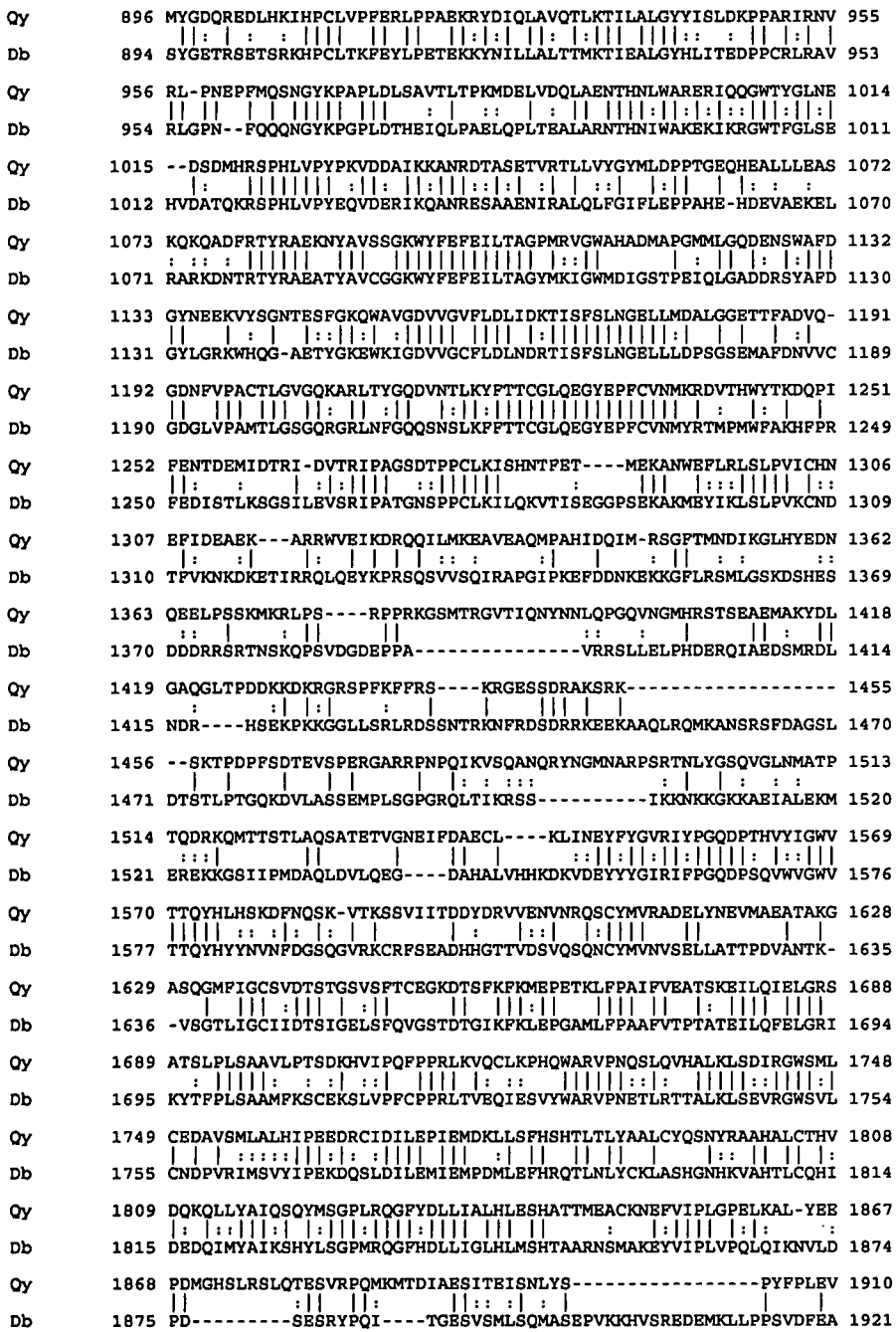
Qy        597 KHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVG 656
              | |||||||||| ||| |||:|||||| |  ||||||:||||:: |||||: ||: :| 
Db        601 KVGRDPKVLDVLSSLCEGNGMAVRSSQNLITQYLLPGKDLLLQTSMRDHVSSMMPNVMLG 660

Qy        657 RVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLY 716
              |||||::||||||  ::|||  |   |:|||||||: |: |:|| |:| | |||||| | 
Db        661 VVEGSALFRKWYFEAEVEHIETMTKQTPYLRIGWANSVGFKPFPGSGDKMGCNGVGDDFY 720

Qy        717 SYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTN 776
              ||||||  :: ||:  |          : |||||||::|||:| | |  ||  ::|||  
Db        721 SYGFDGKSMYFGGKSRRVG-----HKLLEKGDVIGCSIDLTIPEIKFSVNGTYMSGSFKK 775

Qy        777 FNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFG 836
              ||::| |||||:| |:|:||||:|||  |||||  | |:| :||::  :  | :  |  || 
Db        776 FNIDGYFFPVMSLSAKVSCRFILGGNQGRLRYGPPTGFSAVVEAVNGE--LQITDCLSFG 833

Qy        837 NLSKRALAGPPLVQDD-TAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895
              :| |   :||  : ::   |:|||:|     |  :  ::  | |||:||:||| ||| || 
Db        834 DLGKNIFSGPQTIFNNLEPPIPTPIDVSATQLNHHATEMHQKYAENLHELWAMRKIELGW 893
```


Qy 896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955
Db 894 SYGETRSETSRKHPCLTKFEYLPETEKKYNILLALTTMKTIEALGYHLITEDPPCRLRAV 953
Qy 956 RL-PNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNE 1014
Db 954 RLGPN--FQQQNGYKPGPLDTHEIQLPAELQPLTEALARNTHNIWAKEKIKRGWTFGLSE 1011
Qy 1015 --DSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEAS 1072
Db 1012 HVDATQKRSPHLVPYEQVDERIKQANRESAAENIRALQLFGIFLEPPAHE-HDEVAEKEL 1070
Qy 1073 KQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFD 1132
Db 1071 RARKDNTRTYRAEATYAVCGGKWYFEFEILTAGYMKIGWMDIGSTPEIQLGADDRSYAFD 1130
Qy 1133 GYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQ- 1191
Db 1131 GYLGRKWHQG-AETYGKEWKIGDVVGCFLDLNDRTISFSLNGELLLDPSGSEMAFDNVVC 1189
Qy 1192 GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPI 1251
Db 1190 GDGLVPAMTLGSGQRGRLNFGQQSNSLKFPTTCGLQEGYEPFCVNMYRTMPMWFAKHFPR 1249
Qy 1252 FENTDEMIDTRI-DVTRIPAGSDTPPCLKISHNTFET----MEKANWEFLRLSLPVICHN 1306
Db 1250 FEDISTLKSGSILEVSRIPATGNSPPCLKILQKVTISEGGPSEKAKMEYIKLSLPVKCND 1309
Qy 1307 EFIDEAEK---ARRWVEIKDRQQILMKEAVEAQMPAHIDQIM-RSGFTMNDIKGLHYEDN 1362
Db 1310 TFVKNKDKETIRRQLQEYKPRSQSVVSQIRAPGIPKEFDDNKEKKGFLRSMLGSKDSHES 1369
Qy 1363 QEELPSSKMKRLPS----RPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDL 1418
Db 1370 DDDRRSRTNSKQPSVDGDEPPA--------------VRRSLLELPHDERQIAEDSMRDL 1414
Qy 1419 GAQGLTPDDKKDKRGRSPFKFFRS----KRGESSDRAKSRK------------------- 1455
Db 1415 NDR----HSEKPKKGGLLSRLRDSSNTRKNFRDSDRRKEEKAAQLRQMKANSRSFDAGSL 1470
Qy 1456 --SKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATP 1513
Db 1471 DTSTLPTGQKDVLASSEMPLSGPGRQLTIKRSS----------IKKNKKGKKAEIALEKM 1520
Qy 1514 TQDRKQMTTSTLAQSATETVGNEIFDAECL----KLINEYFYGVRIYPGQDPTHVYIGWV 1569
Db 1521 EREKKGSIIPMDAQLDVLQEG----DAHALVHHKDKVDEYYYGIRIFPGQDPSQVWVGWV 1576
Qy 1570 TTQYHLHSKDFNQSK-VTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKG 1628
Db 1577 TTQYHYYNVNFDGSQGVRKCRFSEADHHGTTVDSVQSQNCYMVNVSELLATTPDVANTK- 1635
Qy 1629 ASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRS 1688
Db 1636 -VSGTLIGCIIDTSIGELSFQVGSTDTGIKFKLEPGAMLFPAAFVTPTATEILQFELGRI 1694
Qy 1689 ATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSML 1748
Db 1695 KYTFPLSAAMFKSCEKSLVPFCPPRLTVEQIESVYWARVPNETLRTTALKLSEVRGWSVL 1754
Qy 1749 CEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHV 1808
Db 1755 CNDPVRIMSVYIPEKDQSLDILEMIEMPDMLEFHRQTLNLYCKLASHGNHKVAHTLCQHI 1814
Qy 1809 DQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPELKAL-YEE 1867
Db 1815 DEDQIMYAIKSHYLSGPMRQGFHDLLIGLHLMSHTAARNSMAKEYVIPLVPQLQIKNVLD 1874
Qy 1868 PDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYS----------------PYFPLEV 1910
Db 1875 PD---------SESRYPQI----TGESVSMLSQMASEPVKKHVSREDEMKLLPPSVDFEA 1921
Qy 1911 AREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMT 1970
Db 1922 LKKHVMESLQSATHHAVMNCRDLIGGDNTNHFEPLFKLFDQLLVIGLINDEELECLLRLI 1981
Qy 1971 NPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDF 2030
Db 1982 HPQAFDENYE---TGTTQKGLTQLELAEPVKIQLVSILDHLCDIQLRYRIESLVAFTEGF 2038
Qy 2031 VGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKE----- 2085
Db 2039 VGELQSDQCKRYMEIKQTDMPPAEAAKKTKEFRCPPKEQMFRLLMCKVKEERDPELMEED 2098
Qy 2086 ----NCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAE-----NQEPEAKPGAFGKLYN 2136
Db 2099 ADVDQCPMAEGLQQQLRDFCELLVGKIG--NVKEGDSDDQLALIESEEGSWVDSFARI-- 2154
Qy 2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196
Db 2155 VVKVPPPVLEEGMEMQ----KKGTQNFREIIVTMLREWAQADFIESKSLIRNMFRLLLRQ 2210
Qy 2197 YDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2256
Db 2211 YSGIREIRDAMSQTYVFHERNEKDVTDFLVYLIQIRELLTVQFEHTEEAILKRGLWKLMN 2270
Qy 2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVV 2316
Db 2271 NRIFFQHPDLMRLLSVHENVMSIMMNIL---TAQQGTVEHEGDELKEKAPIKDAS-EMVV 2326
Qy 2317 ACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELA 2376
Db 2327 ACSRFLCYFCRTSRQNQKAMFEHLSFLLDNATMLLARPSLRGSVPLDVAYSSFMDNNELA 2386
Qy 2377 LALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVE 2436
Db 2387 LALKEEELDKVAVYLSRCGLQPNSELITKGYPDIGWDPVEGERYIDFLRFCVWINGENVE 2446
Qy 2437 ENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFS 2496
Db 2447 ENANLVIRLLIRRPECLGVALKGEGQGLFSAFKEAIALSEDI------RLLE-----NDS 2495
Qy 2497 HP-------------LPESD-EDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNE 2542
Db 2496 HPSLLSSGLLGENPTYPSKDAEGEDYIDLGAATLDFYSSLVDLLAKCAPDPMAIQAGKGD 2555
Qy 2543 SLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERV 2602
Db 2556 SLRARAILRSLISLDDLGQILALRFTIPNLAAPSIEDTGPLP-GLLPNHKGSVLLFLDRV 2614
Qy 2603 YGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFY 2662
Db 2615 YGIDQQDMLFHVLEQSFLPDLRAATMMDSPRALESDTALALNRYLCNSVLPLLTNHSHFF 2674
Qy 2663 NEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVD 2722
Db 2675 ADAEHHSALLDATLHTVYRMNRLKSLTKNQRDAVSDFLVAITRELPPAMMIKLLKKVITD 2734
Qy 2723 VSKLSEYTT-VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLS 2781
Db 2735 ILTMNDMNVLVPLRLITLHYERCGKYYGS----GNHYGVASEQEKRLSMLLFDAIFDTLG 2790
Qy 2782 KMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTS 2841
Db 2791 SRPYDPELFGKALPCMTAIGSAISPDYTLTSGLEDVRNKRREEEG-----AWIPRTVDVS 2845
Qy 2842 SVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKE 2901
Db 2846 RCEINRDLEKMTELFAEHFHDSWASRKLEKGWVHGDLYSRANFTHPRLKPFALLKDFEKS 2905
Qy 2902 RYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPF-DYN 2960
Db 2906 FYKERCSECLKALMA--WNYSFEMMDRDANDRASAAR------------TLSGTSISNFA 2951
Qy 2961 PHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000

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                 | |:|::::|| ::| | ||::|:::| |||||   :| |
Db       2952 PKPIDLSSMTLEKDMVNAAEKMAEHSHLIWAKKVMNDLNT 2991


RESULT 5
Q60WP5_CAEBR
ID   Q60WP5_CAEBR PRELIMINARY;      PRT;  5207 AA.
AC   Q60WP5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein CBG19042.
GN   Name=CBG19042;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   The C.briggsae Sequencing Consortium;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAC01000098; CAE71970.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005262; F:calcium channel activity; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0016165; F:lipoxygenase activity; IEA.
DR   GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR   GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000907; Lipoxygenase.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00036; efhand; 2.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS50919; MIR; 5.
KW   Hypothetical protein.
SQ   SEQUENCE   5207 AA;  591778 MW;  C8C3C7992E814468 CRC64;

  Query Match             44.9%;  Score 7078.5;  DB 2;  Length 5207;
  Best Local Similarity   45.2%;  Pred. No. 0;
  Matches 1454;  Conservative  527;  Mismatches  874;  Indels  363;  Gaps   56;

Qy         12 DDVSFLRTEDMVCLSCTAT--------GERVCLAAEGFGNRHCFLENIADKNIPPDLSQC 63
              :| :::   |:||||| |:         |||||  |||||| | |||::||:||||:: |
Db         11 EDHNYVTKGDIVCLSCVASHNRDGVLGSERVCLCTEGFGNRMCTLENVSDKDIPPDIAMC 70

Qy         64 VFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLSTSSS 123
              :  |: |||:|||||:::|           ||:|||||:|: |:|: |:|||||||: ||
Db         71 MLYIDNALSMRALQEMMSADSDHKSASGAGGHKTLLYGHAVQLKHVQSEMYLACLSSCSS 130

Qy        124 QDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTKENE 183
              |||||||:|: ::|||||||:|||||||||||||||||:||||||||||||
Db        131 NDKLAFDVGVQETNEGEACWWTIHPASKQRSEGEKVRVGDDVILVSVATERYLHMAYSKG 190

Qy        184 VSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDGGQN 243
              :: |||| | |::|   :|  | : :|::|| |||| ||| |||||||  |::    |
Db        191 YMVI-ASFHQTLWNIQSVSSGSMRTRNMGFLFGNDVLRLFHGNDECLTIPENWSEHPQHN 249

Qy        244 IVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELYLVS 303
              :|:|||: ::|||||||:|| | || |  : |    ||:|||:|||||| | | : |
Db        250 MVIYEGGAAVTQARSLWRVELVRMKWHGALVGWEQVFRIKHITSGRYLGVLD-NAVQLYH 308

Qy        304 REEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSYKSY 363
              :|:|     || : | || :||:|::|: | :|   |:||::   :|| :| |||||::
Db        309 KEKADFELTAFVMCQNKDPKKQMLDEKEEEGMGNATIRYGETNAFIQHVKTQLWLSYQTS 368

Qy        364 ETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETL 423
              |  |||:||||||:|:  ::| |||   |  : ||||::|||||||||:  ||: |:: |
Db        369 EVTKKGLGKVEEKKAVALKDGHMDDCYTFFMALEEESKSARVIRKCSSVLNKFLKGIDAL 428

Qy        424 QENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGI 483
              |     |  :  |:| |::  :|||| |||||:|: : |||||  ||||:|||||||:
Db        429 QLEGNQSTDWTRVDLNEVLKLMEDLIEYFAQPNEEQDFEEKQNHLRALRSRQDLFQEEGV 488

Qy        484 LNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFAN 543
              ||:||: ||| : : :    || | |:|:   || || ||| |:||:|||| ||||||:
Db        489 LNMILDTIDKFSQMEALPDFAG-LIGEETHIKWEQISTYLYLLVAAMIKGNHYNCAQFAS 547

Qy        544 SNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPK 603
              : ||:||| || :  | |  |:||||:||| :|||||||: : ||: :|||||  |||||
Db        548 AQRLDWLFGRLSNPQSAE--GILDVLYCVLTESPEALNMINEGHIRSVISLLEKVGRDPK 605

Qy        604 VLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEGSAV 663
              ||||| ||| |||:|||||| |  ||||||:|||||:: |||||: ||: :| |:|||:
Db        606 VLDVLSSLCEGNGMAVRSSQNLITQYLLPGKDLLLQTSMRDHVSSMMPNVMLGVVDGSAL 665

Qy        664 YRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGFDGA 723
              :||||||  ::|||  |   |:|||||||: |: |:|| |:||| |||||| |||||||
Db        666 FRKWYFEAEVEHIETMTKQTPYLRIGWANSVGFKPFPGSGDKWGCNGVGDDFYSYGFDGK 725

Qy        724 YLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLEGMF 783
              :: ||:   |          : |||||||:|||:| | |  ||  ::|||  || :| |
Db        726 SMFFGGKSRIVG-----HKLLEKGDVIGCSIDLTIPEIRFSVNGSYMSGSFKKFNTDGYF 780

Qy        784 FPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSKRAL 843
              |||:| |:|:||||:||| |||||  | |:| :||::  :  | :  |  ||:| |
Db        781 FPVMSLSAKVSCRFILGGNQGRLRYGPPTGFSAVVEAVNGE--LGITDCLSFGDLGKNIF 838

Qy        844 AGPPLVQDD-TAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQRE 902
              ||  : ::   |:|||:|     |  :  ::  | |||:||:||| ||| || ||: |
Db        839 CGPQTIFNNLEPPIPTPIDVSTTQLTHHAMEMHQKYAENLHELWAMRKIELGWSYGETRS 898

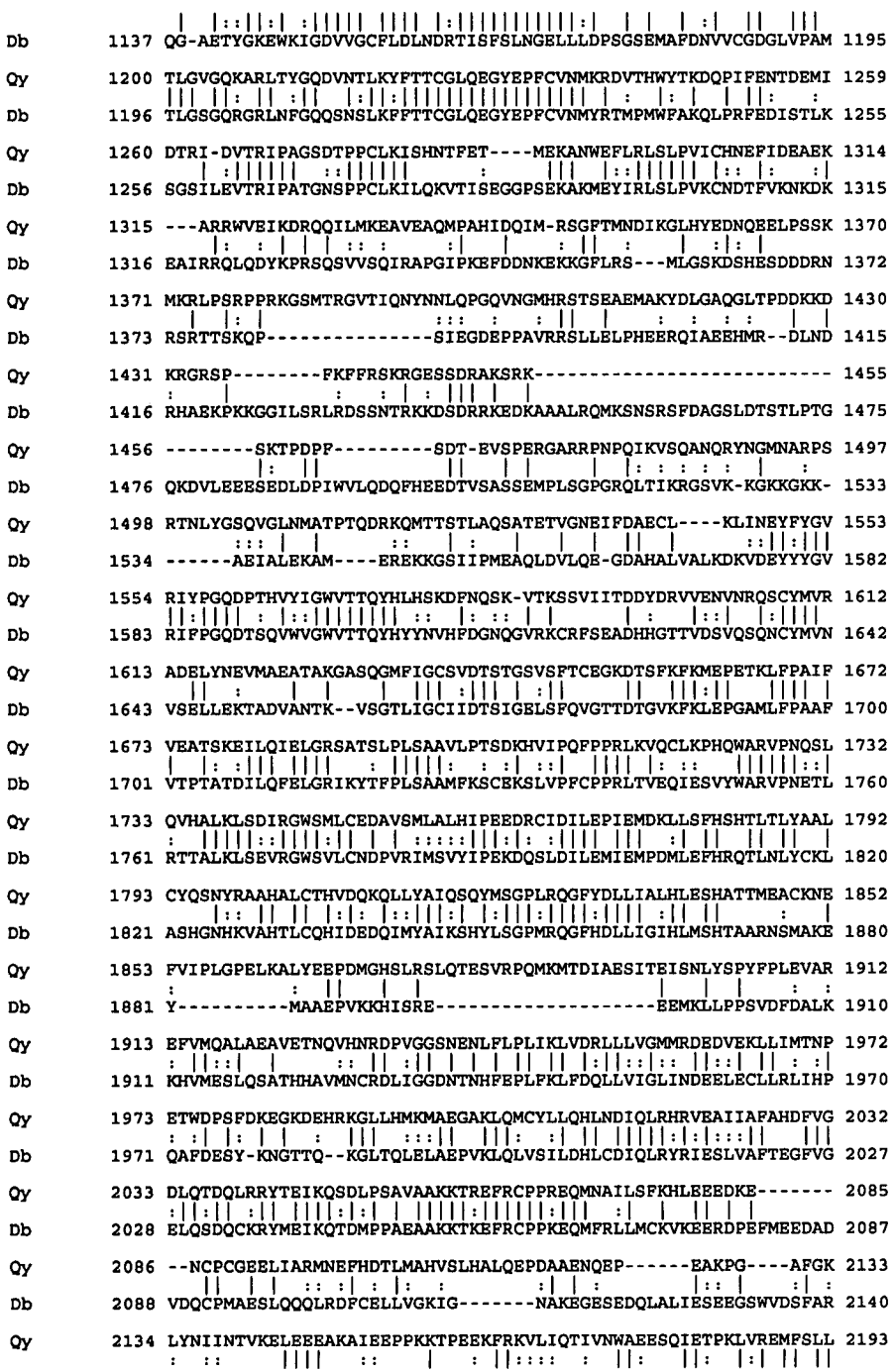
Qy        903 DLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNEPF 962
              :  : |||  || ||  ||:|:| ||: |:||| ||||::  | ||| |:| ||| : |
Db        899 ETSRKHPCLTRFELLPETEKKYNIMLALTTMKTIEALGYHLITDDPPCRLRAVRLA-QNF 957

Qy        963 MQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNE--DSDMHR 1020
              ||||||| |||   : |  ::  | : || ||||:||:|:|::|||:||:|  |:   |
Db        958 QQSNGYKPGPLDTHEIQLPVELQPLTEALARNTHNIWAKEKIKRGWTFGLSEHVDATQKR 1017

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||| :||: ||:|||::|:|  :| | ::|   |:||   | |: :  :  : :: : |
Db       1018 SPHLVPYEQVDERIKQANRESAAENIRALQLFGIFLEPPAHE-HDEIAEKELRARKDNTR 1076

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAPDGYNEEKVY 1140
              |||||  |||: |||||||||||||| |::||      | : || |: |:|||||   | :
Db       1077 TYRAEATYAVNGGKWYFEFEILTAGYMKIGWMDIGSTPEIQLGADDRSYAFDGYLGRKWH 1136

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQ-GDNFVPAC 1199
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RESULT 6
Q8TA74_HEMPU
ID Q8TA74_HEMPU PRELIMINARY; PRT; 5317 AA.
AC Q8TA74;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

```
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ryanodine receptor.
OS   Hemicentrotus pulcherrimus (Sea urchin).
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC   Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC   Hemicentrotus.
OX   NCBI_TaxID=7650;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21821894; PubMed=11832393;
RA   Shiwa M., Murayama T., Ogawa Y.;
RT   "Molecular cloning and characterization of ryanodine receptor from
RT   unfertilized sea urchin eggs.";
RL   Am. J. Physiol. Regul. Integr. Comp. Physiol. 282:R727-R737(2002).
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position
CC       (By similarity).
DR   EMBL; AB051576; BAB84714.1; -; mRNA.
DR   HSSP; P09860; 1DTL.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005262; F:calcium channel activity; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR   GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00036; efhand; 2.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR   PROSITE; PS50919; MIR; 4.
KW   Calcium; Ion transport; Ionic channel; Receptor; Repeat;
KW   Transmembrane; Transport.
SQ   SEQUENCE   5317 AA;  597224 MW;  2FA8A1D8CBE28A78 CRC64;

  Query Match             44.4%;  Score 6986.5;  DB 2;  Length 5317;
  Best Local Similarity   45.8%;  Pred. No. 0;
  Matches 1445;  Conservative  545;  Mismatches  905;  Indels  257;  Gaps   52;

Qy         11 QDDVSFLRTEDMVCLSCTATG-ERVCLAAEGFGNRHCFLENIADKNIPPDLSQCVFVIEQ 69
              :|:|||||| | : | |::     | | |||||||:| ||  :::|:|||| |||| |
Db          7 EDEVSFLRTGDQLNLVCSSQSLGHVLLGAEGFGNRNCVLEEASNQNVPPDLSICVFVLNQ 66

Qy         70 ALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLSTSSSQDKLAF 129
              |||||||||:|    :  :|  :||||||||:|:||:|  | |:|||| ||||:|||||
Db         67 ALSVRALQEMVIT--DQIDQGGQAGHRTLLYGHAMLLQHSLSSMHLACLPTSSSKDKLAF 124

Qy        130 DVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTT--KENEVSIV 187
              |||||: :|||||||||:|| |||||||||||||||||:|||||||| :  :::: ||
Db        125 DVGLQESTQGEACWWTIHPVSKQRSEGEKVRVGDDLILVNVATERYLHLSVERDDQPMIV 184

Qy        188 NASFHVTHWSVQPYGTGISRM----------KYVGYVFGGDVLRFFHGG-DECLTIPST 235
              |||  | |:| |  :|| ::           | :|:: | | |||  |  || ||:|
Db        185 VASFQQTLWTVAPVSSGIVKIKAMAKKYGDTEKVLGFLNGLDTLRFSRGHMDEYLTVPPV 244

Qy        236 WTKDGGQNI--VVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGV 293
               ||   ||  | |: |:|   ||||| ||   || | :::|  | ||||:|:|:|| |
Db        245 GCKD-DDNISEVSYDTGAVAQYARSLWRAELILKKWNGSYVSWGPPCRIRHLTSGKYLAV 303

Qy        294 NDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSE 353
              :  : :| |:           || :| ::|    : |    :|:  |||||||::|| :
Db        304 LENGTVCIVPRKSCNLDDTIFCFQQSREDLAN-YDSKQDHGMGSADIKYGDSTVLIQHMK 362

Qy        354 TGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
              || ||||   |:     |:  |:: ::  || ||||    |:: ||||:| :||| : ||
Db        363 TGHWLSYLVVESVVG--GRAAERKVVMLPEGHMDDGFSVVRARAEESRSAGIIRKSTLLF 420

Qy        414 TKFINGLETLQ-ENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALR 472
              :| : |::|: |     : : | ||  :|  ||||| || :|:|| :|||| | :|||
Db        421 NQFFDALDSLRGEKEDDQLAWNSFNLSSVVDILEDLIEYFGEPEEDEDHEEKQKKLKALR 480

Qy        473 NRQDLFQEEGILNLILEAIDKINVITS-QGFLAGFLAGDESGQSWEMISGYLYQLLAAII 531
              |||||| |||:: |:|| |||:::  | : | |  : |:::|  |: |  |||:||||:|
Db        481 NRQDLFHEEGMVKLVLETIDKLSIFKSGRDFAA--IVGEDAGDLWQDIVTYLYKLLAAMI 538

Qy        532 KGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVI 591
              : || ||| || | ||:|| :|| || : :  |:|:|||||: ||||||:::: ||| :
Db        539 RHNHNNCALFAQSVRLDWLINRLESQQASK--GVLEVLHCVLLGSPEALNIIKENHIKSM 596

Qy        592 ISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRP 651
              || |||||||||||||||||||||||||:|| ||| ||| ::|||||:|| |  :||
Db        597 ISQLEKHGRDPKVLDVLCSLCVGNGVAVRSNQNLICDNLLPSRDLLLQTAVVDEVVCMRP 656

Qy        652 NIFVGRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGV 711
              |: :   : | ||:|||||| :|  |  |  | |:||| | |:  |  ||| || :||
Db        657 NVSISVDKNSTVYKKWYFEVAIDKQEAGTSRPVHFRVGWATTQGFRTYLRGGEGWGNSGV 716

Qy        712 GDDLYSYGFDGAYLWSGG--RKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVR 769
              |||||:|||| ||:||  :  | :        : |||::|   ||:|| | :  ||
Db        717 VDDLYSFGFDGLNLWTGGVSKAAPWSGNR----LLSKGDIVGVCFDLSVPRILYHVNGSP 772

Qy        770 VTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSL 829
              :  ||  ||||||||||:| |:::  ||:|||:||| :|: |:|:: : ||:||:: | :
Db        773 IKASFEGINLEGMFFPVLSFSARVCARFILGGKHGRFKYSPPKGFAAVCESVLPKERLKI 832

Qy        830 EPCFYFGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMN 889
              ||||  |:::: : ||  || :||:| |||| : || |:| :||||||||||:| ||
Db        833 EPCFALGHVTEGIIQGPTASQDHSAFIPAPVDTANVNLPGYIEMLRDKLAENIHELWCMN 892

Qy        890 KIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPP 949
              |||||| :|  |:|  |:|  |: |  || :|| :| :||:|::|||:||:|:
Db        893 KIEAGWTWGPVRDDSKKVHDSLMFFSSLSEQEKNFDITMAYETLRTLMALGYHISIDEET 952

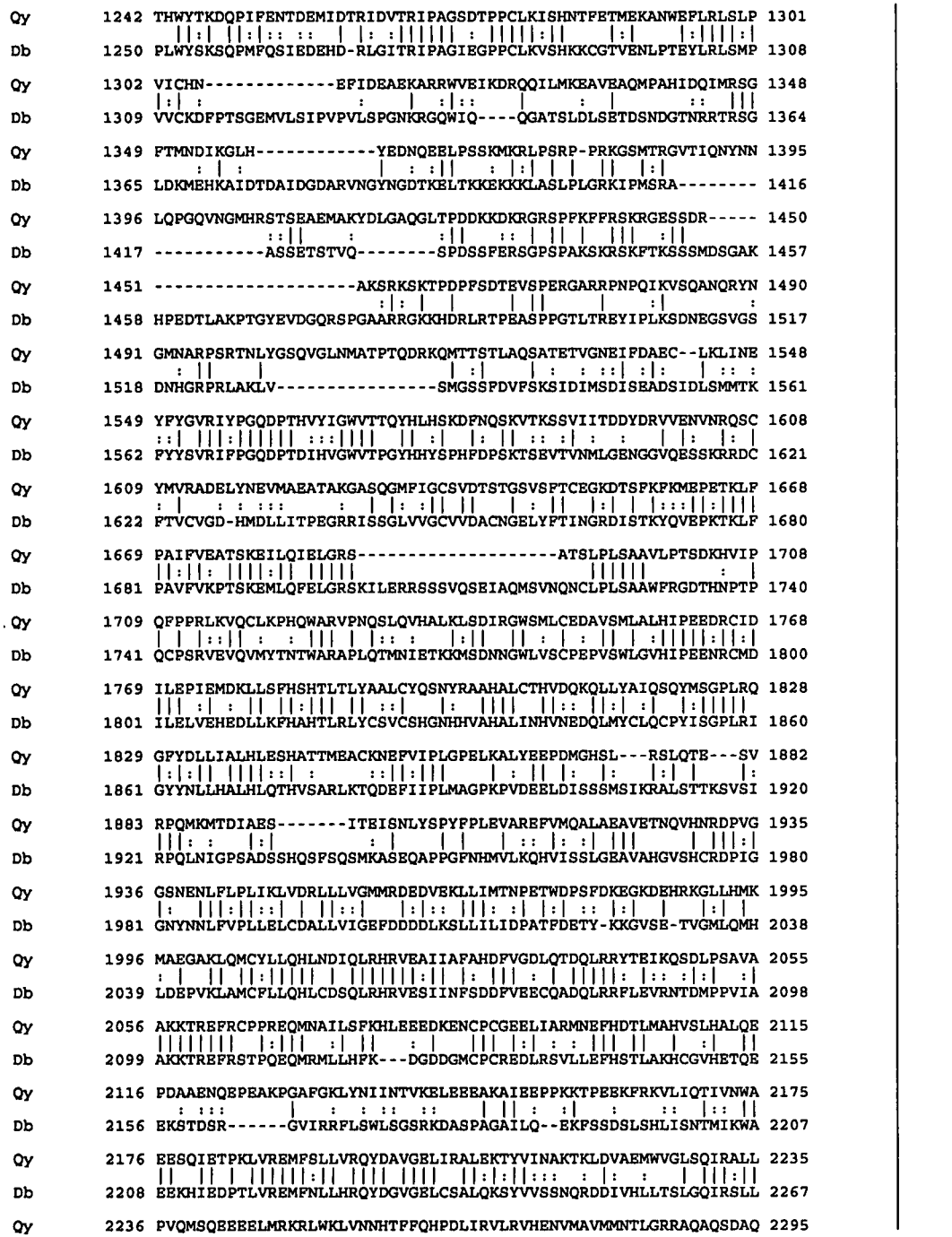
Qy        950 AR--IRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQG 1007
              ::  :: :|||   :: |||||||| :|| : |  ||::||: |||| ||:||:|| ||
Db        953 SKSTLKRLRLPMN-YLMSNGYKPAPYNLSTIHLNVKMEKLVELLAENAHNVWAKDRIAQG 1011

Qy       1008 WTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGE----- 1062
              |||||:|::   |:| |||| :::|  || |||||||:||:| :|| |:||| |
Db       1012 WTYGLSEETSYKRNPQLVPYNQLNDQAKKLNRDTASETIRTILGFGYALEPPTNEGQSDP 1071

Qy       1063 QHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMML 1122
                 |  |  |::  ||:||||:||| ||:|||||| :| | |||||    :|    :
Db       1072 SFRGLAREIS-DKKSHTRTFRAEKSYAVKSGRWYFEFEAMTTGYMRVGWGRPTIAARSEV 1130

Qy       1123 GQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALG 1182
              | |  |:|||:   | : | :|:||| |   ||:|  |:|:| ||||::||| | |::|
Db       1131 GTDGCSFAFDGFLARKWHQG-SETFGKTWGEMDVIGCMLNLVDNTISFTMNGEYLCDSVG 1189

Qy       1183 GETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPPFCVNMKRDV 1241
              |  | |:: |: ||| | |  |:|| | :|||| ||||| |||||||||||||||: :
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RESULT 7
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ID   Q94279_CAEEL PRELIMINARY;      PRT;  5107 AA.
AC   Q94279;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Uncoordinated protein 68.
GN   Name=unc-68; ORFNames=K11C4.5;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
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RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; U64854; AAB18318.1; -; Genomic_DNA.
DR   PIR; T29144; T29144.
DR   HSSP; P09860; 1DTL.
DR   Ensembl; K11C4.5; Caenorhabditis elegans.
DR   WormBase; WBGene00006801; K11C4.5.
DR   WormPep; K11C4.5; CE12116.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005262; F:calcium channel activity; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0016165; F:lipoxygenase activity; IEA.
DR   GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR   GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR002202; HMG-CoA_red.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000907; LipOase.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00036; efhand; 2.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00472; MIR; 3.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_2.
DR   PROSITE; PS00066; HMG_COA_REDUCTASE_1; UNKNOWN_1.
DR   PROSITE; PS50919; MIR; 4.
KW   Complete proteome.
SQ   SEQUENCE   5107 AA;  580736 MW;  462B7C01B799D152 CRC64;

  Query Match           43.4%;  Score 6828;  DB 2;  Length 5107;
  Best Local Similarity   45.0%;  Pred. No. 0;
  Matches 1407;  Conservative  519;  Mismatches  850;  Indels  350;  Gaps   52;

Qy        113 MYLACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVAT 172
              |||||||: || ||||||||:|: ::|||||||:||||||||||||||||:|||||||
Db          1 MYLACLSSCSSNDKLAFDVGVQETNEGEACWWTIHPASKQRSEGEKVRVGDDVILVSVAT 60

Qy        173 ERYLHTTK---ENEVSI----------------------VNASFHVTHWSVQPYGTGI 205
              |||||  |   | | |:                     | |||| | |::|   :|
Db         61 ERYLHLKKGKTEEEASLMLLFCGRNVLLLFHQHMAYSKGYMVIASFHQTLWNIQSVSSGS 120

Qy        206 SRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELA 265
              | : :|::|| |||| ||| |||||||  |::    |:|:|||: ::||||||:||
Db        121 MRTRNMGFLFGNDVLRLFHGNDECLTIPENWSEHPQHNMVIYEGGAAVTQARSLWRVELI 180

Qy        266 RTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQ 325
              | || |  : |    ||:|||:|||||| | | : |  :|:|    || : | || :||
Db        181 RMKWHGALVGWEQVFRIKHITSGRYLGVLD-NSVQLYHKEKADFDLTAFVMCQNKDPKKQ 239

Qy        326 VLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGK 385
              :|::|: | :|   |:||::   :|| :| |||||:: |  |||:|||||||:|:  ::|
Db        240 MLDEKEEEGMGNATIRYGETNAFIQHVKTQLWLSYQTTEVTKKGLGKVEEKKAVALKDGH 299

Qy        386 MDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEMVMCL 445
              |||   |  : ||||::|||||||||:  ||: |:: ||      |  :  |:| |::  :
Db        300 MDDCYTFFMALEEESKSARVIRKCSSVLNKFLKGIDALQLEGNQSTDWTRVDLNEVLKLM 359

Qy        446 EDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAG 505
              |||| ||||:::  : |||||  ||||:|||||||||:||:||: ||| : : :    ||
Db        360 EDLIEYFAQPNDEQDFEEKQNHLRALRSRQDLFQEEGVLNMILDTIDKFSQMEALPDFAG 419

Qy        506 FLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGM 565
              | |:|:   || || ||| |:||:|||| |||||:: ||:||| || :  | |  |:
Db        420 -LIGEETHVKWEQISTYLYLLVAAMIKGNHYNCAQFASAQRLDWLFGRLSNPQSAE--GI 476

Qy        566 LDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNN 625
              ||||:||| :|||||||: : ||: :|||||| |||||||||| ||| |||:|||||||
Db        477 LDVLYCVLTESPEALNMINEGHIRSVISLLEKVGRDPKVLDVLSSLCEGNGMAVRSSQNL 536

Qy        626 ICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEKTTHMMPH 685
              |  ||||||:||||:: ||||| ||: :| |||||::|||||  ::||| |   |:
Db        537 ITQYLLPGKDLLLQTSMRDHVSSMMPNVMLGVVEGSALFRKWYFEAEVEHIETMTKQTPY 596

Qy        686 LRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIR 745
              |||||||: |: |:|| |:| | |||||| |||||||  :: ||:    |        :
Db        597 LRIGWANSVGFKPFPGSGDKMGCNGVGDDFYSYGFDGKSMYFGGKSRRVG-----HKLLE 651

Qy        746 KGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLEGMFPPVISCSSKLSCRFLLGGEHGR 805
              |||||||::|||:| | |  ||  ::|||  ||::| ||||:| |:|:||||:|||  ||
Db        652 KGDVIGCSIDLTIPEIKFSVNGTYMSGSFKKFNIDGYFFPVMSLSAKVSCRFILGGNQGR 711

Qy        806 LRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSKRALAGPPLVQDD-TAFVPTPVDTLQ 864
              |||  | |:| :||:  :  |  :  | ||:| |   :||  : ::   |:|||:|
Db        712 LRYGPPTGFSAVVEAVNGE--LQITDCLSFGDLGKNIFSGPQTIFNNLEPPIPTPIDVSA 769

Qy        865 ITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRY 924
              |  :  ::  | |||:||:||| ||| || ||: | :  : ||||  || ||  ||:|
Db        770 TQLNHHATEMHQKYAENLHELWAMRKIELGWSYGETRSETSRKHPCLTKFEYLPETEKKY 829

Qy        925 DIQLAVQTLKTILALGYYISLDKPPARIRNVRL-PNEPFMQSNGYKPAPLDLSAVTLTPK 983
              :| ||: |:||| ||||::  : || |:| ||| ||  | | ||||| |||   : |  :
Db        830 NILLALTTMKTIEALGYHLITEDPPCRLRAVRLGPN--FQQQNGYKPGPLDTHEIQLPAE 887

Qy        984 MDELVDQLAENTHNLWARERIQQGWTYGLNE--DSDMHRSPHLVPYPKVDDAIKKANRDT 1041
              :  | : || ||||:||:|:|::|||:||:|  |:   |||||||| :||: ||:|||::
Db        888 LQPLTEALARNTHNIWAKEKIKRGWTFGLSEHVDATQKRSPHLVPYEQVDERIKQANRES 947

Qy       1042 ASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEI 1101
              |:| :| | ::|  |:||  | |: :  :  : :: : ||||||  |||  |||||||||
Db        948 AAENIRALQLFGIFLEPPAHE-HDEVAEKELRARKDNTRTYRAEATYAVCGGKWYFEFEI 1006

Qy       1102 LTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFL 1161
              |||| |::||       | : || |: |:|||||   | : |  |::||:| :||||| ||
Db       1007 LTAGYMKIGWMDIGSTPEIQLGADDRSYAFDGYLGRKWHQG-AETYGKEWKIGDVVGCFL 1065

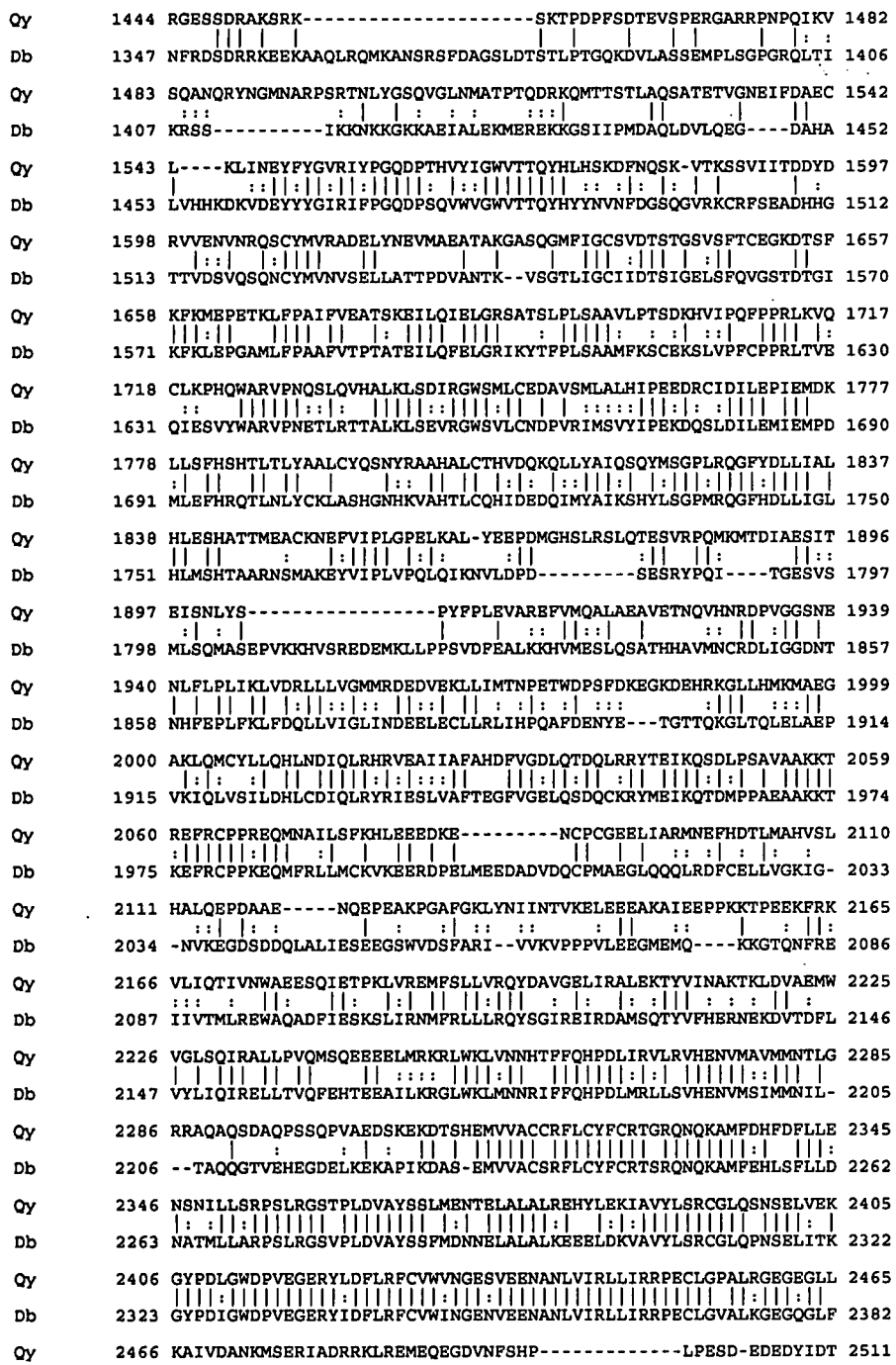
Qy       1162 DLIDKTISFSLNGELLMDALGGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKY 1220
              || |:|||||||||:|  | |  | :|  ||  ||| ||| ||: || :||  |:||:
Db       1066 DLNDRTISFSLNGELLLDPSGSEMAFDNVVCGDGLVPAMTLGSGQRGRLNFGQQSNSLKF 1125

Qy       1221 FTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMIDTRI-DVTRIPAGSDTPPCLK 1279
              |||||||||||||||| | :  |: |  | ||:   :    | :|:|||| ::|||||
Db       1126 FTTCGLQEGYEPFCVNMYRTMPMWFAKQLPRFEDISTLKSGSILEVSRIPATGNSPPCLK 1185

Qy       1280 ISHNTFET----MEKANWEFLRLSLPVICHNEFIDEAEK---ARRWVEIKDRQQILMKEA 1332
              |      :     |||  |:::|||||  |:: |:   :|    |:  | | | | :: :
Db       1186 ILQKVTISEGGPSEKAKMEYIKLSLPVKCNDTFVKNKDKETIRRQLQEYKPRSQSVVSQI 1245

Qy       1333 VEAQMPAHIDQIM-RSGFTMNDIKGLHYEDNQEELPSSKMKRLPS----RPPRKGSMTRG 1387
                :|    |    :  ||  : :      :: ::  |    :  ||    ||
Db       1246 RAPGIPKEFDDNKEKKGFLRSMLGSKDSHESDDDRRSRTNSKQPSVDGDEPPA------- 1298

Qy       1388 VTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFFRS----K 1443
                ::   :   |     || :  ||  :      :| |:|   :   |    |
Db       1299 --------VRRSLLELPHDERQIAEDSMRDLNDR----HSEKPKKGGLLSRLRDSSNTRK 1346
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RESULT 8
Q29621_RABIT
ID Q29621_RABIT PRELIMINARY; PRT; 4968 AA.
AC Q29621;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cardiac ryanodine receptor.
GN Name=RyR-2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=91032060; PubMed=2226801; DOI=10.1016/0014-5793(90)80399-4;
RA Nakai J., Imagawa T., Hakamat Y., Shigekawa M., Takeshima H., Numa S.;
RT "Primary structure and functional expression from cDNA of the cardiac
RT ryanodine receptor/calcium release channel.";
RL FEBS Lett. 271:169-177(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;

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RX   MEDLINE=93147068; PubMed=1337083;
RA   Imagawa T., Nakai J., Takeshima H., Nakasaki Y., Shigekawa M.;
RT   "Expression of Ca(2+)-induced Ca2+ release channel activity from
RT   cardiac ryanodine receptor cDNA in Chinese hamster ovary cells.";
RL   J. Biochem. 112:508-513(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RA   Nakai J.;
RL   Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Regulatory light chain of myosin. Does not bind calcium
CC       (By similarity).
CC   -!- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light chains
CC       (By similarity).
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position
CC       (By similarity).
DR   EMBL; U50465; AAA93465.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005262; F:calcium channel activity; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR   GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00036; efhand; 1.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50919; MIR; 5.
KW   Ion transport; Ionic channel; Motor protein; Muscle protein; Myosin;
KW   Receptor; Repeat; Transmembrane; Transport.
SQ   SEQUENCE   4968 AA;  565086 MW;  04B16A35D06B852D CRC64;

  Query Match             43.0%;  Score 6778;  DB 2;  Length 4968;
  Best Local Similarity   45.6%;  Pred. No. 0;
  Matches 1401;  Conservative  530;  Mismatches  851;  Indels  290;  Gaps   57;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
              |:||   | |:: ||||:|  | | ||||     :::||||||||||| ||||: :: ||:||
Db          2 ADGGEGE-DEIQFLRTDDEVVLQCTATIHKEQQKLCLAAEGFGNRLCFLESTSNSKNVPP 60

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKG-------------TGSGHRTLLYGNAI 104
              ||| | ||:||:|||||||:: |    |  :|               | |||||||:||
Db         61 DLSICTFVLEQSLSVRALQEML-ANTVEKSEGQVDVEKWKFMMKTAQGGGHRTLLYGHAI 119

Qy        105 LLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGD 163
              ||||  | ||| ||||| || ||||||||||: : |||||||:||||||||||||||||
Db        120 LLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVRVGD 179

Qy        164 DLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFF 223
              |||||||::||||| :  |    |:|:|  | ||| |  :|    :  ||: ||||||
Db        180 DLILVSVSSERYLHLSYGNGSLHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVLRLL 237

Qy        224 HGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRI 282
              ||  |||||:||    :  :  | ||||:|   |||||||  |  |:|  | |  | |:
Db        238 HGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGSHIRWGQPFRL 297

Qy        283 RHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKY 342
              ||:|||:|| : :   | |: :|:|   | ||  |  |:      :  |::: :|   |||
Db        298 RHVTTGKYLSLMEDKNLLLMDKEKADVKSTAFTFRSSKEKLDGGVR-KEVDGMGTSEIKY 356

Qy        343 GDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRT 402
              |||   :|| :|||||:|:| : |   :|  :: | ||:|  || |||||: |||| |||||
Db        357 GDSICYIQHVDTGLWLTYQSVDVKSVRMGSIQRK-AIMHHEGHMDDGLNLSRSQHEESRT 415

Qy        403 ARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNL--GEMVMCLEDLINYFAQPDEDME 460
              |||||     || :|| ||: | :  : |    ||:|    : : |:||| ||  ||| :|
Db        416 ARVIRSTVFLFNRFIRGLDALSKKAKAS----SVDLPIESVSLSLQDLIGYFHPPDEHLE 471

Qy        461 HEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMIS 520
              ||:|||: |||:|||:||||||::||:|| ||:::| :|    |  :|| |:|::||: |
Db        472 HEDKQNRLRALKNRQNLFQEEGMINLVLECIDRLHVYSSAAHFAD-VAGREAGESWKSIL 530

Qy        521 GYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEAL 580
              ||:||||:|:|| |||||: |  |:|| ||| :     :|:|:||||||::|||||
Db        531 NSLYELLAALIRGNRKNCAQFSGS--LDWLISRL--ERLEASSGILEVLHCVLVESPEAL 586

Qy        581 NMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQT 640
              |:::: ||| |||||:||||: ||||||||||| :||||||:|: ||| ||||::|||||
Db        587 NIIKEGHIKSIISLLDKHGRNHKVLDVLCSLCVCHGVAVRSNQHLICDNLLPGRDLLLQT 646

Qy        641 ALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPY 699
              ||:||||:|||||:|  |||| |:|||:|: :|| |    |    |||:|||:| || ||
Db        647 RLVNHVSSMRPNIFLGVSEGSAQYKKWYYELMVDHTEPPVTAEATHLRVGWASTEGYSPY 706

Qy        700 PGGGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVP 759
              |||||:||||||||||:|||||| :||||     |:  :  :  :|  ||| | |||: |
Db        707 PGGGEEWGGNGVGDDLFSYGFDGLHLWSGCIARTVSSPN--QHLLRTDDVISCCLDLSAP 764

Qy        760 IINFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVE 819
              |:|  ||  | | | ||||:|:||||:| |: :  ||||| ||  ::  | ||:|  |
Db        765 SISFRINGQPVQGMFENFNIDGLFFPVVSFSAGIKVRFLLGGRHGEFKFLPPPGYAPCYE 824

Qy        820 SLLPQQILSLEPC--FYFGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDK 877
              ::||:: | :|    :       | | || :     || | |||| || || ::|:||:|
Db        825 AVLPKEKLKVEHSREYKQERTYTRDLLGPTVSLTQAAFTPIPVDTSQIVLPPHLERIREK 884

Qy        878 LAENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTIL 937
              |||||||:| ||||| || ||  |:|  : ||||| | :||  |: |::|::::||||:|
Db        885 LAENIHELWVMNKIELGWQYGPVRDDNKRQHPCLVEFSKLPEQERNYNLQMSLETLKTLL 944

Qy        938 ALGYYISLDKPPA--RIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENT 995
              ||| :: :    |  ::: ::||   :  ::||||||:||| : |||  : :||:||||
Db        945 ALGCHVGISDEHAEEKVKKMKLPKN-YQLTSGYKPAPMDLSFIKLTPSQEAMVDKLAENA 1003

Qy        996 HNLWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYM 1055
              ||:|||:||:|||||: :|    |:|  |||| :||  ||:|:|:  | ||||| |||
Db       1004 HNVWARDRIRQGWTYGIQQDVKNRRNPRLVPYTLLDDRTKKSNKDSLREAVRTLLGYGYN 1063

Qy       1056 LDPPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHAD 1115
              |: |  :|  |   |         || :|||| ||| :|:|||||| :|:| |||||:
Db       1064 LEAP--DQDHAARAEVCSGTGERFRIFRAEKTYAVKAGRWYFEFEAVTSGDMRVGWSRPG 1121

Qy       1116 MAPGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGE 1175
                |   || || ::|||||:  :: : || | :|: |  |||||  :|: : |: |:||||
Db       1122 CQPDQELGSDERAFAFDGFKAQRWHQGN-EHYGRSWQAGDVVGCMVDMNEHTMMFTLNGE 1180

Qy       1176 LLMDALGGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFC 1234
              :|:|  | |  | |  || |:| |:||| |  |: :|:||:|||||| ||||||||||
Db       1181 ILLDDSGSELAFKDFDVGDGFIPVCSLGVAQVGRMNFGKDVSTLKYFTICGLQEGYEPFA 1240

Qy       1235 VNMKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE 1294
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Db       1241 VNTNRDITMWLSKRLPQFLQVPSNHE-HIEVTRIDGTIDSSPCLKVTQKSFGS-QNSNTD 1298

Qy       1295 --FLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMN 1352

Db       1299 IMFYRLSMPIECAEVF---------------------------------------------- 1314

Qy       1353 DIKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAE 1412

Db       1315 -----------------SKTVPGGLPGAGLF-------------GPKNDLEDYDADSD 1342

Qy       1413 MAKYDLGAQG-LTPDDKKDKRGRSPFKPFRSKRGESSDRAKSRKSKTPDPFSDTEVSPER 1471

Db       1343 FEVLMKTAHGHLVP----------------------DRVDKDKETTKAEFNN------- 1372

Qy       1472 GARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATE 1531

Db       1373 --HKDYAQEKPSRLKQRFLLRRTKP---------------------DYSTSHSARLTED 1408

Qy       1532 TVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVI 1591

Db       1409 VLADDRDDYDFLMQTSTYYYSVRIFPGQEPANVWVGWITSDFHQYDTGFDLDRVRTVTVT 1468

Qy       1592 ITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCE 1651

Db       1469 LGDEKGKVHESIKRSNCYMVCA----GESMSPGQGRN-NNGLEIGCVVDAASGLLTFIAN 1523

Qy       1652 GKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFP 1711

Db       1524 GKELSTYYQVEPSTKLFPAVFAQATSPNVFQFELGRIKNVMPLSAGLFKSEHKNPVPQCP 1583

Qy       1712 PRLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILE 1771

Db       1584 PRLHVQFLSHVLWSRMPNQFLKVDVSRISERQGWLVQCLDPLQFMSLHIPEENRSVDILE 1643

Qy       1772 PIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFY 1831

Db       1644 LTEQEELLKFHYHTLRLYSAVCALGNHRVAHALCSHVDEPQLLYAIENKYMPGLLRTGYY 1703

Qy       1832 DLLIALHLESHATTMEACKNEFVIPLGPELKA--LYEEPDMGHSLRSL-QTESVRPQMKM 1888

Db       1704 DLLIDIHLSSYATARLMMNNEFIVPMTEETKSITLFPDENKKHGLPGIGLSTSLRPRMQF 1763

Qy       1889 TDIAESITEISN---LYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPL 1945

Db       1764 S--SPSFVSINNECYQYSPEFPLDILKAKTIQMLTEAVKEGSLHARDPVGGTTEFLFVPL 1821

Qy       1946 IKLVDRLLLVGMMRDEDVEKLLIMTNPETW---------------DPSFDK---EGKDEH 1987

Db       1822 IKLFYTLLIMGIFHNEDLRHILQLIEPSVFKDAATPEEEGDTLEEEPSVEDTKLEGAGEE 1881

Qy       1988 --------RKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQL 2039

Db       1882 EAKMGKRPKEGLLQMKLPEPVKLQMCLLLQYLCDCQVRHRIEAIVAFSDDFVAKLQDNQR 1941

Qy       2040 RRYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMN 2098

Db       1942 FRYNEVMQALNMSAALTARKTKEFRSPPQEQINMLLNFK----DDKSECPCPEEIRDQLL 1997

Qy       2099 EFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEE--AKAIEEPPK 2156

Db       1998 DFHEDLMTHCGIELDEDGSLDGNSDLTIR----GRLLSLVEKVTYLKKKQTEKPVESDSR 2053

Qy       2157 KTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAK 2216

Db       2054 KS--STLQQLISETMVRWAQESVIEDPELVRAMFVLLHRQYDGIGGLVRALPKTYTINGV 2111

Qy       2217 TKLDVAEMWVGLSQIRALLPVQMSQEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENV 2276

Db       2112 SVEDTINLLASLGQIRSLLSVRMGKEEEKLMIRGLGDIMNNKVFYQHPNLMRALGMHETV 2171

Qy       2277 MAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAM 2336

Db       2172 MEVMVNVLG----------------GGESKE-ITFPKMVANCCRFLCYFCRISRQNQKAM 2214

Qy       2337 FDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGL 2396

Db       2215 FDHLSYLLENSSVGLASPAMRGSTPLDVAAASVMDNNELALALREPDLEKVVRYLAGCGL 2274

Qy       2397 QSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPA 2456

Db       2275 QSCQMLVSKGYPDIGWNPVEGERYLDFLRFAVFCNGESVEENANVVVRLLIRRPECFGPA 2334

Qy       2457 LRGE-GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPES---------DEDE 2506

Db       2335 LRGEGGNGLLAAMEEAIKIAE----------------DPSRDGPSPTSGSSKTLDTEEEED 2379

Qy       2507 DYIDTGAAILNPYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLR 2566

Db       2380 DTIHMGNAIMTPYAALIDLLGRCAPEMHLIHAGKGEAIRIRSILRSLIPLGDLVGVISIA 2439

Qy       2567 FTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAA 2626

Db       2440 FQMPTIAKDGNVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRAA 2499

Qy       2627 TMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNR 2686

Db       2500 ASLDTAALSATDMALALNRYLCTAVLPLLTRCAPLFAGTEHHASLIDSLLHTVYRLSKGC 2559

Qy       2687 MLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAK 2746

Db       2560 SLTKAQRDSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCWK 2619

Qy       2747 YYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPP 2806

Db       2620 YYCLPG-GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALPP 2678

Qy       2807 DYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWAS 2866

Db       2679 DY-MESNYVSMM--EKQSSMDSEG-NFNPQPVDTSNIIIPEKLEYFINKYAEHSHDKWSM 2734

Qy       2867 RKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEV 2926

Db       2735 DKLANGWIYGEIYSDSSKIQPLMKPYKLLSEKEKEIYRWPIKESLKTMLAWGWRIERTR- 2793

Qy       2927 DIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNA 2986

Db       2794 ---EGDSMALYNRTRRISQTSQVSVDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAENY 2848

Qy       2987 HDIWAKKKKEEL 2998

Db       2849 HNIWAKKKKLEL 2860
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RESULT 9
RYR2_RABIT
ID   RYR2_RABIT     STANDARD;      PRT;  4969 AA.
AC   P30957;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ryanodine receptor 2 (Cardiac muscle-type ryanodine receptor) (RyR2)
DE   (RYR-2) (Cardiac muscle ryanodine receptor-calcium release channel).
GN   Name=RYR2;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart muscle;
RX   MEDLINE=90337947; PubMed=2380170;
RA   Otsu K., Willard H.F., Khanna V.K., Zorzato F., Green N.M.,
RA   Maclennan D.H.;
RT   "Molecular cloning of cDNA encoding the Ca2+ release channel
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RT   (ryanodine receptor) of rabbit cardiac muscle sarcoplasmic
RT   reticulum.";
RL   J. Biol. Chem. 265:13472-13483(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8841406;
RA   Nishida K., Otsu K., Hori M., Kuzuya T., Tada M.;
RT   "Cloning and characterization of the 5'-upstream regulatory region of
RT   the Ca(2+)-release channel gene of cardiac sarcoplasmic reticulum.";
RL   Eur. J. Biochem. 240:408-415(1996).
RN   [3]
RP   PHOSPHORYLATION SITE SER-2809.
RX   MEDLINE=91250425; PubMed=1645727;
RA   Witcher D.R., Kovacs R.J., Schulman H., Cefali D.C., Jones L.R.;
RT   "Unique phosphorylation site on the cardiac ryanodine receptor
RT   regulates calcium channel activity.";
RL   J. Biol. Chem. 266:11144-11152(1991).
CC   -!- FUNCTION: Communication between transverse-tubules and
CC       sarcoplasmic reticulum. Contraction of cardiac muscle is triggered
CC       by release of calcium ions from SR following depolarization of T-
CC       tubules.
CC   -!- SUBUNIT: Homotetramer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Heart and brain.
CC   -!- MISCELLANEOUS: The calcium release channel is modulated by calcium
CC       ions, magnesium ions, ATP and calmodulin.
CC   -!- MISCELLANEOUS: The calcium release channel activity resides in the
CC       C-terminal region while the remaining part of the protein
CC       constitutes the 'foot' structure spanning the junctional gap
CC       between the SR and the T-tubule. It is possible that the foot
CC       structure interacts with the cytoplasmic region of the
CC       dihydropyridine receptor.
CC   -!- MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Ca-
CC       release channel in junctional SR and modulates its activity.
CC   -!- SIMILARITY: Belongs to the ryanodine receptor family.
CC   -!- SIMILARITY: Contains 1 EF-hand domain.
CC   -!- SIMILARITY: Contains 5 MIR domains.
CC   -!- SIMILARITY: Contains 3 SPRY domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; M59743; AAA31179.1; -; mRNA.
DR   PIR; A37113; A37113.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecpt_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   PANTHER; PTHR13715:SF1; Ryanodn_receptor; 10.
DR   Pfam; PF00036; efhand; 1.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50222; EF_HAND_2; 1.
DR   PROSITE; PS50919; MIR; 5.
KW   Calcium; Calcium channel; Calcium transport; Calmodulin-binding;
KW   Glycoprotein; Ion transport; Ionic channel; Multigene family;
KW   Phosphorylation; Receptor; Repeat; Transmembrane; Transport.
FT   TOPO_DOM      1   3090       Cytoplasmic.
FT   TRANSMEM   3091   3110       M' (Potential).
FT   TRANSMEM   3154   3172       M'' (Potential).
FT   TRANSMEM   3941   3960       M1 (Potential).
FT   TRANSMEM   3979   3996       M2 (Potential).
FT   TRANSMEM   4234   4257       M3 (Potential).
FT   TRANSMEM   4295   4315       M4 (Potential).
FT   TRANSMEM   4501   4521       M5 (Potential).
FT   TRANSMEM   4580   4602       M6 (Potential).
FT   TRANSMEM   4722   4742       M7 (Potential).
FT   TRANSMEM   4770   4788       M8 (Potential).
FT   TRANSMEM   4812   4829       M9 (Potential).
FT   TRANSMEM   4847   4869       M10 (Potential).
FT   DOMAIN      110    165       MIR 1.
FT   DOMAIN      172    217       MIR 2.
FT   DOMAIN      225    280       MIR 3.
FT   DOMAIN      286    345       MIR 4.
FT   DOMAIN      351    408       MIR 5.
FT   DOMAIN      670    808       SPRY 1.
FT   REPEAT      853    966       1.
FT   REPEAT      967   1080       2.
FT   DOMAIN     1098   1221       SPRY 2.
FT   DOMAIN     1423   1561       SPRY 3.
FT   REPEAT     2693   2811       3.
FT   REPEAT     2813   2926       4.
FT   DOMAIN     4024   4059       EF-hand.
FT   REGION      853   2926       4 X approximate repeats.
FT   REGION     2619   3016       Modulator (Potential).
FT   REGION     2775   2807       Calmodulin-binding (Potential).
FT   REGION     2877   2898       Calmodulin-binding (Potential).
FT   REGION     2998   3016       Calmodulin-binding (Potential).
FT   MOD_RES    2809   2809       Phosphoserine (by CaMK).
FT   CARBOHYD   4105   4105       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   4796   4796       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   4969 AA;  565073 MW;  FF6E0684B974BB4D CRC64;

  Query Match           43.0%;  Score 6770.5;  DB 1;  Length 4969;
  Best Local Similarity  45.6%;  Pred. No. 0;
  Matches 1401;  Conservative  530;  Mismatches  851;  Indels  291;  Gaps   58;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
              |:||  | |:: ||||:| | | ||||     :::||||||||| ||||: :: ||:||
Db          2 ADGGEGE-DEIQFLRTDDEVVLQCTATIHKEQQKLCLAAEGFGNRLCFLESTSNSKNVPP 60

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKG-------------TGSGHRTLLYGNAI 104
              ||| | ||:||:| ||||||:: |   |  :|               | |||||||:||
Db         61 DLSICTFVLEQSLLVRALQEML-ANTVEKSEGQVDVEKWKFMMKTAQGGGHRTLLYGHAI 119

Qy        105 LLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGD 163
              |||| | ||| ||||| || |||||||||: : |||||||:|||||||||||||||||
Db        120 LLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVRVGD 179

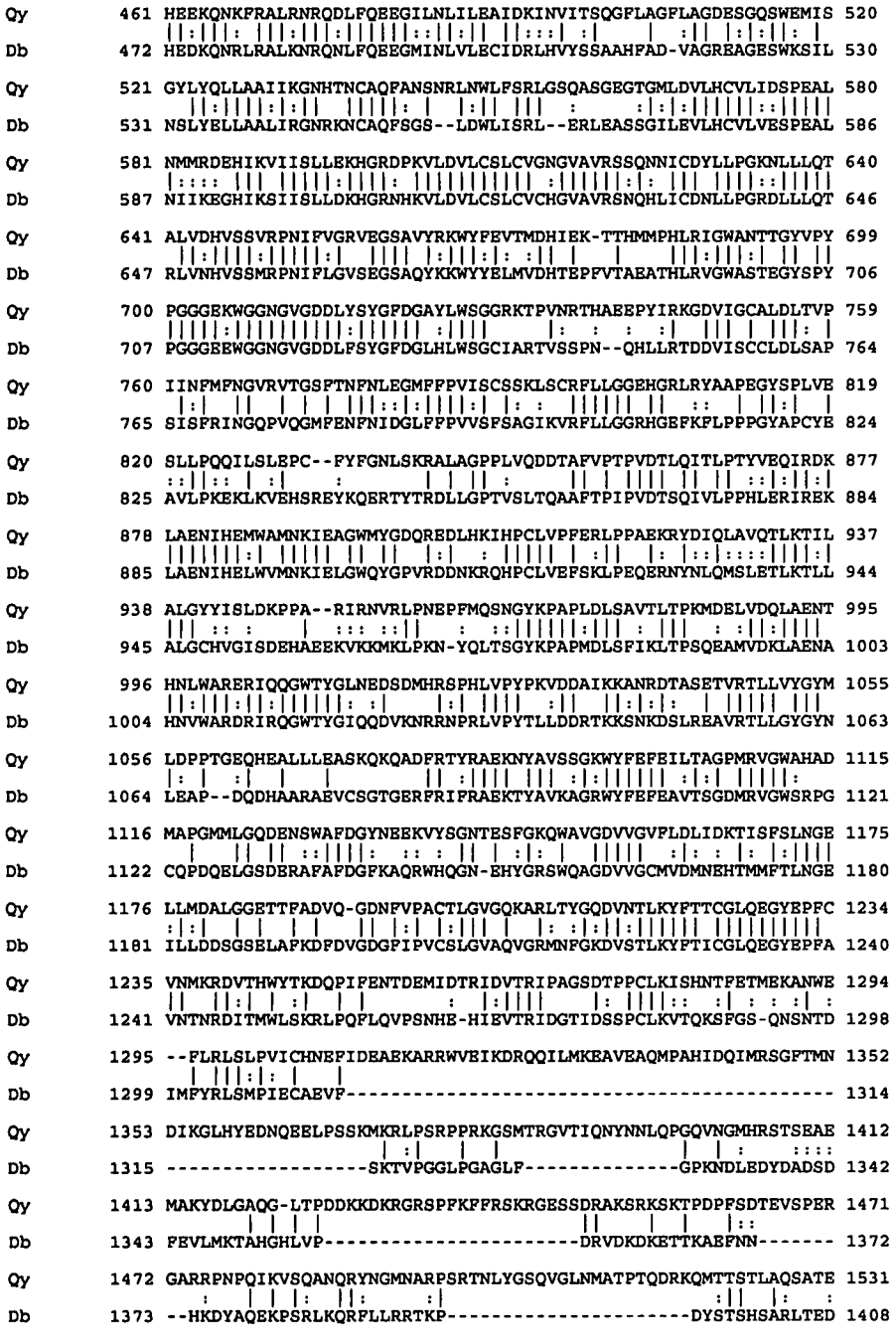
Qy        164 DLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFF 223
              |||||||::||||| :  |     |:|:|  | ||| |  :|    :  ||: ||||||
Db        180 DLILVSVSSERYLHLSYGNGSLHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVLRLL 237

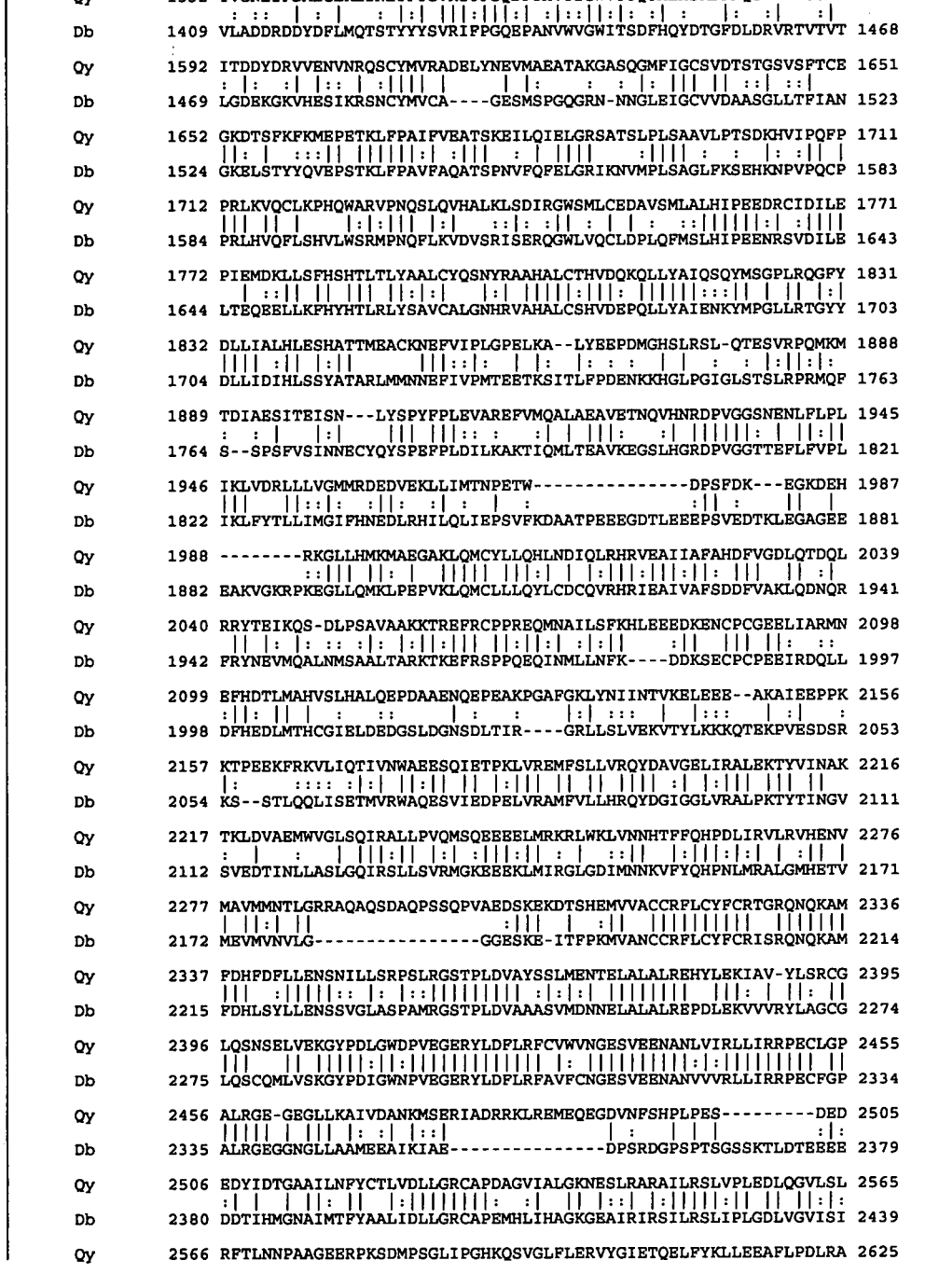
Qy        224 HGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRI 282
              ||  |||||:||    :  :  | ||||:|   |||||||  |  |:|  | |  | |:
Db        238 HGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGSHIRWGQPFRL 297

Qy        283 RHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKY 342
              ||:|||:|| : :   | |: :|:|   | ||  |  |:     :  |::: :|   |||
Db        298 RHVTTGKYLSLMEDKNLLLMDKEKADVKSTAFTFRSSKEKLDGGVR-KEVDGMGTSEIKY 356

Qy        343 GDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRT 402
              |||   :|| :|||||:|:| : |   :| :: | ||:| || ||||| |||| |||||
Db        357 GDSICYIQHVDTGLWLTYQSVDVKSVRMGSIQRK-AIMHHEGHMDDGLNLSRSQHEESRT 415

Qy        403 ARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNL--GEMVMCLEDLINYFAQPDEDME 460
              |||||    || :|| ||: | :  : |    ||:|    : : |:||| ||  ||| :|
Db        416 ARVIRSTVFLFNRFIRGLDALSKKAKAS----SVDLPIESVSLSLQDLIGYFHPPDEHLE 471
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                  | :    |       : || :|  | || :: |||:|||||| |:    |||  |||||||
Db       2440 AFQMPTIAKDGNVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRA 2499

Qy       2626 ATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKN 2685
                |  ||       :||||::|||:  ::|||| : |   :   |::|||:|: |||||||||
Db       2500 AASLDTAALSATDMALALNRYLCTAVLPLLTRCAPLFAGTEHHASLIDSLLHTVYRLSKG 2559

Qy       2686 RMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745
                 ||| ||:::   |:::   ::|||:  |||:|  ||  |:|:  : |:||| |||||
Db       2560 CSLTKAQRDSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCW 2619

Qy       2746 KYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALP 2805
                 |||   | | | |||:|:||  |:  ||  |||:||:  || |||  ||||| |:  |||
Db       2620 KYYCLPG-GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALP 2678

Qy       2806 PDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWA 2865
                 ||| :  ||       ::|:: | :   ::|||::||:: :    |   : |::|| || |:
Db       2679 PDY-MESNYVSMM--EKQSSMDSEG-NFNPQPVDTSNIIIPEKLEYFINKYAEHSHDKWS 2734

Qy       2866 SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE 2925
                |: |||:||| :||| |  | :||| :|:: ||| |: |::|||| :|| || :| :
Db       2735 MDKLANGWIYGEIYSDSSKIQPLMKPYKLLSEKEKEIYRWPIKESLKTMLAWGWRIERTR 2794

Qy       2926 VDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADN 2985
                    :  ::  :::   :  ::  |:|    |:|  :||:|:|||::  ||| :|:|
Db       2795 ----EGDSMALYNRTRRISQTSQVSVDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAEN 2848

Qy       2986 AHDIWAKKKKEEL 2998
                |:|||||| ||
Db       2849 YHNIWAKKKKLEL 2861


RESULT 10
RYR2_HUMAN
ID   RYR2_HUMAN     STANDARD;      PRT;  4967 AA.
AC   Q92736; Q15411;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ryanodine receptor 2 (Cardiac muscle-type ryanodine receptor) (RyR2)
DE   (RYR-2) (Cardiac muscle ryanodine receptor-calcium release channel)
DE   (hRYR-2).
GN   Name=RYR2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
RC   TISSUE=Heart muscle;
RX   MEDLINE=96404895; PubMed=8809036;
RA   Tunwell R.E.A., Wickenden C., Bertrand B.M.A., Shevchenko V.I.,
RA   Walsh M.B., Allen P.D., Lai F.A.;
RT   "The human cardiac muscle ryanodine receptor-calcium release channel:
RT   identification, primary structure and topological analysis.";
RL   Biochem. J. 318:477-487(1996).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 9-87 AND 533-681, DEVELOPMENTAL STAGE, AND
RP   INDUCTION.
RC   TISSUE=Heart muscle, and Myometrium;
RX   MEDLINE=97220386; PubMed=9148749;
RA   Awad S.S., Lamb H.K., Morgan J.M., Dunlop W., Gillespie J.I.;
RT   "Differential expression of ryanodine receptor RyR2 mRNA in the non-
RT   pregnant and pregnant human myometrium.";
RL   Biochem. J. 322:777-783(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 4292-4479, AND TISSUE SPECIFICITY.
RC   TISSUE=Cerebellum, and Hippocampus;
RX   MEDLINE=98268728; PubMed=9607712; DOI=10.1016/S0306-4522(97)00612-X;
RA   Martin C., Chapman K.E., Seckl J.R., Ashley R.H.;
RT   "Partial cloning and differential expression of ryanodine
RT   receptor/calcium-release channel genes in human tissues including the
RT   hippocampus and cerebellum.";
RL   Neuroscience 85:205-216(1998).
RN   [4]
RP   VARIANTS VTSIP LEU-2246; SER-2474; LYS-4104 AND CYS-4497.
RX   PubMed=11208676;
RA   Priori S.G., Napolitano C., Tiso N., Memmi M., Vignati G., Bloise R.,
RA   Sorrentino V.V., Danieli G.A.;
RT   "Mutations in the cardiac ryanodine receptor gene (hRyR2) underlie
RT   catecholaminergic polymorphic ventricular tachycardia.";
RL   Circulation 103:196-200(2001).
RN   [5]
RP   VARIANTS FPVT SER-2328; ARG-4201 AND PHE-4653, AND VARIANT ARG-2958.
RX   MEDLINE=21112862; PubMed=11157710;
RA   Laitinen P.J., Brown K.M., Piippo K., Swan H., Devaney J.M.,
RA   Brahmbhatt B., Donarum E.A., Marino M., Tiso N., Viitasalo M.,
RA   Toivonen L., Stephan D.A., Kontula K.;
RT   "Mutations of the cardiac ryanodine receptor (RyR2) gene in familial
RT   polymorphic ventricular tachycardia.";
RL   Circulation 103:485-490(2001).
RN   [6]
RP   VARIANTS ARVD2 PRO-433 AND ILE-2386.
RX   MEDLINE=21096894; PubMed=11159936; DOI=10.1093/hmg/10.3.189;
RA   Tiso N., Stephan D.A., Nava A., Bagattin A., Devaney J.M., Stanchi F.,
RA   Larderet G., Brahmbhatt B., Brown K., Bauce B., Muriago M., Basso C.,
RA   Thiene G., Danieli G.A., Rampazzo A.;
RT   "Identification of mutations in the cardiac ryanodine receptor gene in
RT   families affected with arrhythmogenic right ventricular cardiomyopathy
RT   type 2 (ARVD2).";
RL   Hum. Mol. Genet. 10:189-194(2001).
CC   -!- FUNCTION: Communication between transverse-tubules and
CC       sarcoplasmic reticulum. Contraction of cardiac muscle is triggered
CC       by release of calcium ions from SR following depolarization of T-
CC       tubules (By similarity).
CC   -!- SUBUNIT: Homotetramer (Potential).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q92736-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q92736-2; Sequence=VSP_005953;
CC   -!- TISSUE SPECIFICITY: Heart muscle, brain (cerebellum and
CC       hippocampus) and placenta.
CC   -!- DEVELOPMENTAL STAGE: Expressed in myometrium during pregnancy.
CC   -!- INDUCTION: By TGF-beta.
CC   -!- DISEASE: Defects in RYR2 are the cause of familial arrhythmogenic
CC       right ventricular dysplasia 2 (ARVD2) [MIM:600996]; also known as
CC       arrhythmogenic right ventricular cardiomyopathy 2 (ARVC2). ARVD is
CC       an autosomal dominant disease characterized by partial
CC       degeneration of the myocardium of the right ventricle, electrical
CC       instability, and sudden death. It is clinically defined by
CC       electrocardiographic and angiographic criteria; pathologic
CC       findings, replacement of ventricular myocardium with fatty and
CC       fibrous elements, preferentially involve the right ventricular
CC       free wall.
CC   -!- DISEASE: Defects in RYR2 are the cause of an autosomal dominant
CC       form of stress-induced polymorphic ventricular tachycardia (VTSIP)
CC       [MIM:604772]; also known as catecholaminergic polymorphic
CC       ventricular tachycardia. VTSIP is a genetic arrhythmogenic
CC       disorder characterized by stress-induced, bidirectional
CC       ventricular tachycardia that may degenerate into cardiac arrest
CC       and cause sudden death.
CC   -!- DISEASE: Defects in RYR2 are a cause of familial polymorphic
CC       ventricular tachycardia (FPVT) [MIM:192605]. FPVT is an autosomal-
CC       dominant, inherited disease with a relatively early onset and a
CC       mortality rate of approximately 30% by the age of 30 years.
CC       Phenotypically, it is characterized by salvoes of bidirectional
CC       and polymorphic ventricular tachycardias in response to vigorous
CC       exercise, with no structural evidence of myocardial disease.
CC   -!- MISCELLANEOUS: The calcium release channel is modulated by calcium
CC       ions, magnesium ions, ATP and calmodulin.
CC   -!- MISCELLANEOUS: The calcium release channel activity resides in the
CC       C-terminal region while the remaining part of the protein
```

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CC       constitutes the 'foot' structure spanning the junctional gap
CC       between the SR and the T-tubule. It is possible that the foot
CC       structure interacts with the cytoplasmic region of the
CC       dihydropyridine receptor.
CC   -!- MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Ca-
CC       release channel in junctional SR and modulates its activity.
CC   -!- SIMILARITY: Belongs to the ryanodine receptor family.
CC   -!- SIMILARITY: Contains 1 EF-hand domain.
CC   -!- SIMILARITY: Contains 5 MIR domains.
CC   -!- SIMILARITY: Contains 3 SPRY domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X98330; CAA66975.1; -; mRNA.
DR   EMBL; Y08218; CAA69395.1; -; mRNA.
DR   EMBL; X91869; CAA62975.1; -; mRNA.
DR   EMBL; AJ002511; CAA05502.1; -; mRNA.
DR   PIR; S72269; S72269.
DR   Ensembl; ENSG00000198626; Homo sapiens.
DR   HGNC; HGNC:10484; RYR2.
DR   MIM; 180902; -.
DR   MIM; 600996; -.
DR   MIM; 604772; -.
DR   MIM; 192605; -.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0015278; F:calcium-release channel activity; TAS.
DR   GO; GO:0006936; P:muscle contraction; TAS.
DR   GO; GO:0008016; P:regulation of heart contraction rate; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   PANTHER; PTHR13715:SF1; Ryanodn_receptor; 10.
DR   Pfam; PF00036; efhand; 1.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50222; EF_HAND_2; 1.
DR   PROSITE; PS50919; MIR; 5.
KW   Alternative splicing; Calcium; Calcium channel; Calcium transport;
KW   Calmodulin-binding; Cardiomyopathy; Disease mutation; Glycoprotein;
KW   Ion transport; Ionic channel; Multigene family; Phosphorylation;
KW   Polymorphism; Receptor; Repeat; Transmembrane; Transport.
FT   TOPO_DOM      1   3089       Cytoplasmic (By similarity).
FT   TRANSMEM   3090   3109       M' (Potential).
FT   TRANSMEM   3153   3171       M'' (Potential).
FT   TRANSMEM   3940   3959       M1 (Potential).
FT   TRANSMEM   3978   3995       M2 (Potential).
FT   TRANSMEM   4233   4256       M3 (Potential).
FT   TRANSMEM   4294   4314       M4 (Potential).
FT   TRANSMEM   4500   4520       M5 (Potential).
FT   TRANSMEM   4578   4600       M6 (Potential).
FT   TRANSMEM   4720   4740       M7 (Potential).
FT   TRANSMEM   4768   4786       M8 (Potential).
FT   TRANSMEM   4810   4827       M9 (Potential).
FT   TRANSMEM   4845   4867       M10 (Potential).
FT   DOMAIN      110    165       MIR 1.
FT   DOMAIN      172    217       MIR 2.
FT   DOMAIN      225    280       MIR 3.
FT   DOMAIN      286    343       MIR 4.
FT   DOMAIN      351    408       MIR 5.
FT   DOMAIN      670    808       SPRY 1.
FT   REPEAT      853    966       1.
FT   REPEAT      967   1080       2.
FT   DOMAIN     1098   1221       SPRY 2.
FT   DOMAIN     1423   1561       SPRY 3.
FT   REPEAT     2692   2810       3.
FT   REPEAT     2812   2925       4.
FT   DOMAIN     4023   4058       EF-hand.

  Query Match             43.0%;  Score 6769;  DB 1;  Length 4967;
  Best Local Similarity   45.6%;  Pred. No. 0;
  Matches 1399;  Conservative  536;  Mismatches  854;  Indels  276;  Gaps   58;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
              |:||  | |:: ||||:| | | ||||     :::|||||||||| ||||: :: ||:||
Db          2 ADGGEGE-DEIQFLRTDDEVVLQCTATIHKEQQKLCLAAEGFGNRLCFLESTSNSKNVPP 60

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKG-------------TGSGHRTLLYGNAI 104
              ||| | ||:||:|||||||:: |   |  :|               | |||||||:||
Db         61 DLSICTFVLEQSLSVRALQEML-ANTVEKSEGQVDVEKWKFMMKTAQGGGHRTLLYGHAI 119

Qy        105 LLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGD 163
              ||||  | ||| ||||| || ||||||||||: : |||||||:|||||||||||||||||
Db        120 LLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVRVGD 179

Qy        164 DLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFF 223
              |||||||::|||||  :  |    |:|:|  | ||| |  :|    :  ||: ||||||
Db        180 DLILVSVSSERYLHLSYGNGSLHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVLRLL 237

Qy        224 HGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRI 282
              ||  |||||:||    :  :  | ||||:|   ||||||||  |  |:|  | |  | |:
Db        238 HGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGGSHIRWGQPFRL 297

Qy        283 RHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKY 342
              ||:|||:|| : :   | |: :|:|   | ||  |  | ::  |   |::: :|   |||
Db        298 RHVTTGKYLSLMEDKNLLLMDKEKADVKSTAFTFRSSK-EKLDVGVRKEVDGMGTSEIKY 356

Qy        343 GDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRT 402
              |||   :|| :|||||:|:| : |   :| :: | ||:| || ||||:  |||| |||||
Db        357 GDSVCYIQHVDTGLWLTYQSVDVKSVRMGSIQRK-AIMHHEGHMDDGISLSRSQHEESRT 415

Qy        403 ARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHE 462
              |||||     || :|| ||: | :  : |      : :  :  :|||| ||  ||| :|||
Db        416 ARVIRSTVFLFNRFIRGLDALSKKAKAST--VDLPIESVSLSLQDLIGYFHPPDEHLEHE 473

Qy        463 EKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGY 522
              :|||: |||:|||:|||||::||:|| ||:::| :|     |  :|| |:|:||: |
Db        474 DKQNRLRALKNRQNLFQEEGMINLVLECIDRLHVYSSAAHFAD-VAGREAGESWKSILNS 532

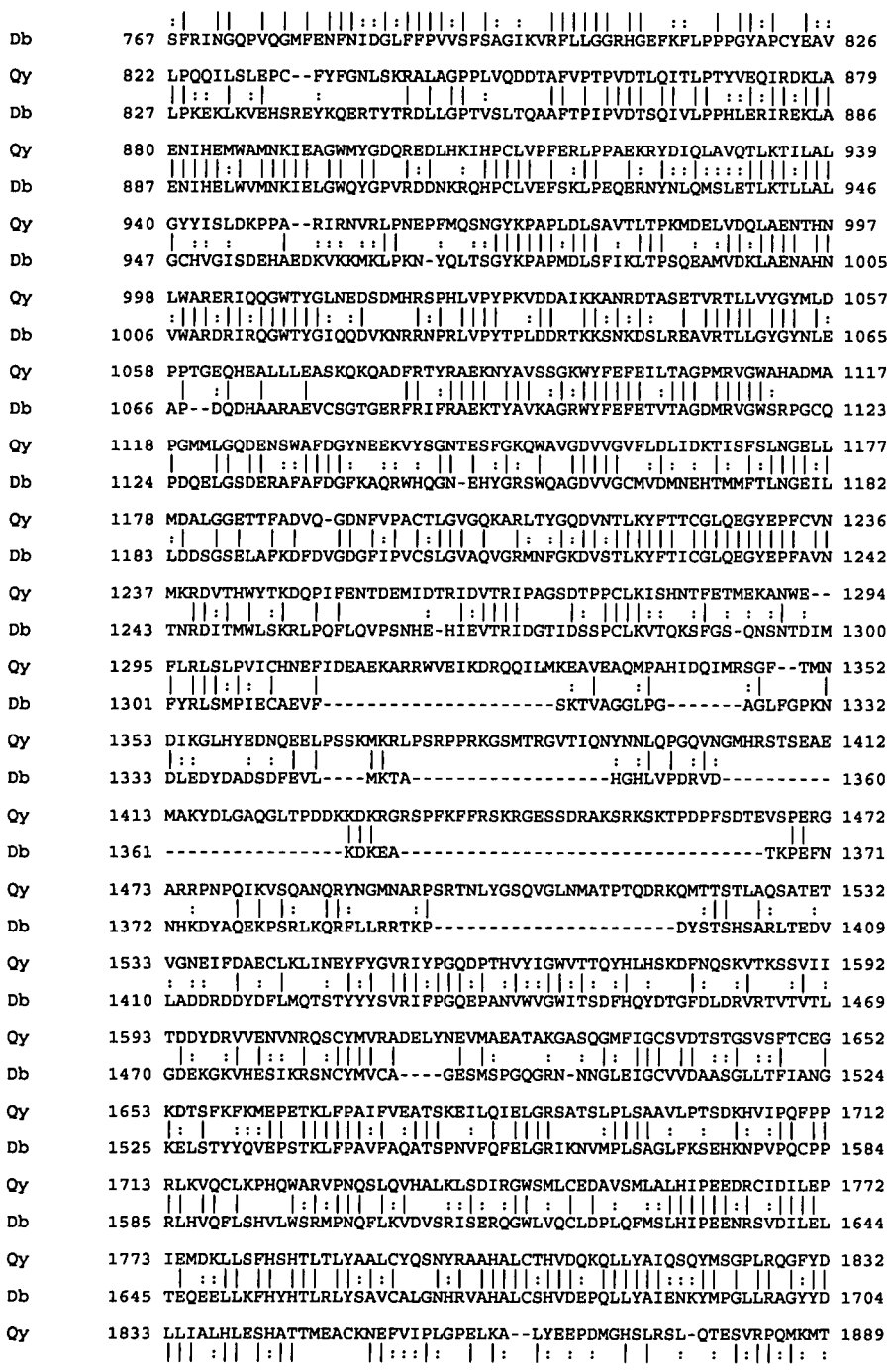
Qy        523 LYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNM 582
              ||:||||:|:||  |||||: |  |:|| ||| :     :|:|:||||||::||||||:
Db        533 LYELLAALIRGNRKNCAQFSGS--LDWLISRL--ERLEASSGILEVLHCVLVESPEALNI 588

Qy        583 MRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTAL 642
              ::: ||| |||||:||||: |||||||||| :|||||||:|: ||| ||||::||||| |
Db        589 IKEGHIKSIISLLDKHGRNHKVLDVLCSLCVCHGVAVRSNQHLICDNLLPGRDLLLQTRL 648

Qy        643 VDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYPG 701
              |:||||:|||||:|  |||| |:|||:|: :|| |   |    |||:|||:| || ||||
Db        649 VNHVSSMRPNIFLGVSEGSAQYKKWYYELMVDHTEPFVTAEATHLRVGWASTEGYSPYPG 708

Qy        702 GGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPII 761
              |||:||||||||:|||||| :||||      |:  :  :  :|  ||| | |||: | |
Db        709 GGEEWGGNGVGDDLFSYGFDGLHLWSGCIARTVSSPN--QHLLRTDDVISCCLDLSAPSI 766

Qy        762 NFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESL 821
```


Db 767 SFRINGQPVQGMFENFNIDGLFFPVVSFSAGIKVRPLLGGRHGEFKFLPPPGYAPCYEAV 826
Qy 822 LPQQILSLEPC--FYFGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLA 879
Db 827 LPKEKLKVEHSREYKQERTYTRDLLGPTVSLTQAAFTPIPVDTSQIVLPPHLERIREKLA 886
Qy 880 ENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILAL 939
Db 887 ENIHELWVMNKIELGWQYGPVRDDNKRQHPCLVEFSKLPEQERNYNLQMSLETLKTLLAL 946
Qy 940 GYYISLDKPPA--RIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHN 997
Db 947 GCHVGISDEHAEDKVKKMKLPKN-YQLTSGYKPAPMDLSFIKLTPSQEAMVDKLAENAHN 1005
Qy 998 LWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLD 1057
Db 1006 VWARDRIRQGWTYGIQQDVKNRRNPRLVPYTPLDDRTKKSNKDSLREAVRTLLGYGYNLE 1065
Qy 1058 PPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMA 1117
Db 1066 AP--DQDHAARAEVCSGTGERFRIFRAEKTYAVKAGRWYFEFETVTAGDMRVGWSRPGCQ 1123
Qy 1118 PGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELL 1177
Db 1124 PDQELGSDERAFAFDGFKAQRWHQGN-EHYGRSWQAGDVVGCMVDMNEHTMMFTLNGEIL 1182
Qy 1178 MDALGGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVN 1236
Db 1183 LDDSGSELAFKDFDVGDGFIPVCSLGVAQVGRMNFGKDVSTLKYFTICGLQEGYEPFAVN 1242
Qy 1237 MKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE-- 1294
Db 1243 TNRDITMWLSKRLPQFLQVPSNHE-HIEVTRIDGTIDSSPCLKVTQKSFGS-QNSNTDIM 1300
Qy 1295 FLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGF--TMN 1352
Db 1301 FYRLSMPIECAEVF--------------------SKTVAGGLPG-------AGLFGPKN 1332
Qy 1353 DIKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAE 1412
Db 1333 DLEDYDADSDFEVL----MKTA------------------HGHLVPDRVD---------- 1360
Qy 1413 MAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERG 1472
Db 1361 ----------------KDKEA---------------------------------TKPEFN 1371
Qy 1473 ARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATET 1532
Db 1372 NHKDYAQEKPSRLKQRFLLRRTKP----------------------DYSTSHSARLTEDV 1409
Qy 1533 VGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVII 1592
Db 1410 LADDRDDYDFLMQTSTYYYSVRIFPGQEPANVWVGWITSDFHQYDTGFDLDRVRTVTVTL 1469
Qy 1593 TDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEG 1652
Db 1470 GDEKGKVHESIKRSNCYMVCA----GESMSPGQGRN-NNGLEIGCVVDAASGLLTFIANG 1524
Qy 1653 KDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPP 1712
Db 1525 KELSTYYQVEPSTKLFPAVFAQATSPNVFQFELGRIKNVMPLSAGLFKSEHKNPVPQCPP 1584
Qy 1713 RLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEP 1772
Db 1585 RLHVQFLSHVLWSRMPNQFLKVDVSRISERQGWLVQCLDPLQFMSLHIPEENRSVDILEL 1644
Qy 1773 IEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYD 1832
Db 1645 TEQEELLKFHYHTLRLYSAVCALGNHRVAHALCSHVDEPQLLYAIENKYMPGLLRAGYYD 1704
Qy 1833 LLIALHLESHATTMEACKNEFVIPLGPELKA--LYEEPDMGHSLRSL-QTESVRPQMKMT 1889
Db 1705 LLIDIHLSSYATARLMMNNEYIVPMTEETKSITLFPDENKKHGLPGIGLSTSLRPRMQFS 1764
Qy 1890 DIAESITEISN---LYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLI 1946
Db 1765 --SPSFVSISNECYQYSPEFPLDILKSKTIQMLTEAVKEGSLHARDPVGGTTEFLFVPLI 1822
Qy 1947 KLVDRLLLVGMMRDEDVEKLLIM---------TNPETWDPSFDKE----------GKDE 1986
Db 1823 KLFYTLLIMGIFHNEDLKHILQLIEPSVFKEAATPEEESDTLEKELSVDDAKLQGAGEEE 1882
Qy 1987 ------HRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040
Db 1883 AKGGKRPKEGLLQMKLPEPVKLQMCLLLQYLCDCQVRHRIEAIVAFSDDFVAKLQDNQRF 1942
Qy 2041 RYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNE 2099
Db 1943 RYNEVMQALNMSAALTARKTKEFRSPPQEQINMLLNFK----DDKSECPCPEEIRDQLLD 1998
Qy 2100 FHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEE--AKAIEEPPKK 2157
Db 1999 FHEDLMTHCGIELDEDGSLDGNSDLTIR----GRLLSLVEKVTYLKKKQAEKPVESDSKK 2054
Qy 2158 TPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKT 2217
Db 2055 S--STLQQLISETMVRWAQESVIEDPELVRAMFVLLHRQYDGIGGLVRALPKTYTINGVS 2112
Qy 2218 KLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVM 2277
Db 2113 VEDTINLLASLGQIRSLLSVRMGKEEEKLMIRGLGDIMNNKVFYQHPNLMRALGMHETVM 2172
Qy 2278 AVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMF 2337
Db 2173 EVMVNVLG----------------GGESKE-ITFPKMVANCCRFLCYFCRISRQNQKAMF 2215
Qy 2338 DHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQ 2397
Db 2216 DHLSYLLENSSVGLASPAMRGSTPLDVAAASVMDNNELALALREPDLEKVVRYLAGCGLQ 2275
Qy 2398 SNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPAL 2457
Db 2276 SCQMLVSKGYPDIGWNPVEGERYLDFLRFAVFCNGESVEENANVVVRLLIRRPECFGPAL 2335
Qy 2458 RGE-GEGLLKAIVDANKMSERIADRRKLREMEQEG---DVNFSHPLPESDEDEDYIDTGA 2513
Db 2336 RGEGGNGLLAAMEEAIKIAE---------DPSRDGPSPNSGSSKTLDTEEEEDDTIHMGN 2386
Qy 2514 AILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPA 2573
Db 2387 AIMTFYSALIDLLGRCAPEMHLIHAGKGEAIRIRSILRSLIPLGDLVGVISIAFQMPTIA 2446
Qy 2574 AGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRND 2633
Db 2447 KDGNVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRAAASLDTAA 2506
Qy 2634 GCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQR 2693
Db 2507 LSATDMALALNRYLCTAVLPLLTRCAPLFAGTEHHASLIDSLLHTVYRLSKGCSLTKAQR 2566
Qy 2694 EAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGA 2753
Db 2567 DSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCWKYYCLPG- 2625
Qy 2754 GQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKN 2813
Db 2626 GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALPPDY-MESN 2684
Qy 2814 YDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGW 2873
Db 2685 YVSMM--EKQSSMDSEG-NFNPQPVDTSNITIPEKLEYFINKYAEHSHDKWSMDKLANGW 2741
Qy 2874 VYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNR 2933
Db 2742 IYGEIYSDSSKVQPLMKPYKLLSEKEKEIYRWPIKESLKTMLARTMRTERTR----EGDS 2797

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Qy       2934 SSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKK 2993
              ::  :::   :  ::  |:|    |:|  :||:|:||||::  ||| :|:| |:|||||
Db       2798 MALYNRTRRISQTSQVSVDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAENYHNIWAKK 2855

Qy       2994 KKEEL 2998
              || ||
Db       2856 KKMEL 2860


RESULT 11
Q546N8_HUMAN
ID   Q546N8_HUMAN PRELIMINARY;      PRT;  4967 AA.
AC   Q546N8;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Ryanodine receptor 2.
GN   Name=RYR2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21096894; PubMed=11159936; DOI=10.1093/hmg/10.3.189;
RA   Tiso N., Stephan D.A., Nava A., Bagattin A., Devaney J.M., Stanchi F.,
RA   Larderet G., Brahmbhatt B., Brown K., Bauce B., Muriago M., Basso C.,
RA   Thiene G., Danieli G.A., Rampazzo A.;
RT   "Identification of mutations in the cardiac ryanodine receptor gene in
RT   families affected with arrhythmogenic right ventricular cardiomyopathy
RT   type 2 (ARVD2).";
RL   Hum. Mol. Genet. 10:189-194(2001).
CC   -!- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light chains
CC       (By similarity).
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position
CC       (By similarity).
DR   EMBL; AJ300340; CAC18855.1; -; Genomic_DNA.
DR   EMBL; AJ300341; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300342; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300343; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300347; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300349; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300351; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300353; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300355; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300364; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300363; CAC18855.1; JOINED; Genomic_DNA.
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DR   EMBL; AJ300361; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300360; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300359; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300358; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300357; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300356; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300373; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300372; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300371; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300370; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300369; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300368; CAC18855.1; JOINED; Genomic_DNA.
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DR   EMBL; AJ300366; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300365; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300382; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300381; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300380; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300379; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300378; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300377; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300376; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300375; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300374; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300399; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300398; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300397; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300396; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300395; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300394; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300393; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300392; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300391; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300416; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300415; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300414; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300413; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300412; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300411; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300410; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300409; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300408; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300433; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300432; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300431; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300430; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300429; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300428; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300427; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300426; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300425; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300444; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300443; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300442; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300441; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300440; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300439; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300438; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300437; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300436; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300435; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300434; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300424; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300423; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300422; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300421; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300420; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300419; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300418; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300417; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300407; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300406; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300405; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300404; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300403; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300402; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300401; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300400; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300390; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300389; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300388; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300387; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300386; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300385; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300384; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300383; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300354; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300352; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300350; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300348; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300346; CAC18855.1; JOINED; Genomic_DNA.
DR   EMBL; AJ300345; CAC18855.1; JOINED; Genomic_DNA.
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DR   EMBL; AJ300344; CAC18855.1; JOINED; Genomic_DNA.
DR   Ensembl; ENSG00000198626; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005262; F:calcium channel activity; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR   GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00036; efhand; 1.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50919; MIR; 5.
KW   Ion transport; Ionic channel; Motor protein; Muscle protein; Myosin;
KW   Receptor; Repeat; Transmembrane; Transport.
SQ   SEQUENCE   4967 AA;  564498 MW;  9A57C0BF9CC34E8A CRC64;

  Query Match             43.0%;  Score 6769;  DB 2;  Length 4967;
  Best Local Similarity   45.6%;  Pred. No. 0;
  Matches 1399;  Conservative  536;  Mismatches  854;  Indels  276;  Gaps   58;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
              |:||  | |:: ||||:| | | ||||     :::||||||||| ||||: :: ||:||
Db          2 ADGGEGE-DEIQFLRTDDEVVLQCTATIHKEQQKLCLAAEGFGNRLCFLESTSNSKNVPP 60

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKG--------------TGSGHRTLLYGNAI 104
              ||| | ||:||:|||||||:: |   |  :|              | ||||||||:||
Db         61 DLSICTFVLEQSLSVRALQEML-ANTVEKSEGQVDVEKWKFMMKTAQGGGHRTLLYGHAI 119

Qy        105 LLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGD 163
              ||||  | ||| ||||| || ||||||||||: : |||||||:||||||||||||||||||
Db        120 LLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVRVGD 179

Qy        164 DLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFF 223
              |||||||::||||| :  |     |:|:|  | ||| |  :|    :  ||: ||||||
Db        180 DLILVSVSSERYLHLSYGNGSLHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVLRLL 237

Qy        224 HGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRI 282
              ||  |||||:||    :  :  | ||||:|   |||||||  |  |:|  | |  | |:
Db        238 HGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGSHIRWGQPFRL 297

Qy        283 RHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKY 342
              ||:|||:|| : :   | |: :|:|   | ||  |  | ::  |   |::: :|   |||
Db        298 RHVTTGKYLSLMEDKNLLLMDKEKADVKSTAFTFRSSK-EKLDVGVRKEVDGMGTSEIKY 356

Qy        343 GDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRT 402
              |||   :|| :|||||:|:| : |   :| :: | ||:| || ||||:  |||| |||||
Db        357 GDSVCYIQHVDTGLWLTYQSVDVKSVRMGSIQRK-AIMHHEGHMDDGISLSRSQHEESRT 415

Qy        403 ARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHE 462
              |||||    || :|| ||: | : : |     : :  : : |:||| ||  ||| :|||
Db        416 ARVIRSTVFLFNRFIRGLDALSKKAKAST--VDLPIESVSLSLQDLIGYFHPPDEHLEHE 473

Qy        463 EKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGY 522
              :|||: |||:|||:||||||::||:|| ||:::| :|    |  :|| |:|:||: |
Db        474 DKQNRLRALKNRQNLFQEEGMINLVLECIDRLHVYSSAAHFAD-VAGREAGESWKSILNS 532

Qy        523 LYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNM 582
              ||:||||:|:||  |||||: |  |:|| |||  :     :|:|:||||||::||||||:
Db        533 LYELLAALIRGNRKNCAQFSGS--LDWLISRL--ERLEASSGILEVLHCVLVESPEALNI 588

Qy        583 MRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTAL 642
              ::: ||| |||||:|||||: ||||||||||| :||||||:|: ||| ||||::|||| |
Db        589 IKEGHIKSIISLLDKHGRNHKVLDVLCSLCVCHGVAVRSNQHLICDNLLPGRDLLLQTRL 648

Qy        643 VDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYPG 701
              |:||||:|||||:|  |||| |:|||:|: :|| |   |    |||:|||:| || ||||
Db        649 VNHVSSMRPNIFLGVSEGSAQYKKWYYELMVDHTEPFVTAEATHLRVGWASTEGYSPYPG 708

Qy        702 GGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPII 761
              |||:|||||||||:|||||| :||||      |:  :  :  :|  ||| | |||: | |
Db        709 GGEEWGGNGVGDDLFSYGFDGLHLWSGCIARTVSSPN--QHLLRTDDVISCCLDLSAPSI 766

Qy        762 NFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESL 821
              :|  ||  | | |||::|:||||:| |: :  |||||| ||  ::  | ||:|  |::
Db        767 SFRINGQPVQGMFENFNIDGLFFPVVSFSAGIKVRFLLGGRHGEFKFLPPPGYAPCYEAV 826

Qy        822 LPQQILSLEPC--FYFGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLA 879
              ||:: | :|    :        | | || :     || | |||| || || ::|:||:|||
Db        827 LPKEKLKVEHSREYKQERTYTRDLLGPTVSLTQAAFTPIPVDTSQIVLPPHLERIREKLA 886

Qy        880 ENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILAL 939
              |||||:| ||||| || ||  |:|  : |||||  | :||  |: |::|::::||||:|||
Db        887 ENIHELWVMNKIELGWQYGPVRDDNKRQHPCLVEFSKLPEQERNYNLQMSLETLKTLLAL 946

Qy        940 GYYISLDKPPA--RIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHN 997
              | :: :    |  ::: ::||   :  ::|||||:||| : |||  : :||:|||| ||
Db        947 GCHVGISDEHAEDKVKKMKLPKN-YQLTSGYKPAPMDLSFIKLTPSQEAMVDKLAENAHN 1005

Qy        998 LWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLD 1057
              :|||:||:|||||: :|    |:| |||| :||  ||:|:|:  | ||||| ||| |:
Db       1006 VWARDRIRQGWTYGIQQDVKNRRNPRLVPYTPLDDRTKKSNKDSLREAVRTLLGYGYNLE 1065

Qy       1058 PPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMA 1117
                |  :|  |   |        || :|||| ||| :|:|||||| :||| |||||:
Db       1066 AP--DQDHAARAEVCSGTGERFRIFRAEKTYAVKAGRWYFEPETVTAGDMRVGWSRPGCQ 1123

Qy       1118 PGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELL 1177
              |   || || ::||||:  :: : || | :|: |  |||||  :|: : |: |:||||:|
Db       1124 PDQELGSDERAFAFDGFKAQRWHQGN-EHYGRSWQAGDVVGCMVDMNEHTMMFTLNGEIL 1182

Qy       1178 MDALGGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVN 1236
              :|  | |  | |   || |:| |:||| |  |: :|:||:|||||| |||||||||| ||
Db       1183 LDDSGSELAFKDFDVGDGFIPVCSLGVAQVGRMNFGKDVSTLKYFTICGLQEGYEPFAVN 1242

Qy       1237 MKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE-- 1294
                ||:| | :|  | |       :  |:|||     |: ||||::  :| : : :| :
Db       1243 TNRDITMWLSKRLPQFLQVPSNHE-HIEVTRIDGTIDSSPCLKVTQKSFGS-QNSNTDIM 1300

Qy       1295 FLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGF--TMN 1352
              | |||:|: |   |                    : |  :|      :|    |
Db       1301 FYRLSMPIECAEVF--------------------SKTVAGGLPG-------AGLFGPKN 1332

Qy       1353 DIKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAE 1412
              |::   : : | |   ||                  : :| | :|:
Db       1333 DLEDYDADSDFEVL----MKTA-----------------HGHLVPDRVD---------- 1360

Qy       1413 MAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERG 1472
                              |||                                    ||
Db       1361 ----------------KDKEA---------------------------------TKPEFN 1371

Qy       1473 ARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATET 1532
                :   | | |:  ||:     :|              :||  |:   :
Db       1372 NHKDYAQEKPSRLKQRFLLRRTKP--------------------DYSTSHSARLTEDV 1409

Qy       1533 VGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVII 1592
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Db       1410 LADDRDDYDFLMQTSTYYYSVRIFPGQEPANVWVGWITSDFHQVDTGFDLDRVRTVTVTL 1469

Qy       1593 TDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEG 1652

Db       1470 GDEKGKVHESIKRSNCYMVCA----GESMSPGQGRN-NNGLEIGCVVDAASGLLTFIANG 1524

Qy       1653 KDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPP 1712

Db       1525 KELSTYYQVEPSTKLFPAVFAQATSPNVFQFELGRIKNVMPLSAGLFKSEHKNPVPQCPP 1584

Qy       1713 RLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEP 1772

Db       1585 RLHVQFLSHVLWSRMPNQFLKVDVSRISERQGWLVQCLDPLQFMSLHIPEENRSVDILEL 1644

Qy       1773 IEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYD 1832

Db       1645 TEQEELLKFHYHTLRLYSAVCALGNHRVAHALCSHVDEPQLLYAIENKYMPGLLRAGYYD 1704

Qy       1833 LLIALHLESHATTMEACKNEFVIPLGPELKA--LYEEPDMGHSLRSL-QTESVRPQMKMT 1889

Db       1705 LLIDIHLSSYATARLMMNNEYIVPMTEETKSITLFPDENKKHGLPGIGLSTSLRPRMQFS 1764

Qy       1890 DIAESITEISN---LYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLI 1946

Db       1765 --SPSFVSISNECYQYSPEFPLDILKSKTIQMLTEAVKEGSLHARDPVGGTTEFLFVPLI 1822

Qy       1947 KLVDRLLLVGMMRDEDVEKLLIM---------TNPETWDPSFDKE----------GKDE 1986

Db       1823 KLFYTLLIMGIFHNEDLKHILQLIEPSVFKEAATPEEESDTLEKELSVDDAKLQGAGEEE 1882

Qy       1987 ------HRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040

Db       1883 AKGGKRPKEGLLQMKLPEPVKLQMCLLLQYLCDCQVRHRIEAIVAFSDDFVAKLQDNQRF 1942

Qy       2041 RYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNE 2099

Db       1943 RYNEVMQALNMSAALTARKTKEFRSPPQEQINMLLNFK----DDKSECPCPEEIRDQLLD 1998

Qy       2100 FHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEE--AKAIEEPPKK 2157

Db       1999 FHEDLMTHCGIELDEDGSLDGNSDLTIR----GRLLSLVEKVTYLKKKQAEKPVESDSKK 2054

Qy       2158 TPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKT 2217

Db       2055 S--STLQQLISETMVRWAQESVIEDPELVRAMFVLLHRQYDGIGGLVRALPKTYTINGVS 2112

Qy       2218 KLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVM 2277

Db       2113 VEDTINLLASLGQIRSLLSVRMGKEEEKLMIRGLGDIMNNKVFYQHPNLMRALGMHETVM 2172

Qy       2278 AVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMF 2337

Db       2173 EVMVNVLG----------------GGESKE-ITFPKMVANCCRFLCYFCRISRQNQKAMF 2215

Qy       2338 DHFDPLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQ 2397

Db       2216 DHLSYLLENSSVGLASPAMRGSTPLDVAAASVMDNNELALALREPDLEKVVRYLAGCGLQ 2275

Qy       2398 SNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPAL 2457

Db       2276 SCQMLVSKGYPDIGWNPVEGERYLDFLRFAVFCNGESVEENANVVVRLLIRRPECFGPAL 2335

Qy       2458 RGE-GEGLLKAIVDANKMSERIADRRKLREMEQEG---DVNFSHPLPESDEDEDYIDTGA 2513

Db       2336 RGEGGNGLLAAMEEAIKIAE---------DPSRDGPSPNSGSSKTLDTEEEEDDTIHMGN 2386

Qy       2514 AILNPYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPA 2573

Db       2387 AIMTFYSALIDLLGRCAPEMHLIHAGKGEAIRIRSILRSLIPLGDLVGVISIAFQMPTIA 2446

Qy       2574 AGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRND 2633

Db       2447 KDGNVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRAAASLDTAA 2506

Qy       2634 GCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQR 2693

Db       2507 LSATDMALALNRYLCTAVLPLLTRCAPLFAGTEHHASLIDSLLHTVYRLSKGCSLTKAQR 2566

Qy       2694 EAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGA 2753

Db       2567 DSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCWKYYCLPG- 2625

Qy       2754 GQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKN 2813

Db       2626 GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALPPDY-MESN 2684

Qy       2814 YDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGW 2873

Db       2685 YVSMM--EKQSSMDSEG-NFNPQPVDTSNITIPEKLEYFINKYAEHSHDKWSMDKLANGW 2741

Qy       2874 VYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNR 2933

Db       2742 IYGEIYSDSSKVQPLMKPYKLLSEKEKEIYRWPIKESLKTMLARTMRTERTR----EGDS 2797

Qy       2934 SSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKK 2993

Db       2798 MALYNRTRRISQTSQVSVDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAENYHNIWAKK 2855

Qy       2994 KKEEL 2998

Db       2856 KKMEL 2860
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RESULT 12
Q9ERN6_MOUSE
ID Q9ERN6_MOUSE PRELIMINARY; PRT; 4967 AA.
AC Q9ERN6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cardiac Ca2+ release channel.
GN Name=Ryr2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99403027; PubMed=10473538; DOI=10.1074/jbc.274.37.25971;
RA Zhao M., Li P., Li X., Zhang L., Winkfein R.J., Chen S.R.;
RT "Molecular identification of the ryanodine receptor pore-forming
RT segment.";
RL J. Biol. Chem. 274:25971-25974(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chen S.W.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF295105; AAG34081.1; -; mRNA.
DR Ensembl; ENSMUSG00000021313; Mus musculus.
DR MGI; MGI:99685; Ryr2.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005262; F:calcium channel activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR000699; Ca-rel_channel.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002048; EF_hand_Ca_bd.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003608; MIR.
DR InterPro; IPR003032; Ryanodine_recept.

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DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00036; efhand; 1.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00054; EFh; 2.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50919; MIR; 5.
SQ   SEQUENCE   4967 AA;  564900 MW;  81A27F4DCFF4E4FB CRC64;

  Query Match             42.9%;  Score 6758;  DB 2;  Length 4967;
  Best Local Similarity   45.4%;  Pred. No. 0;
  Matches 1396;  Conservative  539;  Mismatches  851;  Indels  286;  Gaps   57;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KN 55
              ||:|  |   :|:: ||||:| | | ||||     :::|||||||||| ||||: :: ||
Db          1 MADAGEG---EDEIQFLRTDDEVVLQCTATIHKEQQKLCLAAEGFGNRLCFLESTSNSKN 57

Qy         56 IPPDLSQCVFVIEQALSVRALQELVTAAGSETGKG--------------TGSGHRTLLYG 101
              :|||||  | ||:||:||||||||:: |    |  :|                | ||||||||
Db         58 VPPDLSICTFVLEQSLSVRALQEML-ANTVEKSEGQVDVEKWKFMMKTAQGGGHRTLLYG 116

Qy        102 NAILLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVR 160
              :||||||  | ||| |||||  || ||||||||||: : |||||||:|||||||||||||
Db        117 HAILLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVR 176

Qy        161 VGDDLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVL 220
              ||||||||||::||||| :  |    |:|:|  | ||| |  :|    :  ||: |||||
Db        177 VGDDLILVSVSSERYLHLSYGNSSWHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVL 234

Qy        221 RFFHGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHP 279
              |  ||  |||||:||    :  :  | ||||:|  |||||||  |  |:|  | |  |
Db        235 RLLHGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGSHIRWGQP 294

Qy        280 MRIRHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPI 339
              |:|||:|||:|| : :   | |: :|:|  | ||  |  | ::  |   |::: :|
Db        295 FRLRHVTTGKYLSLMEDKNLLLMDKEKADVKSTAFAFRSSK-EKLDVGVRKEVDGMGTSE 353

Qy        340 IKYGDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEE 399
              ||||||   :|| :|||||:|:: : |   :| :: | ||:|  || |||||: |||| ||
Db        354 IKYGDSICYIQHVDTGLWLTYQAVDVKSARMGSIQRK-AIMHHEGHMDDGLNLSRSQHEE 412

Qy        400 SRTARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDM 459
              ||||||||     || :|| ||: |  :::  :    : :  : : |:||| ||   ||| :
Db        413 SRTARVIRSTVFLFNRFIRGLDAL--SKKVKLPTIDLPIESVSLSLQDLIGYFHPPDEHL 470

Qy        460 EHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMI 519
              |||:|||: |||:|||:||||||::||:|| ||:::| :|    | :|| |:|:||: |
Db        471 EHEDKQNRLRALKNRQNLFQEEGMINLVLECIDRLHVYSSAAHFAD-VAGREAGESWKSI 529

Qy        520 SGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEA 579
                ||:||||:|:||  |||||: |  |:|| |||  :     :|:|:||||||::||||
Db        530 LNSLYELLAALIRGNRKNCAQFSGS--LDWLISRL--ERLEASSGILEVLHCVLVESPEA 585

Qy        580 LNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQ 639
              ||:::: ||| |||||:|||| |||||||||| :||||||:|: ||| ||||::||||
Db        586 LNIIKEGHIKSIISLLDKHGRNHKVLDVLCSLCVCHGVAVRSNQHLICDNLLPGRDLLLQ 645

Qy        640 TALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVP 698
              | ||:||||:|||||:|  |||| |:|||:|: :|| |   |    |||:|||:| || |
Db        646 TRLVNHVSSMRPNIFLGVSEGSAQYKKWYYELMVDHTEPFVTAEATHLRVGWASTEGYSP 705

Qy        699 YPGGGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTV 758
              ||||||:|||||||||:|||||| :||||      |:  :  :  :|  ||| | |||:
Db        706 YPGGGEEWGGNGVGDDLFSYGFDGLHLWSGCIARTVSSPN--QHLLRTDDVISCCLDLSA 763

Qy        759 PIINFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLV 818
              | |:|  ||  | | | |||::|:||||:| |: :  ||||| ||  ::  | ||:
Db        764 PSISFRINGQPVQGMFENFNIDGLFFPVVSFSAGIKVRFLLGGRHGEFKFLPPPGYAACY 823

Qy        819 ESLLPQQILSLEPC--FYFGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRD 876
              |::||:: | :|    :        | | || :      || | |||| || || ::|:||:
Db        824 EAVLPKEKLKVEHSREYKQERTYTRDLLGPTVSLTQAAFTPVPVDTSQIVLPPHLERIRE 883

Qy        877 KLAENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTI 936
              :|||||||:| ||||| || ||  |:|  : |||||  | :||  |: |::|::::||||:
Db        884 RLAENIHELWVMNKIELGWQYGPVRDDNKRQHPCLVEFCKLPEQERNYNLQMSLETLKTL 943

Qy        937 LALGYYISL--DKPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAEN 994
              |||| :: :  :    ::: ::||   :  ::|||||:||| : |||  : :||:||||
Db        944 LALGCHVGIADEHAEEKVKKMKLPKN-YQLTSGYKPAPMDLSFIKLTPSQEAMVDKLAEN 1002

Qy        995 THNLWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGY 1054
              ||:|||:||:|||||: :|    |:| |||| :||  ||:|:|:  | ||||| |||
Db       1003 AHNVWARDRIRQGWTYGIQQDVKNRRNPRLVPYTLLDDRTKKSNKDSLREAVRTLLGYGY 1062

Qy       1055 MLDPPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHA 1114
              |: |  :|  |  |      || :|||| ||| :|:|||||| :||| |||||:
Db       1063 HLEAP--DQDHASRAEVCSGTGERFRIFRAEKTYAVKAGRWYFEFEAVTAGDMRVGWSRP 1120

Qy       1115 DMAPGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNG 1174
                | : || |: ::||||:  :: : || | :|: |  |||||  :|: : |: |:|||
Db       1121 GCQPDLELGSDDRAFAFDGFKAQRWHQGN-EHYGRSWQAGDVVGCMVDMNEHTMMFTLNG 1179

Qy       1175 ELLMDALGGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPF 1233
              |:|:|  | |  | |    || |:|  |:||| |  |: :|:||:|||||  ||||||||
Db       1180 EILLDDSGSELAFKDFDVGDGFIPVCSLGVAQVGRMNFGKDVSTLKYFTICGLQEGYEPF 1239

Qy       1234 CVNMKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTPETM-EKAN 1292
              ||  ||:| | :|  | |        :  |:||||    |: ||||::  :| :    :
Db       1240 AVNTNRDITMWLSKRLPQFLQVPSNHE-HIEVTRIDGTIDSSPCLKVTQKSFGSQNNNTD 1298

Qy       1293 WEFLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGP--T 1350
                | |||:|: |   |                        ::|   :|        :||
Db       1299 IMFYRLSMPIECAEVF--------------------SKSVAGGLPG-------AGFYGP 1330

Qy       1351 MNDIKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSE 1410
                :|::    : : | |     ||                  : :| | :::
Db       1331 KSDLEDFDVDSDFEVL----MKTA-----------------HGHLVPDRID-------- 1360

Qy       1411 AEMAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPE 1470
                                 |||                    :||          ||
Db       1361 -----------------KDK-----------------------ETP--------KPE 1369

Qy       1471 RGARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSAT 1530
                :  | | |:  ||:     :|                        :|   |:
Db       1370 FNNHKDYAQEKPSRLKQRFLLRRTKP--------------------DYSTGHSARLTE 1407

Qy       1531 ETVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSV 1590
              : :  :  | | |    : |:| |||:|||:| :|::||:|: :| :    |:  :|   :|
Db       1408 DVLAGDRDDYEYLMQTSTYYYSVRIFPGQEPANVWVGWITSDFHQYDTGFDLDRVRTVTV 1467

Qy       1591 IITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTC 1650
              : |:  :| |:: | :|||| |     | |:    :  | |: ||| || ::| ::|
Db       1468 TLGDEKGKVHESIKRSNCYMVCA----GESMSPGQGRNNSNGLEIGCVVDAASGLLTFIA 1523

Qy       1651 EGKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQF 1710
                ||: |  :::|| |||||:| :|||  : | ||||    :|||| :  :  |: :||
Db       1524 NGKELSTYYQVEPSTKLFPAVFAQATSPNVFQFELGRIKNVMPLSAGLFKSEHKNPVPQC 1583

Qy       1711 PPRLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDIL 1770
              |||| ||  |    |:|:|||  :|  ::|: :|| : | | :  ::|||||:| :|||
Db       1584 PPRLHVQFLSHVLWSRMPNQFLKVDVSRISERQGWLVQCLDPLQFMSLHIPEENRSVDIL 1643

Qy       1771 EPIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGF 1830
              |  | ::|| || ||| ||:|:|   |:| |||||:|||: ||||||:::|| | || |:
Db       1644 ELTEQEELLQFHYHTLRLYSAVCALGNHRVAHALCSHVDEPQLLYAIENKYMPGLLRAGY 1703
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Qy       1831 YDLLIALHLESHATTMEACKNEFVIPLGPELKA--LYEEPDMGHSLRSL-QTESVRPQMK 1887
Db       1704 YDLLIDIHLSSYATARLMMNNEFIVPMTEETKSITLFPDENKKHGLPGIGLSTSLRPRMR 1763

Qy       1888 MTDIAESITEISN---LYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLP 1944
Db       1764 FS--SPSFVSISNDCYQYSPEFPLDILKAKTIQMLTEAVKEGSLHARDPVGGTTEFLFVP 1821

Qy       1945 LIKLVDRLLLVGMMRDEDVEKLLIMTNPETW--------------------DPSFDKE-- 1982
Db       1822 LIKLFYTLLIMGIFHNEDLKHILQLIEPSVFKEAAVPEEEGGTPEKEISIEDAKLEGEEE 1881

Qy       1983 --GKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040
Db       1882 AKGGKRPKEGLLQMKLPEPVKLQMCLLLQYLCDCQVRHRIEAIVAFSDDFVAKLQDNQRF 1941

Qy       2041 RYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNE 2099
Db       1942 RYNEVMQALNMSAALTARKTKEFRSPPQEQINMLLNFK----DDKSECPCPEEIRDQLLD 1997

Qy       2100 FHDTLMAHVSLHALQEPDAAENQEPEAKPGAPGKLYNIINTVKELEEEAKAIEEPPKKTP 2159
Db       1998 FHEDLMTHCGIELDEDGSLDGSNDLTIR----GRLLSLVEKVTYLKK--KQAEKPVASDS 2051

Qy       2160 EE--KFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKT 2217
Db       2052 RKCSSLQQLISETMVRWAQESVIEDPELVRAMFVLLHRQYDGIGGLVRALPKTYTINGVS 2111

Qy       2218 KLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVM 2277
Db       2112 VEDTINLLASLGQIRSLLSVRMGKEEEKLMIRGLGDIMNNKVFYQHPNLMRALGMHETVM 2171

Qy       2278 AVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMF 2337
Db       2172 EVMVNVLG----------------GGESKE-ITFPKMVANCCRFLCYFCRISRQNQKAMF 2214

Qy       2338 DHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEK-IAVYLSRCGL 2396
Db       2215 DHLSYLLENSSVGLASPAMRGSTPLDVAAASVMDNNELALALREPDLEKVVARYLAGCGL 2274

Qy       2397 QSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPA 2456
Db       2275 QSCQMLVSKGYPDIGWNPVEGERYLDFLRFAVFCNGESVEENANVVVRLLIRRPECFGPA 2334

Qy       2457 LRGE-GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPES---------DEDE 2506
Db       2335 LRGEGGNGLLAAMEEAIKIAE----------------DPSRDGPSPTSGSSKTLDIEEEED 2379

Qy       2507 DYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLR 2566
Db       2380 DTIHMGNAIMTFYAALIDLLGRCAPEMHLIHAGKGEAIRIRSILRSLIPLGDLVGVISIA 2439

Qy       2567 FTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAA 2626
Db       2440 FQMPTIAKDGKVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRAA 2499

Qy       2627 TMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNR 2686
Db       2500 ASLDTAALSATDMALALNRYLCTAVLPLLTRCARLFAGTEHHASLIDSLLHTVYRLSKGC 2559

Qy       2687 MLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAK 2746
Db       2560 SLTKAQRDSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCWK 2619

Qy       2747 YYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPP 2806
Db       2620 YYCLPG-GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALPP 2678

Qy       2807 DYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWAS 2866
Db       2679 DY-MESNYVSMM--EKQSSMDSEG-NFNPQPVDTSNITIPEKLEYFINKYAEHSHDKWSM 2734

Qy       2867 RKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEV 2926
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Db       2735 DKLANGWIYGEIYSDSSKIQPLMKPYKLLSEKEKEIYRWPIKESLKTMLAWGWRIERTR- 2793

Qy       2927 DIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNA 2986

Db       2794 ---EGDSMALYNRTRRISQTSQVSIDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAENY 2848

Qy       2987 HDIWAKKKKEEL 2998

Db       2849 HNIWAKKKKLEL 2860
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RESULT 13
Q5VWP1_HUMAN
ID Q5VWP1_HUMAN PRELIMINARY; PRT; 4965 AA.
AC Q5VWP1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Ryanodine receptor 2 (Cardiac).
GN ORFNames=RP4-626J7.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wall M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Coville G.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Moore M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Pearce A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Griffiths C.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RA Clark S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light chains
CC (By similarity).
CC -!- DOMAIN: Each of the four internal repeats contains five
CC hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC positively charged transmembrane segment (S4). S4 segments
CC probably represent the voltage-sensor and are characterized by a
CC series of positively charged amino acids at every third position
CC (By similarity).
DR EMBL; AL391809; CAI14440.1; -; Genomic_DNA.
DR EMBL; AL442065; CAI15350.1; -; Genomic_DNA.
DR EMBL; AL513130; CAI15936.1; -; Genomic_DNA.
DR EMBL; AL356773; CAH73918.1; -; Genomic_DNA.
DR EMBL; AL445473; CAH71393.1; -; Genomic_DNA.
DR EMBL; AL365332; CAH71369.1; -; Genomic_DNA.
DR EMBL; AL359924; CAI22065.1; -; Genomic_DNA.
DR EMBL; AL513130; CAI22065.1; JOINED; Genomic_DNA.
DR EMBL; AL359924; CAI14440.1; JOINED; Genomic_DNA.
DR EMBL; AL356773; CAI14440.1; JOINED; Genomic_DNA.
DR EMBL; AL365332; CAI14440.1; JOINED; Genomic_DNA.

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DR   EMBL; AL445473; CAI14440.1; JOINED; Genomic_DNA.
DR   EMBL; AL359924; CAI15350.1; JOINED; Genomic_DNA.
DR   EMBL; AL391809; CAI15350.1; JOINED; Genomic_DNA.
DR   EMBL; AL445473; CAI15936.1; JOINED; Genomic_DNA.
DR   EMBL; AL442065; CAI15936.1; JOINED; Genomic_DNA.
DR   EMBL; AL391809; CAI15936.1; JOINED; Genomic_DNA.
DR   EMBL; AL365332; CAI15936.1; JOINED; Genomic_DNA.
DR   EMBL; AL359924; CAI15936.1; JOINED; Genomic_DNA.
DR   EMBL; AL356773; CAI15936.1; JOINED; Genomic_DNA.
DR   EMBL; AL513130; CAI15350.1; JOINED; Genomic_DNA.
DR   EMBL; AL445473; CAI15350.1; JOINED; Genomic_DNA.
DR   EMBL; AL513130; CAH73918.1; JOINED; Genomic_DNA.
DR   EMBL; AL445473; CAH73918.1; JOINED; Genomic_DNA.
DR   EMBL; AL442065; CAH73918.1; JOINED; Genomic_DNA.
DR   EMBL; AL391809; CAH73918.1; JOINED; Genomic_DNA.
DR   EMBL; AL365332; CAH73918.1; JOINED; Genomic_DNA.
DR   EMBL; AL359924; CAH73918.1; JOINED; Genomic_DNA.
DR   EMBL; AL365332; CAI15350.1; JOINED; Genomic_DNA.
DR   EMBL; AL356773; CAH71393.1; JOINED; Genomic_DNA.
DR   EMBL; AL513130; CAH71369.1; JOINED; Genomic_DNA.
DR   EMBL; AL445473; CAH71369.1; JOINED; Genomic_DNA.
DR   EMBL; AL442065; CAH71369.1; JOINED; Genomic_DNA.
DR   EMBL; AL391809; CAH71369.1; JOINED; Genomic_DNA.
DR   EMBL; AL359924; CAH71369.1; JOINED; Genomic_DNA.
DR   EMBL; AL356773; CAH71369.1; JOINED; Genomic_DNA.
DR   EMBL; AL445473; CAI22065.1; JOINED; Genomic_DNA.
DR   EMBL; AL442065; CAI22065.1; JOINED; Genomic_DNA.
DR   EMBL; AL391809; CAI22065.1; JOINED; Genomic_DNA.
DR   EMBL; AL365332; CAI22065.1; JOINED; Genomic_DNA.
DR   EMBL; AL356773; CAI22065.1; JOINED; Genomic_DNA.
DR   EMBL; AL513130; CAH71393.1; JOINED; Genomic_DNA.
DR   EMBL; AL442065; CAH71393.1; JOINED; Genomic_DNA.
DR   EMBL; AL391809; CAH71393.1; JOINED; Genomic_DNA.
DR   EMBL; AL365332; CAH71393.1; JOINED; Genomic_DNA.
DR   EMBL; AL359924; CAH71393.1; JOINED; Genomic_DNA.
DR   EMBL; AL356773; CAI15350.1; JOINED; Genomic_DNA.
DR   EMBL; AL513130; CAI14440.1; JOINED; Genomic_DNA.
DR   EMBL; AL442065; CAI14440.1; JOINED; Genomic_DNA.
DR   Ensembl; ENSG00000198626; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005262; F:calcium channel activity; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR   GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00036; efhand; 1.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50919; MIR; 5.
KW   Ion transport; Ionic channel; Motor protein; Muscle protein; Myosin;
KW   Receptor; Repeat; Transmembrane; Transport.
SQ   SEQUENCE   4965 AA;  564742 MW;  04ECD3C1676C3ADB CRC64;
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  Query Match             41.7%;  Score 6566.5;  DB 2;  Length 4965;
  Best Local Similarity   45.0%;  Pred. No. 0;
  Matches 1354;  Conservative  529;  Mismatches  848;  Indels  275;  Gaps   54;

Qy         44 RHCFLENIADKNIPPDLSQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNA 103
              | |:|    ::    |: :  |::: |                       | |||||||:|
Db         77 RRCWLTPWRNQKGQVDVEKWKFMMKTA-------------------QGGGHRTLLYGHA 116

Qy        104 ILLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVG 162
              |||||  | ||| ||||| || ||||||||||: : |||||||:||||||||||||||||
Db        117 ILLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVRVG 176

Qy        163 DDLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRF 222
              ||||||||::||||| :  |    |:|:|  | ||| |  :|    :  ||: ||||||
Db        177 DDLILVSVSSERYLHLSYGNGSLHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVLRL 234

Qy        223 FHGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMR 281
              ||  |||||:||    :  :  | ||||:|   ||||||||  |  |:|  | |  | |
Db        235 LHGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGSHIRWGQPFR 294

Qy        282 IRHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIK 341
              :||:|||:|| : :   | |: :|:|  | ||  |  | ::  |  |::: :|   ||
Db        295 LRHVTTGKYLSLMEDKNLLLMDKEKADVKSTAFTFRSSK-EKLDVGVRKEVDGMGTSEIK 353

Qy        342 YGDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESR 401
              ||||   :|| :|||||:|:| : |   :| :: | ||:| || ||||:  |||| ||||
Db        354 YGDSVCYIQHVDTGLWLTYQSVDVKSVRMGSIQRK-AIMHHEGHMDDGISLSRSQHEESR 412

Qy        402 TARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEH 461
              ||||||    || :|| ||: | :  : |     : :  : : |:||| ||  ||| :||
Db        413 TARVIRSTVFLFNRFIRGLDALSKKAKAST--VDLPIESVSLSLQDLIGYFHPPDEHLEH 470

Qy        462 EEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISG 521
              |:|||: |||:|||:||||||::||:|| ||:::| :|    |  :|| |:|:||: |
Db        471 EDKQNRLRALKNRQNLFQEEGMINLVLECIDRLHVYSSAAHFAD-VAGREAGESWKSILN 529

Qy        522 YLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALN 581
              ||:||||:|:||  |||||: |  |:|| |||  :     :|:|:||||||::||||||
Db        530 SLYELLAALIRGNRKNCAQFSGS--LDWLISRL--ERLEASSGILEVLHCVLVESPEALN 585

Qy        582 MMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTA 641
              :::: ||| |||||:|||: |||||||||| :||||||:|: ||| |||||::|||||
Db        586 IIKEGHIKSIISLLDKHGRNHKVLDVLCSLCVCHGVAVRSNQHLICDNLLPGRDLLLQTR 645

Qy        642 LVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYP 700
              ||:||||:|||||:|  |||| |:||||:|: :|| |   |    |||:|||:| || |||
Db        646 LVNHVSSMRPNIFLGVSEGSAQYKKWYYELMVDHTEPFVTAEATHLRVGWASTEGYSPYP 705

Qy        701 GGGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPI 760
              ||||:||||||||:|||||| :||||      |:  :  :  :|  ||| | |||: |
Db        706 GGGEEWGGNGVGDDLFSYGFDGLHLWSGCIARTVSSPN--QHLLRTDDVISCCLDLSAPS 763

Qy        761 INFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVES 820
              |:|  ||  | | | |||::|:||||:| |: :  ||||| ||  ::  | ||:|  |:
Db        764 ISFRINGQPVQGMFENFNIDGLFFPVVSFSAGIKVRFLLGGRHGEFKFLPPPGYAPCYEA 823

Qy        821 LLPQQILSLEPC--FYFGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKL 878
              :||:: | :|    :       | | || :     || | |||| || || ::|:||:||
Db        824 VLPKEKLKVEHSREYKQERTYTRDLLGPTVSLTQAAFTPIPVDTSQIVLPPHLERIREKL 883

Qy        879 AENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILA 938
              ||||||:| ||||| || ||  |:|  : |||||  | :||  |: |::|::::||||:||
Db        884 AENIHELWVMNKIELGWQYGPVRDDNKRQHPCLVEFSKLPEQERNYNLQMSLETLKTLLA 943

Qy        939 LGYYISLDKPPA--RIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTH 996
              || :: :    |  ::: ::||   :  ::||||||:||| : |||  : :||:|||| |
Db        944 LGCHVGISDEHAEDKVKKMKLPKN-YQLTSGYKPAPMDLSFIKLTPSQEAMVDKLAENAH 1002

Qy        997 NLWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYML 1056
              |:|||:||:||||||: :|    |:| |||| :||  ||:|:|:  | ||||| ||| |
Db       1003 NVWARDRIRQGWTYGIQQDVKNRRNPRLVPYTLLDDRTKKSNKDSLREAVRTLLGYGYNL 1062
```

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Qy       1057 DPPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADM 1116
Db       1063 EAP--DQDHAARAEVCSGTGERFRIFRAEKTYAVKAGRWYFEFETVTAGDMRVGWSRPGC 1120

Qy       1117 APGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGEL 1176
Db       1121 QPDQELGSDERAFAFDGFKAQRWHQGN-EHYGRSWQAGDVVGCMVDMNEHTMMFTLNGEI 1179

Qy       1177 LMDALGGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCV 1235
Db       1180 LLDDSGSELAFKDFDVGDGFIPVCSLGVAQVGRMNFGKDVSTLKYFTICGLQEGYEPFAV 1239

Qy       1236 NMKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE- 1294
Db       1240 NTNRDITMWLSKRLPQFLQVPSNHE-HIEVTRIDGTIDSSPCLKVTQKSFGS-QNSNTDI 1297

Qy       1295 -FLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGF--TM 1351
Db       1298 MFYRLSMPIECAEVF----------------------SKTVAGGLPG-------AGLFGPK 1329

Qy       1352 NDIKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEA 1411
Db       1330 NDLEDYDADSDPEVL----MKTA-----------------HGHLVPDRVD--------- 1358

Qy       1412 EMAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPER 1471
Db       1359 ----------------KDKEA--------------------------------TKPEF 1368

Qy       1472 GARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATE 1531
Db       1369 NNHKDYAQEKPSRLKQRFLLRRTKP----------------------DYSTSHSARLTED 1406

Qy       1532 TVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVI 1591
Db       1407 VLADDRDDYDFLMQTSTYYYSVRIFPGQEPANVWVGWITSDFHQYDTGFDLDRVRTVTVT 1466

Qy       1592 ITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCE 1651
Db       1467 LGDEKGKVHESIKRSNCYMVCA----GESMSPGQGRN-NNGLEIGCVVDAASGLLTFIAN 1521

Qy       1652 GKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFP 1711
Db       1522 GKELSTYYQVEPSTKLFPAVFAQATSPNVFQFELGRIKNVMPLSAGLFKSEHKNPVPQCP 1581

Qy       1712 PRLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILE 1771
Db       1582 PRLHVQFLSHVLWSRMPNQFLKVDVSRISERQGWLVQCLDPLQFMSLHIPEENRSVDILE 1641

Qy       1772 PIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFY 1831
Db       1642 LTEQEELLKFHYHTLRLYSAVCALGNHRVAHALCSHVDEPQLLYAIENKYMPGLLRAGYY 1701

Qy       1832 DLLIALHLESHATTMEACKNEFVIPLGPELKA--LYEEPDMGHSLRSL-QTESVRPQMKM 1888
Db       1702 DLLIDIHLSSYATARLMMNNEYIVPMTEETKSITLFPDENKKHGLPGIGLSTSLRPRMQF 1761

Qy       1889 TDIAESITEISN---LYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPL 1945
Db       1762 S--SPSFVSISNECYQYSPEFPLDILKSKTIQMLTEAVKEGSLHARDPVGGTTEFLFVPL 1819

Qy       1946 IKLVDRLLLVGMMRDEDVEKLLIM---------TNPETWDPSFDKE-----------GKD 1985
Db       1820 IKLFYTLLIMGIFHNEDLKHILQLIEPSVFKEAATPEEESDTLEKELSVDDAKLQGAGEE 1879

Qy       1986 E------HRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQL 2039
Db       1880 EAKGGKRPKEGLLQMKLPEPVKLQMCLLLQYLCDCQVRHRIEAIVAFSDDFVAKLQDNQR 1939

Qy       2040 RRYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMN 2098
Db       1940 FRYNEVMQALNMSAALTARKTKEFRSPPQEQINMLLNFK----DDKSECPCPEEIRDQLL 1995

Qy       2099 EFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEE--AKAIEEPPK 2156

Db       1996 DFHEDLMTHCGIELDEDGSLDGNSDLTIR----GRLLSLVEKVTYLKKKQAEKPVESDSK 2051

Qy       2157 KTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAK 2216
Db       2052 KS--STLQQLISETMVRWAQESVIEDPELVRAMFVLLHRQYDGIGGLVRALPKTYTINGV 2109

Qy       2217 TKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENV 2276
Db       2110 SVEDTINLLASLGQIRSLLSVRMGKEEEKLMIRGLGDIMNNKVFYQHPNLMRALGMHETV 2169

Qy       2277 MAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAM 2336
Db       2170 MEVMVNVLG----------------GGESKE-ITFPKMVANCCRFLCYFCRISRQNQKAM 2212

Qy       2337 FDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGL 2396
Db       2213 FDHLSYLLENSSVGLASPAMRGSTPLDVAAASVMDNNELALALREPDLEKVVRYLAGCGL 2272

Qy       2397 QSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPA 2456
Db       2273 QSCQMLVSKGYPDIGWNPVEGERYLDFLRFAVFCNGESVEENANVVVRLLIRRPECFGPA 2332

Qy       2457 LRGE-GEGLLKAIVDANKMSERIADRRKLREMEQEG---DVNFSHPLPESDEDEDYIDTG 2512
Db       2333 LRGEGGNGLLAAMEEAIKIAE---------DPSRDGPSPNSGSSKTLDTEEEEDDTIHMG 2383

Qy       2513 AAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNP 2572
Db       2384 NAIMTFYSALIDLLGRCAPEMHLIHAGKGEAIRIRSILRSLIPLGDLVGVISIAFQMPTI 2443

Qy       2573 AAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRN 2632
Db       2444 AKDGNVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRAAASLDTA 2503

Qy       2633 DGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQ 2692
Db       2504 ALSATDMALALNRYLCTAVLPLLTRCAPLFAGTEHHASLIDSLLHTVYRLSKGCSLTKAQ 2563

Qy       2693 REAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTG 2752
Db       2564 RDSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCWKYYCLPG 2623

Qy       2753 AGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSK 2812
Db       2624 -GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALPPDY-MES 2681

Qy       2813 NYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENG 2872
Db       2682 NYVSMM--EKQSSMDSEG-NFNPQPVDTSNITIPEKLEYFINKYAEHSHDKWSMDKLANG 2738

Qy       2873 WVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNN 2932
Db       2739 WIYGEIYSDSSKVQPLMKPYKLLSEKEKEIYRWPIKESLKTMLAWGWRIERTR----EGD 2794

Qy       2933 RSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAK 2992
Db       2795 SMALYNRTRRISQTSQVSVDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAENYHNIWAK 2852

Qy       2993 KKKEEL 2998
Db       2853 KKKMEL 2858
```

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RESULT 14
Q91313_RANCA
ID   Q91313_RANCA PRELIMINARY;      PRT;  5037 AA.
AC   Q91313;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ryanodine receptor alpha isoform.
GN   Name=FROG-ARR;
```

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OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
OC   Aquarana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=94274714; PubMed=8006029;
RA   Oyamada H., Murayama T., Takagi T., Iino M., Iwabe N., Miyata T.,
RA   Ogawa Y., Endo M.;
RT   "Primary structure and distribution of ryanodine-binding protein
RT   isoforms of the bullfrog skeletal muscle.";
RL   J. Biol. Chem. 269:17206-17214(1994).
CC   -!- DOMAIN: Each of the four internal repeats contains five
CC       hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and one
CC       positively charged transmembrane segment (S4). S4 segments
CC       probably represent the voltage-sensor and are characterized by a
CC       series of positively charged amino acids at every third position
CC       (By similarity).
DR   EMBL; D21070; BAA04646.1; -; mRNA.
DR   PIR; A54161; A54161.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005262; F:calcium channel activity; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005219; F:ryanodine-sensitive calcium-release channel. . .; IEA.
DR   GO; GO:0006874; P:calcium ion homeostasis; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50919; MIR; 5.
KW   Ion transport; Ionic channel; Receptor; Repeat; Transmembrane;
KW   Transport.
SQ   SEQUENCE   5037 AA;  571291 MW;  FF263948A51C3ABF CRC64;

  Query Match             41.5%;  Score 6534.5;  DB 2;  Length 5037;
  Best Local Similarity   44.3%;  Pred. No. 0;
  Matches 1371;  Conservative  539;  Mismatches  875;  Indels  311;  Gaps   64;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
              ||||  | |:: |||||:| | |:||      ::|:  |||||| |:||: :: :| ||
Db          2 AEGGEGE-DEIQFLRTEDVVVLQCSATIRKENLKMCMGVEGFGNRLCYLESTSNAQNAPP 60

Qy         59 DLSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYL 115
              ||: | |::||:|||||||::      |||: :  | ||||||||:|||||| :|||||
Db         61 DLAICCFILEQSLSVRALQEMLANTVEMGSESSQ--GGGHRTLLYGHAILLRHCHSDMYL 118

Qy        116 ACLSTSSS-QDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATER 174
               ||:|| |  |||||||||: : |||||||:|||||||||||||:|||||||::||
Db        119 CCLTTSRSLTDKLAFDVGLQEDASGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSER 178

Qy        175 YLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGG-DECLTIP 233
                ||| :  :    |:|||  | |:: |  :|    :  ||| |||||| ||| ||||||
Db        179 YLHLSTASGDLQVDASFMQTLWNMNPITSGCEIAE--GYVTGGDVLRLFHGHMDECLTIS 236

Qy        234 STWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGV 293
              ||   :  : |  ||||:| | |||||| |  |  |:|  : |  | | ||:||||||
Db        237 STDQGEEQRRIPHYEGGAVCSHARSLWRSEPLRISWSGSHMRWGMPFRARHVTTGRYLAR 296

Qy        294 NDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSE 353
               ::  | ||  |:| | : ||| |  | ::  |   :|:| :|   ||||:|   |||
Db        297 EEERGLVLVDAEKANTKATAFCFRISK-EKLDVAPKRDIEGMGPADIKYGESMCFVQHVN 355

Qy        354 TGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
              :||||:| : ::|   :| :: | ||||:|| ||| |  |||| |||: ||:|   : ||
Db        356 SGLWLTYAAADSKVARLGPLKRK-AILHQEGHMDDALSLSRSQREESQAARMIYSTAGLF 414

Qy        414 TKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRN 473
                || ||::|    : |   |: |  :|: |:||| ||  |:|:::||||| | |:|:|
Db        415 NIFIKGLDSLNGKNKPSKPI-SLPLDMVVLTLQDLIGYFQHPEEELQHEEKQTKLRSLKN 473

Qy        474 RQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKG 533
              ||:|||||||:: :|: ||::|| ::    | | ||:|: :||: |   ||:|||::|:|
Db        474 RQNLFQEEGIISQVLDCIDRLNVYSTAAHFAEF-AGEEAAESWKEIVNLLYELLASLIRG 532

Qy        534 NHTNCAQFANSNRLNWLFSRLGS-QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVII 592
              | :||| |  || |:|: |:|   :||   :|:|:||:||||:||| |||:::  ||| ||
Db        533 NRSNCALF--SNNLDWVVSKLDRLEAS---SGILEVLYCVLIESPEVLNIIKKNHIKSII 587

Qy        593 SLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPN 652
              |||:||||: ||||||||||| |||||||:|| | : ||| ::|||||  :|::|:|:|||
Db        588 SLLDKHGRNHKVLDVLCSLCVCNGVAVRSNQNLITENLLPRRDLLLQTRMVNYVTSMRPN 647

Qy        653 IFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGV 711
              |: |  |||  ::|||||| :| :|   |    |||:||| | || |||| || || ||
Db        648 IYFGTCEGSTQFKKWYFEVIVDQVEPFVTAEATHLRVGWALTEGYSPYPGAGEGWGANGA 707

Qy        712 GDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVT 771
              ||||||: ||| :||| ||       :|  :  :   ||: | |||||| |:| |||  |
Db        708 GDDLYSFAFDGLHLWS-GRVCRAVASH-NQHLLTADDVVSCCLDLTVPSISFRFNGHPVQ 765

Qy        772 GSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEP 831
              | | ||||:|:|||| | |  :  |||||| ||  ::   |  ||:|  |:|||:  : :||
Db        766 GMPENFNLDGLFFPVSSFSPGIKIRFLLGGRHGEFKFLPPPGYAPAYEALLPRDRMRVEP 825

Qy        832 CFYF----GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWA 887
                 :    |::  | | ||       |:||| ||||:|| || ::|:|||:||||||||:||
Db        826 IKEYKHDVGDI--RNLLGPTKSLSHTSFVPCPVDTVQIVLPPHLERIREKLAENIHELWA 883

Qy        888 MNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISL-- 945
              : :|| || ||  |:|  ::|||||: |  ||  |: |:: :: :||||:|||| :: :
Db        884 LTRIEQGWTYGPIRDDNKRLHPCLLDFHSLPEPERNYNLLMSGETLKTLLALGCHVGMAD 943

Qy        946 DKPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQ 1005
              :|    :: ::|| : :| ||||||||||| | |||  : |||:|||| ||:|||:|:|
Db        944 EKAEENLKKIKLP-KTYMMSNGYKPAPLDLSHVKLTPAQNTLVDKLAENGHNVWARDRVQ 1002

Qy       1006 QGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHE 1065
              ||||| : :|    |:| ||||  :|:  || |||:  | ||||: ||| ::||  :|
Db       1003 QGWTYSIIQDIKNKRNPRLVPYVLLDEKTKKTNRDSLCEAVRTLMGYGYNIEPP--DQES 1060

Qy       1066 ALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQD 1125
              :     :| :    | :||||:||| |||||||| :| | ||||||  :: | : || |
Db       1061 SAQGGITKPRAERMRIFRAEKSYAVKSGKWYFEFEAVTTGEMRVGWARPEVRPDVELGAD 1120

Qy       1126 ENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGET 1185
              | :: |:|:  :: : | :| ||: |  |||||  :|| :  | |:||||:|:   | :
Db       1121 ELAYVFNGHRGQRWHIG-SEPFGRNWQPGDVVGCMIDLTEMNIMFTLNGEMLIGDSGSDV 1179

Qy       1186 TFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHW 1244
              | |:: |: |:|  |:||: |  ||  |||| :|:||| |||||:||| :||||::| |
Db       1180 AFKDIEIGEGFIPVCSLGMSQVGRLNLGQDVGSLRYFTICGLQEGFEPFAINMKREITTW 1239

Qy       1245 YTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE--FLRLSLPV 1302
              ::|  | | |        |:|:||    | |||||::| || : : :| :  | |||:||
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Db       1240 FSKSLPQFANV-SADHGHIEVSRIDGTVDNPPCLKVTHKTFGS-QNSNTDMLFFRLSMPV 1297

Qy       1303 ICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDN 1362

Db       1298 ----EFYETFKCTPGATPLTRSFTIVEEEVQDVDMDSEF-EVLKKSAARKEIEA----TN 1348

Qy       1363 QEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQG 1422

Db       1349 EKDL----AKETPKEPPK---------------------------------------- 1362

Qy       1423 LTPDDKKDKRGRSPFKFFRSKRGESSDRAKSR----KSKTPDPFSDTEVSPERGARRPNP 1478

Db       1363 --PENEKD--------------TTTEKTKKRGFLFKPKKPAFISTTPVVP--------- 1396

Qy       1479 QIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIF 1538

Db       1397 ---------------------------------------------TMPRLMKEVVPDDRD 1411

Qy       1539 DAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDR 1598

Db       1412 DPEIIRNTTTYYYSVRVFAGQEPTGVWIGWVTPDYHLYDMNFDLNKVRNATITMGDDKGN 1471

Qy       1599 VVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFK 1658

Db       1472 IFNSINRSNCYMVWGGEFSNNTQ---QARVRKEDLVVGCLIDLATGLMTFTANGKEVNTF 1528

Qy       1659 FKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQC 1718

Db       1529 FQVEPNTKLFPAVFVTPLSQTLFQFELGKLKNIMPISAAMFRSESKNPVPQCPPRLDVQV 1588

Qy       1719 LKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKL 1778

Db       1589 LKPVVWSRMPNDFLKVESSKVSDRHGWMVECTDPLMMMALHIPEEDRCIDILELSERLDL 1648

Qy       1779 LSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALH 1838

Db       1649 LKFHYHTLKLYCSVCALGNNRVAHALTSHVDESQLLYTIESNNLSGLLRSGFYDLLISIH 1708

Qy       1839 LESHATTMEACKNEFVIPLGPELKA--LYEEPDMGHSLRSL-QTESVRPQMKMTDIAESI 1895

Db       1709 LESAKRGRMTMNSEFIVPMTDQTKSITLFPNENKKHGLPGVGMSTCLRPELHFSHTC-FV 1767

Qy       1896 TEISNLY--SPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLL 1953

Db       1768 STISELYQHSPYIPLDILKTKAINMLTESVQDGGQHTRDPVGGSVEFQFVPVLKLISTLL 1827

Qy       1954 LVGMMRDEDVEKLLIMTNPETW---DPSFD---------------------------- 1980

Db       1828 IMGVFQDDDVRHILKMIEPNVFSEEEPAEEGGEEGEEKEATEKGGEEGEVEGEGQEKTED 1887

Qy       1981 ------------KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFA 2027

Db       1888 GEEKTVEDGEAEAKEEEEALEEGLLQMKLPESVKLQMCNLLQYFCDRELQHRVEAIIAFS 1947

Qy       2028 HDFVGDLQTDQLRRYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKEN 2086

Db       1948 ERHMDSLQTNQRHRYKELMQAFTMSAAETARRTREFRPPPQEQINMLVNFKNIPEEE--- 2004

Qy       2087 CPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEE 2146

Db       2005 YPVPEEIRDEHIDFHADLLAHCGVHM-----EGQEEEEQEDTSLARRLLSLVEKIKNLRG 2059

Qy       2147 EAKAIEEPPKKTPEEK---FRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGEL 2203

Db       2060 KKQEPEPEPEEQEEPKPTTLQELISHTMVHWAQESFIQNPELVRVMFSLLHRQYDGLGEL 2119

Qy       2204 IRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQH 2263

Db       2120 IRAMPKAYTINAVSVEDTMNLLESLGQIRSLLIVQMGPEEENLMIQSIGNIMNNKVFYQH 2179

Qy       2264 PDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLC 2323

Db       2180 PNLMRALGMHETVMEVMVNVLG---------------GGESKE-IRFPKMVTNCCRFLC 2222

Qy       2324 YFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHY 2383

Db       2223 YFCRISRQNQRAMFDHLSYLLENSGIGL---GMRGSTPLDVAAASVIDNNELALALQEQD 2279

Qy       2384 LEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVI 2443

Db       2280 LEKVVSYLAGCGLQSCPMLLAKGYPDIGWNPVGGERYLDFLRFAVFVNGESVEENANVVV 2339

Qy       2444 RLLIRRPECLGPALRGE-GEGLLKAIVDANKMSERIA--------DRRKLREMEQEGDVN 2494

Db       2340 RLLIRRPECFGPALRGEGGNGLLGAIEDAIKISEDPARDGPTVKKDRRR----ELYGG-- 2393

Qy       2495 FSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLV 2554

Db       2394 ------EEPHEENRVHLGNAIMSFYAALIDLLGRCAPEMHLIQAGKGEALRIRAILRSLV 2447

Qy       2555 PLEDLQGVLSLRFTLNNPAAGEE----RPKSDMPSGLIPGHKQSVGLFLERVYGIETQEL 2610

Db       2448 PIEDLVGVISL--PLQIPAFGKDGNTIEPK--MSASFVPDHKAPMVLFLDRVYGIDNQDF 2503

Qy       2611 FYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYAS 2670

Db       2504 LLQVLEVGFLPDMRAAASLDTAAFSTTEMALAMNRYLCSAVLPLITKCAPLFSGTEHRAI 2563

Qy       2671 LLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYT 2730

Db       2564 MVDSMLHTIYRLSRGRSLTKAQRDVIEECLMGLCRFLRPSMLQHLLRRLVFDVPILNEFS 2623

Qy       2731 TVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELF 2790

Db       2624 KMPLKLLTNHYERCWKYY-CLPTGWANYGVSSEEELHLTRKLFWGIFESLAHKRFDAELY 2682

Qy       2791 GKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLD-NPQYDPQPINTSSVALNNDL 2849

Db       2683 KITMPCLCAIAGAIPPDY-----VDASYSSKTDKKASVDAEGNFDPKPVETLNVIIPEKL 2737

Qy       2850 NTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRE 2909

Db       2738 DGFINKYAEHTHDKWAFEKIQNNWSYGETIDEEAKTHPMLRPYKTFSEKDKEIYRWPIKE 2797

Qy       2910 SLKALLAIGWSVE---HSEVDIPSNNRSSMRRQSKSGGR--PPEIVTDSATPFDYNPHPV 2964

Db       2798 SLKAMIAWEWLVEKAREGEED-RTEKKTKTRKISQTAQQTYDPMVQT-------FSPTPI 2849

Qy       2965 DMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000

Db       2850 DLTGLTLSRELQSMAEQLAENYHNTWGRKKKVELET 2885
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RESULT 15
RYR1_PIG
ID   RYR1_PIG       STANDARD;      PRT;  5035 AA.
AC   P16960;
DT   01-AUG-1990 (Rel. 15, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ryanodine receptor 1 (Skeletal muscle-type ryanodine receptor) (RyR1)
DE   (RYR-1) (Skeletal muscle calcium release channel).
GN   Name=RYR1; Synonyms=CRC;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Norwegian Landrace; TISSUE=Skeletal muscle;
RX   MEDLINE=93036581; PubMed=1329581;
RA   Harbitz I., Kristensen T., Bosnes M., Kran S., Davies W.;
RT   "DNA sequence of the skeletal muscle calcium release channel cDNA and
RT   verification of the Arg615-->Cys615 mutation, associated with porcine
RT   malignant hyperthermia, in Norwegian landrace pigs.";
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RL   Anim. Genet. 23:395-402(1992).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 1129-2801.
RA   Brenig B.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 1129-2643.
RC   STRAIN=German Landrace; TISSUE=Liver;
RX   MEDLINE=94117003; PubMed=8288238;
RA   Leeb T., Schmolzl S., Brem G., Brenig B.;
RT   "Genomic organization of the porcine skeletal muscle ryanodine
RT   receptor (RYR1) gene coding region 4624 to 7929.";
RL   Genomics 18:349-354(1993).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 4785-5035.
RX   MEDLINE=91065640; PubMed=2174405;
RA   Harbitz I., Chowdhary B., Thomsen P.D., Davies W., Kaufman U.,
RA   Kran S., Gustavsson I., Christensen K., Hauge J.G.;
RT   "Assignment of the porcine calcium release channel gene, a candidate
RT   for the malignant hyperthermia locus, to the 6p11-->q21 segment of
RT   chromosome 6.";
RL   Genomics 8:243-248(1990).
CC   -!- FUNCTION: Communication between transverse-tubules and
CC       sarcoplasmic reticulum. Contraction of skeletal muscle is
CC       triggered by release of calcium ions from SR following
CC       depolarization of T-tubules.
CC   -!- SUBUNIT: Homotetramer (Potential).
CC   -!- MISCELLANEOUS: The calcium release channel is modulated by calcium
CC       ions, magnesium ions, ATP and calmodulin.
CC   -!- MISCELLANEOUS: The calcium release channel activity resides in the
CC       C-terminal region while the remaining part of the protein
CC       constitutes the 'foot' structure spanning the junctional gap
CC       between the SR and the T-tubule. It is possible that the foot
CC       structure interacts with the cytoplasmic region of the
CC       dihydropyridine receptor.
CC   -!- MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Ca-
CC       release channel in junctional SR and modulates its activity.
CC   -!- SIMILARITY: Belongs to the ryanodine receptor family.
CC   -!- SIMILARITY: Contains 5 MIR domains.
CC   -!- SIMILARITY: Contains 3 SPRY domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X62880; CAA44674.1; ALT_SEQ; mRNA.
DR   EMBL; X68247; CAA48318.1; -; Genomic_DNA.
DR   EMBL; X69465; CAA49225.1; -; Genomic_DNA.
DR   EMBL; M32501; AAA31022.1; -; mRNA.
DR   InterPro; IPR000699; Ca-rel_channel.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR003608; MIR.
DR   InterPro; IPR003032; Ryanodine_recept.
DR   InterPro; IPR001215; Ryanodn_receptor.
DR   InterPro; IPR009460; Ryanrecept_TM4-6.
DR   InterPro; IPR003877; SPRY_receptor.
DR   PANTHER; PTHR13715:SF1; Ryanodn_receptor; 10.
DR   Pfam; PF00520; Ion_trans; 1.
DR   Pfam; PF02815; MIR; 1.
DR   Pfam; PF06459; RR_TM4-6; 1.
DR   Pfam; PF01365; RYDR_ITPR; 2.
DR   Pfam; PF02026; RyR; 4.
DR   Pfam; PF00622; SPRY; 3.
DR   PRINTS; PR00795; RYANODINER.
DR   ProDom; PD000012; EF-hand; 1.
DR   SMART; SM00472; MIR; 4.
DR   SMART; SM00449; SPRY; 3.
DR   PROSITE; PS50919; MIR; 5.
KW   Calcium; Calcium channel; Calcium transport; Glycoprotein;
KW   Ion transport; Ionic channel; Phosphorylation; Receptor; Repeat;
KW   Transmembrane; Transport.
FT   TOPO_DOM      1   3124       Cytoplasmic.
FT   TRANSMEM   3125   3145       M' (Potential).
FT   TRANSMEM   3189   3207       M'' (Potential).
FT   TRANSMEM   3980   3999       M1 (Potential).
FT   TRANSMEM   4018   4036       M2 (Potential).
FT   TRANSMEM   4274   4297       M3 (Potential).
FT   TRANSMEM   4339   4359       M4 (Potential).
FT   TRANSMEM   4557   4578       M5 (Potential).
FT   TRANSMEM   4646   4669       M6 (Potential).
FT   TRANSMEM   4787   4807       M7 (Potential).
FT   TRANSMEM   4835   4854       M8 (Potential).
FT   TRANSMEM   4877   4896       M9 (Potential).
FT   TRANSMEM   4921   4935       M10 (Potential).
FT   DOMAIN       98    153       MIR 1.
FT   DOMAIN      160    205       MIR 2.
FT   DOMAIN      211    265       MIR 3.
FT   DOMAIN      271    334       MIR 4.
FT   DOMAIN      336    393       MIR 5.
FT   DOMAIN      659    797       SPRY 1.
FT   REPEAT      842    955       1.
FT   REPEAT      956   1069       2.
FT   DOMAIN     1085   1208       SPRY 2.
FT   REPEAT     1345   1360       3 (incomplete).
FT   REPEAT     1373   1388       4 (incomplete).
FT   DOMAIN     1430   1570       SPRY 3.
FT   REPEAT     2727   2846       5.
FT   REPEAT     2847   2960       6.
FT   REGION      842   2960       6 X approximate repeats.
FT   COMPBIAS   1874   1925       Glu-rich (acidic).
FT   COMPBIAS   4458   4526       Pro-rich.
FT   MOD_RES    2844   2844       Phosphoserine (by PKA and PKG) (By
FT                                similarity).
FT   MOD_RES    3947   3947       Phosphoserine (Potential).
FT   MOD_RES    4320   4320       Phosphothreonine (Potential).
FT   CARBOHYD   3467   3467       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   3475   3475       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   3904   3904       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   3945   3945       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   4144   4144       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   4862   4862       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT   2092   2092       A -> P (in Ref. 2 and 3).
SQ   SEQUENCE   5035 AA;  565332 MW;  E00613F2027B94A4 CRC64;

  Query Match           41.0%;  Score 6453.5;  DB 1;  Length 5035;
  Best Local Similarity  44.2%;  Pred. No. 0;
  Matches 1367;  Conservative  531;  Mismatches  894;  Indels  303;  Gaps   63;

Qy          5 EGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPPD 59
              :||   | |:| ||||:| | | | ||      ::|||||||||| ||||  :: :|:|||
Db          3 DGGEGE-DEVQFLRTDDEVVLQCNATVLKEQLKLCLAAEGFGNRLCFLEPTSNAQNVPPD 61

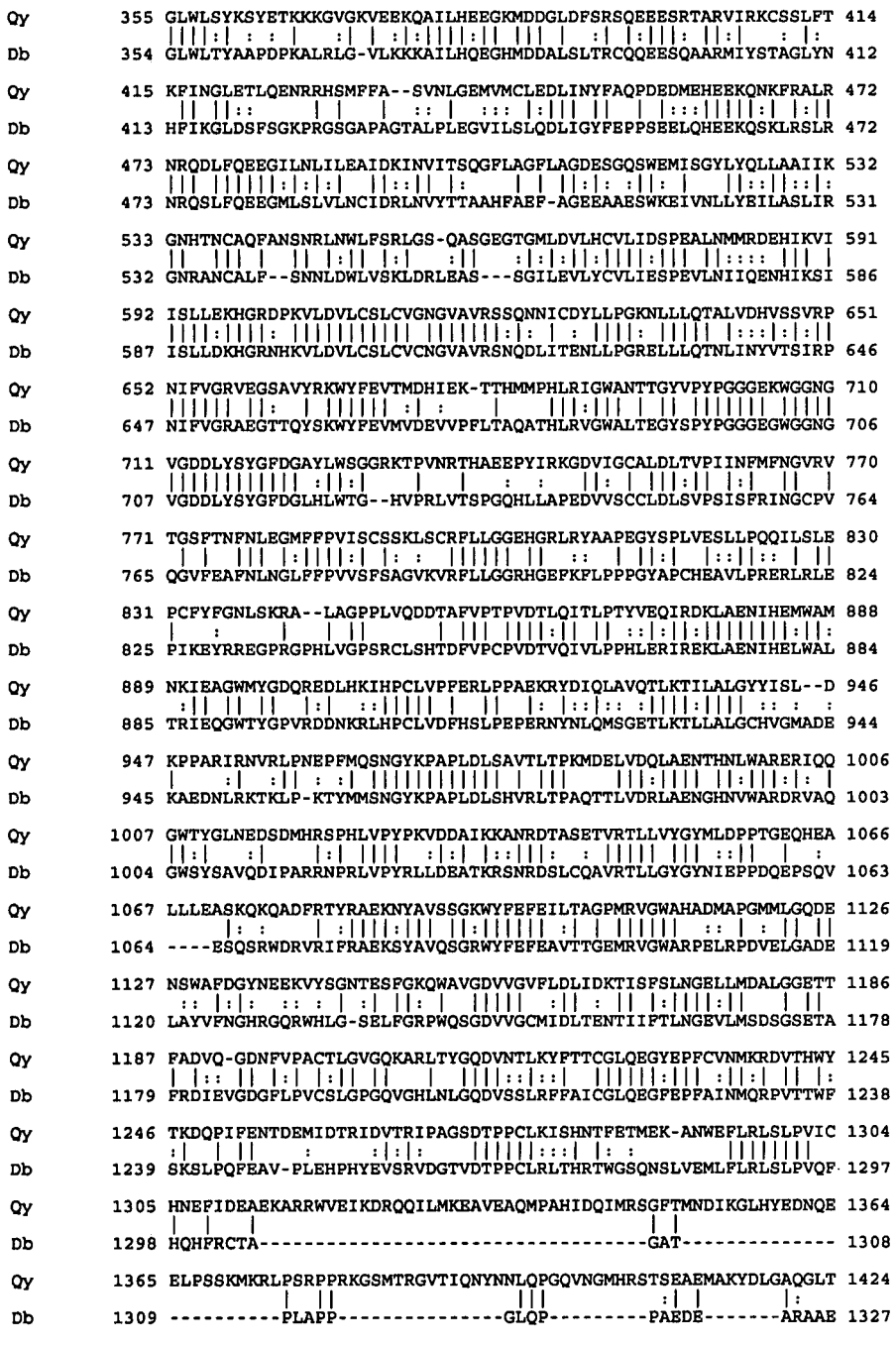
Qy         60 LSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLA 116
              |: | ||:||:||||||||::     || |: :  | ||||||||:|||||| :| |||:
Db         62 LAICCFVLEQSLSVRALQEMLANTVEAGVESSQ--GGGHRTLLYGHAILLRHAHSGMYLS 119

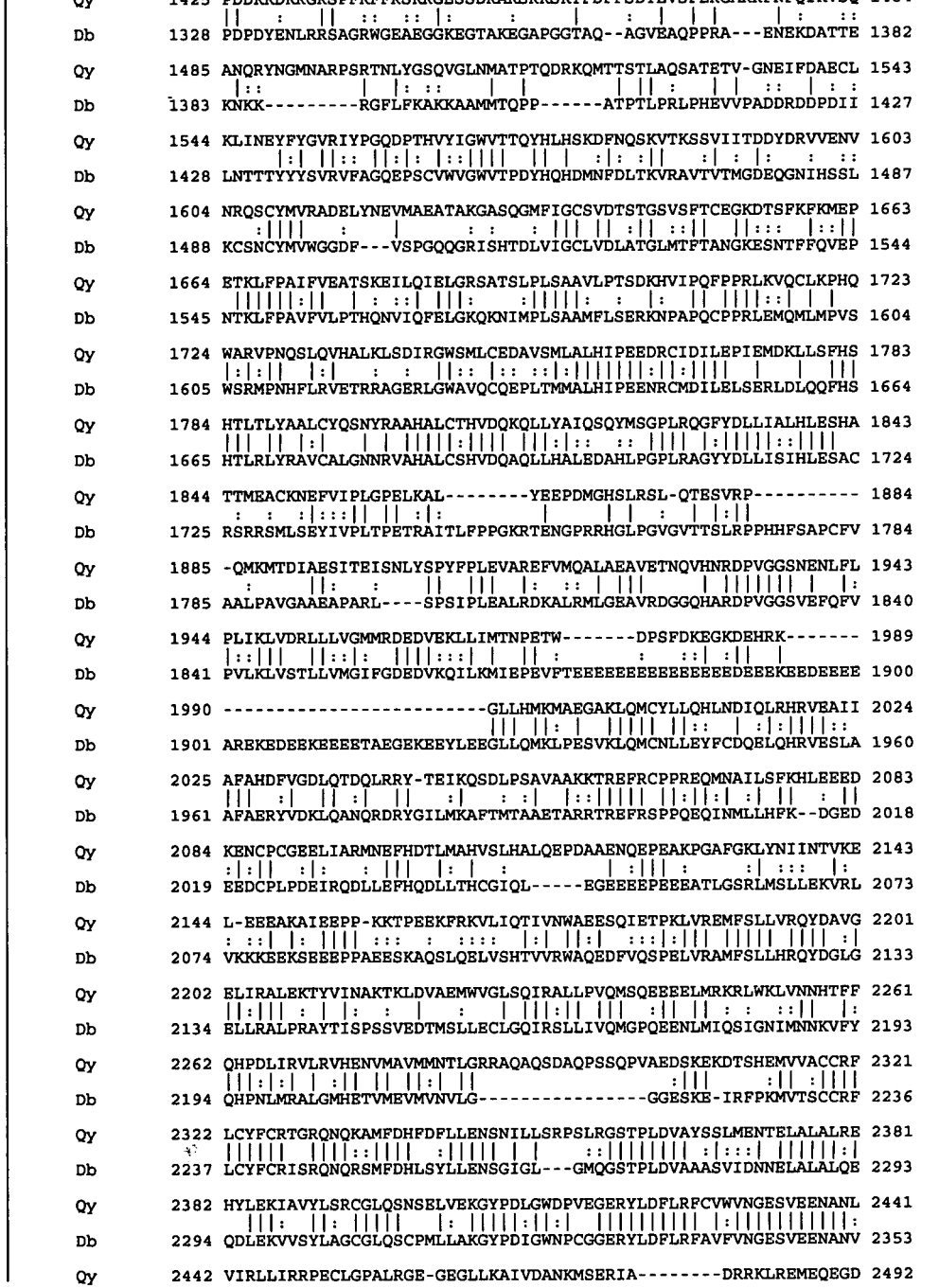
Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              ||:|| |  |||||||||||: : ||||||| |||||||||||||||||||||||::|||
Db        120 CLTTSRSMTDKLAFDVGLQEDATGEACWWTTHPASKQRSEGEKVRVGDDLILVSVSSERY 179

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGG-DECLTIPS 234
              || :  :    |:|||  | |:: |  :|        ||| || ||| |||  |||||| |
Db        180 LHLSTASGELQVDASFMQTLWNMNPICSGCEE----GYVTGGHVLRLFHGHMDECLTI-S 234

Qy        235 TWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVN 294
                |  : :| |||||| : ||||||||  |  |:|  : |  |:||||:|||||| :
Db        235 PADSDDQRRLVYYEGGSVCTHARSLWRLEPLRISWSGSHLRWGQPLRIRHVTTGRYLALI 294

Qy        295 DQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSET 354
              :   | :|   :| | : :|| |  | ::      :|:| :| | ||||:|   |||  :
Db        295 EDQGLVVVDASKAHTKATSFCFRISK-EKLDTAPKRDVEGMGPPEIKYGESLCFVQHVAS 353
```





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          |:|||||:||| ||||||| | ||| | :| ::||  |       |||:    |  |
Db       2354 VVRLLIRKPECFGPALRGEGGSGLLATIEEAIRISEDPARDGPGVRRDRRR----EHFG- 2408

Qy       2493 VNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRS 2552
                |   :|: :  | ||::||  |:||||||||:  :|  || |:|| ||||||
Db       2409 --------EEPPEENRVHLGHAIMSFYAALIDLLGRCAPEMHLIQAGKGEALRIRAILRS 2460

Qy       2553 LVPLEDLQGVLSLRFTLNNPAAGEE----RPKSDMPSGLIPGHKQSVGLFLERVYGIETQ 2608
              ||||:|| |::||   |  |  |::    :||  | :  :| || |: |||:|||||| |
Db       2461 LVPLDDLVGIISL--PLQIPTLGKDGALVQPK--MSASFVPDHKASMVLFLDRVYGIENQ 2516

Qy       2609 ELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENY 2668
              :   :|:  ||||:|||  ||      ::|||::|||:  ::|||: | |  :   |:
Db       2517 DFLLHVLDVGFLPDMRAAASLDTATFSTTEMALALNRYLCLAVLPLITKCAPLFAGTEHR 2576

Qy       2669 ASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSE 2728
              | ::|: |||||||: | ||| ||: : : |:||   ::|||  |||:|  ||  |:|
Db       2577 AIMVDSMLHTVYRLSRGRSLTKAQRDVIEECLMALCRYIRPSMLQHLLRRLVFDVPILNE 2636

Qy       2729 YTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPE 2788
              :  : |:||| ||||| |||     |   || :|:||  ||  ||  |||||:   |:||
Db       2637 FAKMPLKLLTNHYERCWKYY-CLPTGWANFGVTSEEELHLTRKLFWGIFDSLAHKKYDPE 2695

Qy       2789 LFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLD-NPQYDPQPINTSSVALNN 2847
              |:  |:||| ||  ||||||      |  :  | :    :|    :||:|: | :| :
Db       2696 LYRMAMPCLCAIAGALPPDY-----VDASYSSKAEKKATVDAEGNFDPRPVETLNVIIPE 2750

Qy       2848 DLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPV 2907
               |:: : ||:|: |: ||  ||:| | |||   :  |||| |:||  :: :|| |: |:
Db       2751 KLDSFINKFAEYTHEKWAFDKIQNNWSYGENIDEELKTHPMLRPYKTFSEKDKEIYRWPI 2810

Qy       2908 RESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFD----YNPHP 2963
              :|||||::|  |::|          ::    : |:  :    :: ||  :|    ||| |
Db       2811 KESLKAMIAWEWTIE----------KAREGEEEKTEKKKTRKISQSAQTYDAREGYNPQP 2860

Qy       2964 VDMTNLTLSREMQNMAERLADNAHDIWAKKKKEEL 2998
               |:: :|||||:| |||:||:| |: | :|||:||
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Search completed: April 14, 2006, 01:41:40
Job time : 465 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 14, 2006, 01:41:53 ; Search time 74 Seconds
(without alignments)
3351.717 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Perfect score: 15748
Sequence: 1 MAEAEGGASEQDDVSFLRTE.....RLADNAHDIWAKKKKEELVT 3000

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6778	43.0	4968	2	US-09-424-783-5	Sequence 5, Appli
2	6442.5	40.9	5032	2	US-09-538-092-979	Sequence 979, App
3	6439	40.9	5037	2	US-09-424-783-4	Sequence 4, Appli
4	6413	40.7	4872	2	US-09-424-783-3	Sequence 3, Appli
5	6354	40.3	4866	2	US-09-424-783-2	Sequence 2, Appli
6	336.5	2.1	240	1	US-08-114-555A-8	Sequence 8, Appli
7	336.5	2.1	240	2	US-08-559-397A-14	Sequence 14, Appl
8	334.5	2.1	240	1	US-08-114-555A-6	Sequence 6, Appli
9	334.5	2.1	240	2	US-08-559-397A-12	Sequence 12, Appl
10	313.5	2.0	2262	2	US-09-949-016-8849	Sequence 8849, Ap
11	289	1.8	2713	4	PCT-US96-01735-1	Sequence 1, Appli
12	279	1.8	2749	2	US-09-385-222A-4	Sequence 4, Appli
13	222	1.4	604	2	US-09-385-222A-2	Sequence 2, Appli
14	198	1.3	3259	2	US-09-949-016-6507	Sequence 6507, Ap
15	197.5	1.3	2954	2	US-09-150-867-1	Sequence 1, Appli
16	192	1.2	2733	2	US-09-949-016-11433	Sequence 11433, A
17	189.5	1.2	2663	2	US-09-538-092-1252	Sequence 1252, Ap
18	189	1.2	2662	2	US-09-595-684B-31	Sequence 31, Appl
19	187.5	1.2	3878	2	US-09-914-259-11	Sequence 11, Appl
20	186	1.2	5024	2	US-09-710-279-2964	Sequence 2964, Ap
21	185.5	1.2	1530	2	US-09-976-594-736	Sequence 736, App
22	185.5	1.2	1530	2	US-09-949-016-6668	Sequence 6668, Ap
23	185.5	1.2	1938	2	US-09-949-016-6417	Sequence 6417, Ap
24	183.5	1.2	273	2	US-09-270-767-45068	Sequence 45068, A
25	183	1.2	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
26	178.5	1.1	1959	2	US-09-949-016-8134	Sequence 8134, Ap
27	176	1.1	3433	2	US-09-538-092-1136	Sequence 1136, Ap
28	175.5	1.1	2867	2	US-09-902-540-12593	Sequence 12593, A
29	174.5	1.1	2107	2	US-09-949-016-7646	Sequence 7646, Ap
30	174.5	1.1	2107	2	US-09-949-016-7647	Sequence 7647, Ap
31	174.5	1.1	2115	2	US-09-296-662-33	Sequence 33, Appl
32	173.5	1.1	1937	2	US-09-538-092-918	Sequence 918, App
33	173.5	1.1	1939	2	US-09-949-016-11104	Sequence 11104, A
34	172.5	1.1	3210	2	US-09-538-092-1154	Sequence 1154, Ap
35	172.5	1.1	3248	1	US-08-353-700-1	Sequence 1, Appli
36	172.5	1.1	3248	4	PCT-US95-16216-1	Sequence 1, Appli
37	169.5	1.1	2364	2	US-09-538-092-1243	Sequence 1243, Ap
38	169	1.1	1939	2	US-09-538-092-915	Sequence 915, App
39	168	1.1	1581	2	US-09-866-108A-15754	Sequence 15754, A
40	167	1.1	3433	2	US-09-091-501B-10	Sequence 10, Appl
41	166.5	1.1	1976	2	US-09-538-092-1078	Sequence 1078, Ap
42	164.5	1.0	1939	2	US-09-949-016-6925	Sequence 6925, Ap
43	163	1.0	2101	1	US-08-466-390-4	Sequence 4, Appli
44	163	1.0	2101	1	US-08-470-950-4	Sequence 4, Appli
45	163	1.0	2101	1	US-08-467-781-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-424-783-5
; Sequence 5, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seiichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor
; FILE REFERENCE: 0652.2000000
; CURRENT APPLICATION NUMBER: US/09/424,783
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/EP98/02926
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: DE 197 22 317.6
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4968
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-424-783-5

Query Match 43.0%; Score 6778; DB 2; Length 4968;
Best Local Similarity 45.6%; Pred. No. 0;
Matches 1401; Conservative 530; Mismatches 851; Indels 290; Gaps 57;

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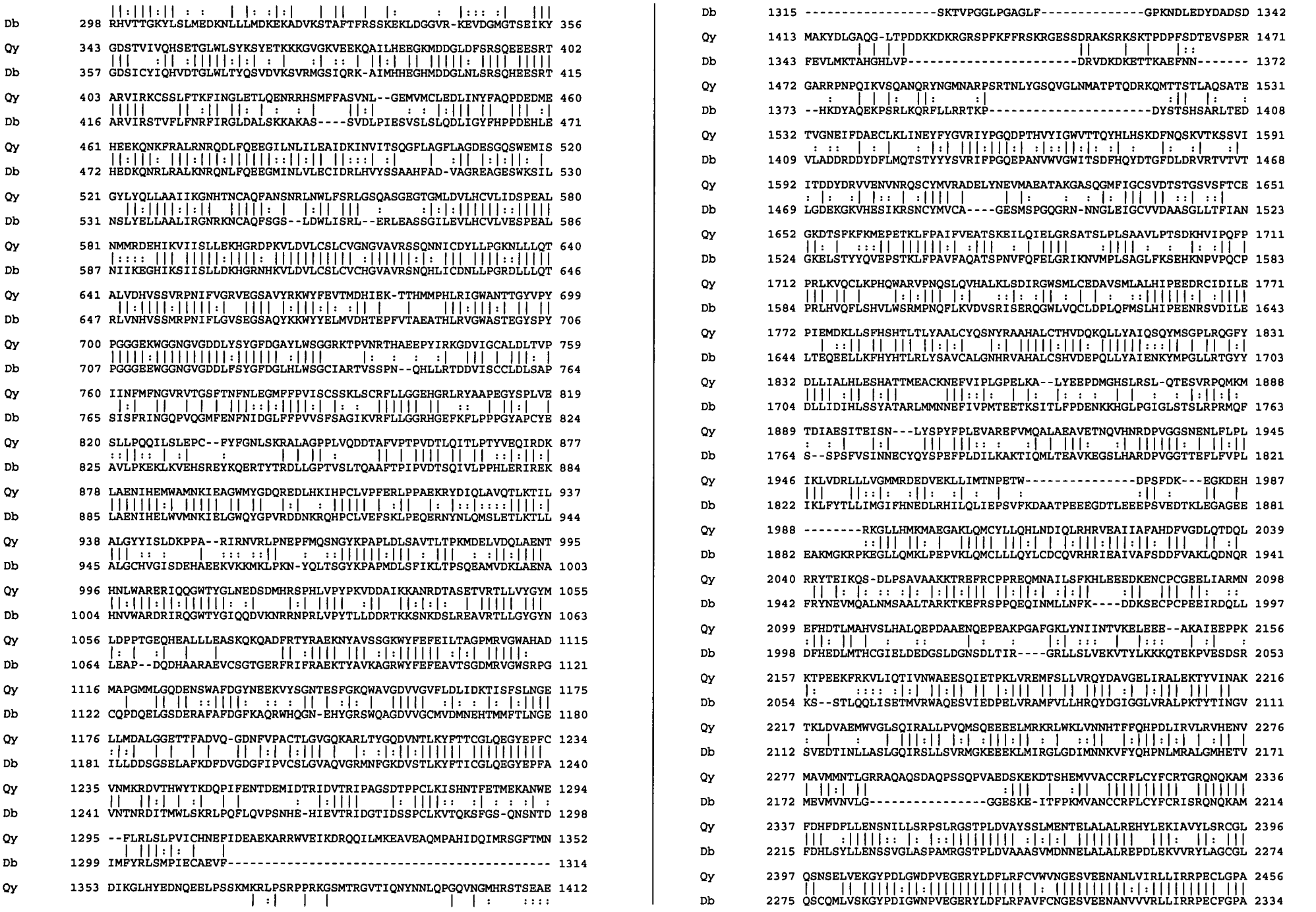
Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKG-------------TGSGHRTLLYGNAI 104
              ||| | ||:||:|||||||:: |   |  :|              | ||||||||:||
Db         61 DLSICTFVLEQSLSVRALQEML-ANTVEKSEGQVDVEKWKFMMKTAQGGGHRTLLYGHAI 119

Qy        105 LLRHLNSDMYLACLSTS-SSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGD 163
              ||||  | ||| ||||| || ||||||||||: : |||||||:|||||||||||||||||
Db        120 LLRHSYSGMYLCCLSTSRSSTDKLAFDVGLQEDTTGEACWWTIHPASKQRSEGEKVRVGD 179

Qy        164 DLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFF 223
              |||||||::||||| :  |     |:|:|  | ||| |  :|    :  ||: ||||||
Db        180 DLILVSVSSERYLHLSYGNGSLHVDAAFQQTLWSVAPISSGSEAAQ--GYLIGGDVLRLL 237

Qy        224 HGG-DECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRI 282
              ||  |||||:||    :  :  | ||||:|   |||||||  |  |:|  | |  | |:
Db        238 HGHMDECLTVPSGEHGEEQRRTVHYEGGAVSVHARSLWRLETLRVAWSGSHIRWGQPFRL 297

Qy        283 RHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKY 342
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Db 298 RHVTTGKYLSLMEDKNLLLMDKEKADVKSTAFTFRSSKEKLDGGVR-KEVDGMGTSEIKY 356
Qy 343 GDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRT 402
Db 357 GDSICYIQHVDTGLWLTYQSVDVKSVRMGSIQRK-AIMHHEGHMDDGLNLSRSQHEESRT 415
Qy 403 ARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNL--GEMVMCLEDLINYFAQPDEDME 460
Db 416 ARVIRSTVFLFNRFIRGLDALSKKAKAS----SVDLPIESVSLSLQDLIGYFHPPDEHLE 471
Qy 461 HEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMIS 520
Db 472 HEDKQNRLRALKNRQNLFQEEGMINLVLECIDRLHVYSSAAHFAD-VAGREAGESWKSIL 530
Qy 521 GYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEAL 580
Db 531 NSLYELLAALIRGNRKNCAQFSGS--LDWLISRL--ERLEASSGILEVLHCVLVESPEAL 586
Qy 581 NMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQT 640
Db 587 NIIKEGHIKSIISLLDKHGRNHKVLDVLCSLCVCHGVAVRSNQHLICDNLLPGRDLLLQT 646
Qy 641 ALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPY 699
Db 647 RLVNHVSSMRPNIFLGVSEGSAQYKKWYYELMVDHTEPFVTAEATHLRVGWASTEGYSPY 706
Qy 700 PGGGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVP 759
Db 707 PGGGEEWGGNGVGDDLFSYGFDGLHLWSGCIARTVSSPN--QHLLRTDDVISCCLDLSAP 764
Qy 760 IINFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVE 819
Db 765 SISFRINGQPVQGMFENFNIDGLFFPVVSFSAGIKVRFLLGGRHGEFKFLPPPGYAPCYE 824
Qy 820 SLLPQQILSLEPC--FYFGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDK 877
Db 825 AVLPKEKLKVEHSREYKQERTYTRDLLGPTVSLTQAAFTPIPVDTSQIVLPPHLERIREK 884
Qy 878 LAENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTIL 937
Db 885 LAENIHELWVMNKIELGWQYGPVRDDNKRQHPCLVEFSKLPEQERNYNLQMSLETLKTLL 944
Qy 938 ALGYYISLDKPPA--RIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENT 995
Db 945 ALGCHVGISDEHAEEKVKKMKLPKN-YQLTSGYKPAPMDLSFIKLTPSQEAMVDKLAENA 1003
Qy 996 HNLWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYM 1055
Db 1004 HNVWARDRIRQGWTYGIQQDVKNRRNPRLVPYTLLDDRTKKSNKDSLREAVRTLLGYGYN 1063
Qy 1056 LDPPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHAD 1115
Db 1064 LEAP--DQDHAARAEVCSGTGERFRIFRAEKTYAVKAGRWYFEFEAVTSGDMRVGWSRPG 1121
Qy 1116 MAPGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGE 1175
Db 1122 CQPDQELGSDERAFAFDGFKAQRWHQGN-EHYGRSWQAGDVVGCMVDMNEHTMMFTLNGE 1180
Qy 1176 LLMDALGGETTFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFC 1234
Db 1181 ILLDDSGSELAFKDFDVGDGFIPVCSLGVAQVGRMNFGKDVSTLKYFTICGLQEGYEPFA 1240
Qy 1235 VNMKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE 1294
Db 1241 VNTNRDITMWLSKRLPQFLQVPSNHE-HIEVTRIDGTIDSSPCLKVTQKSFGS-QNSNTD 1298
Qy 1295 --FLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMN 1352
Db 1299 IMFYRLSMPIECAEVF-- 1314
Qy 1353 DIKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAE 1412
Db 1315 ------------------SKTVPGGLPGAGLF--------------GPKNDLEDYDADSD 1342
Qy 1413 MAKYDLGAQG-LTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPER 1471
Db 1343 FEVLMKTAHGHLVP----------------------DRVDKDKETTKAEFNN------- 1372
Qy 1472 GARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATE 1531
Db 1373 --HKDYAQEKPSRLKQRFLLRRTKP----------------------DYSTSHSARLTED 1408
Qy 1532 TVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVI 1591
Db 1409 VLADDRDDYDFLMQTSTYYYSVRIFPGQEPANVWVGWITSDFHQYDTGFDLDRVRTVTVT 1468
Qy 1592 ITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCE 1651
Db 1469 LGDEKGKVHESIKRSNCYMVCA----GESMSPGQGRN-NNGLEIGCVVDAASGLLTFIAN 1523
Qy 1652 GKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFP 1711
Db 1524 GKELSTYYQVEPSTKLFPAVFAQATSPNVFQFELGRIKNVMPLSAGLFKSEHKNPVPQCP 1583
Qy 1712 PRLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILE 1771
Db 1584 PRLHVQFLSHVLWSRMPNQFLKVDVSRISERQGWLVQCLDPLQFMSLHIPEENRSVDILE 1643
Qy 1772 PIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFY 1831
Db 1644 LTEQEELLKFHYHTLRLYSAVCALGNHRVAHALCSHVDEPQLLYAIENKYMPGLLRTGYY 1703
Qy 1832 DLLIALHLESHATTMEACKNEFVIPLGPELKA--LYEEPDMGHSLRSL-QTESVRPQMKM 1888
Db 1704 DLLIDIHLSSYATARLMMNNEFIVPMTEETKSITLFPDENKKHGLPGIGLSTSLRPRMQF 1763
Qy 1889 TDIAESITEISN---LYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPL 1945
Db 1764 S--SPSFVSINNECYQYSPEFPLDILKAKTIQMLTEAVKEGSLHARDPVGGTTEFLFVPL 1821
Qy 1946 IKLVDRLLLVGMMRDEDVEKLLIMTNPETW---------------DPSFDK---EGKDEH 1987
Db 1822 IKLFYTLLIMGIFHNEDLRHILQLIEPSVFKDAATPEEEGDTLEEEPSVEDTKLEGAGEE 1881
Qy 1988 --------RKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQL 2039
Db 1882 EAKMGKRPKEGLLQMKLPEPVKLQMCLLLQYLCDCQVRHRIEAIVAFSDDFVAKLQDNQR 1941
Qy 2040 RRYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMN 2098
Db 1942 FRYNEVMQALNMSAALTARKTKEFRSPPQEQINMLLNFK----DDKSECPCPEEIRDQLL 1997
Qy 2099 EFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEE--AKAIEEPPK 2156
Db 1998 DFHEDLMTHCGIELDEDGSLDGNSDLTIR----GRLLSLVEKVTYLKKKQTEKPVESDSR 2053
Qy 2157 KTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAK 2216
Db 2054 KS--STLQQLISETMVRWAQESVIEDPELVRAMFVLLHRQYDGIGGLVRALPKTYTINGV 2111
Qy 2217 TKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENV 2276
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Qy 2277 MAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAM 2336
Db 2172 MEVMVNVLG----------------GGESKE-ITFPKMVANCCRFLCYFCRISRQNQKAM 2214
Qy 2337 FDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGL 2396
Db 2215 FDHLSYLLENSSVGLASPAMRGSTPLDVAAASVMDNNELALALREPDLEKVVRYLAGCGL 2274
Qy 2397 QSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPA 2456
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Qy       2457 LRGE-GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPES---------DEDE 2506
Db       2335 LRGEGGNGLLAAMEEAIKIAE--------------DPSRDGPSPTSGSSKTLDTEEEED 2379

Qy       2507 DYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLR 2566
Db       2380 DTIHMGNAIMTFYAALIDLLGRCAPEMHLIHAGKGEAIRIRSILRSLIPLGDLVGVISIA 2439

Qy       2567 FTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAA 2626
Db       2440 FQMPTIAKDGNVVEPDMSAGFCPDHKAAMVLFLDRVYGIEVQDFLLHLLEVGFLPDLRAA 2499

Qy       2627 TMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNR 2686
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Qy       2687 MLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAK 2746
Db       2560 SLTKAQRDSIEVCLLSICGQLRPSMMQHLLRRLVFDVPLLNEHAKMPLKLLTNHYERCWK 2619

Qy       2747 YYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPP 2806
Db       2620 YYCLPG-GWGNFGAASEEELHLSRKLFWGIFDALSQKKYEQELFKLALPCLSAVAGALPP 2678

Qy       2807 DYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWAS 2866
Db       2679 DY-MESNYVSMM--EKQSSMDSEG-NFNPQPVDTSNIIIPEKLEYFINKYAEHSHDKWSM 2734

Qy       2867 RKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEV 2926
Db       2735 DKLANGWIYGEIYSDSSKIQPLMKPYKLLSEKEKEIYRWPIKESLKTMLAWGWRIERTR- 2793

Qy       2927 DIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNA 2986
Db       2794 ---EGDSMALYNRTRRISQTSQVSVDAA--HGYSPRAIDMSNVTLSRDLHAMAEMMAENY 2848

Qy       2987 HDIWAKKKKEEL 2998
Db       2849 HNIWAKKKKLEL 2860
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RESULT 2
US-09-538-092-979
; Sequence 979, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 979
; LENGTH: 5032
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P21817
US-09-538-092-979

Query Match 40.9%; Score 6442.5; DB 2; Length 5032;
Best Local Similarity 44.3%; Pred. No. 0;
Matches 1377; Conservative 517; Mismatches 891; Indels 321; Gaps 66;

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Qy         56 IPPDLSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLYGNAILLRHLNSD 112
Db         57 VPPDLAICCFVLEQSLSVRALQEMLANTVEAGVESSQ--GGGHRTLLYGHAILLRHAHSR 114

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Db        115 MYLSCLTTSRSMTDKLAFDVGLQEDATGEACWWTMHPASKQRSEGEKVRVGDDIILVSVS 174

Qy        172 TERYLHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGG-DECL 230
Db        175 SERYLHLSTASGELQVDASFMQTLWNMNPI---CSRCE-EGFVTGGHVLRLFHGHMDECL 230

Qy        231 TIPSTWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRY 290
Db        231 TI-SPADSDDQRRLVYYEGGAVCTHARSLWRLEPLRISWSGSHLRWGQPLRVRHVTTGQY 289

Qy        291 LGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQ 350
Db        290 LALTEDQGLVVVDASKAHTKATSFCFRISK-EKLDVAPKRDVEGMGPPEIKYGESLCFVQ 348

Qy        351 HSETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCS 410
Db        349 HVASGLWLTYAAPDPKALRLG-VLKKKAMLHQEGHMDDALSLTRCQQEESQAARMIHSTN 407

Qy        411 SLFTKFINGLETLQENRRHS--MFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKF 468
Db        408 GLYNQFIKSLDSFSGKPRGSGPPAGTALPIEGVILSLQDLIIYFEPPSEDLQHEEKQSKL 467

Qy        469 RALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLA 528
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Qy        529 AIIKGNHTNCAQFANSNRLNWLFSRLGS-QASGEGTGMLDVLHCVLIDSPEALNMMRDEH 587
Db        527 SLIRGNRSNCALF--STNLDWLVSKLDRLEAS---SGILEVLYCVLIESPEVLNIIQENH 581

Qy        588 IKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVS 647
Db        582 IKSIISLLDKHGRNHKVLDVLCSLCVCNGVAVRSNQDLITENLLPGRELLLQTNLINYVT 641

Qy        648 SVRPNIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYPGGGEKW 706
Db        642 SIRPNIFVGRAEGTTQYSKWYFEVMVDEVTPFLTAQATHLRVGWALTEGYTPYPGAGEGW 701

Qy        707 GGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFN 766
Db        702 GGNGVGDDLYSYGFDGLHLWTGHVARPV--TSPGQHLLAPEDVISCCLDLSVPSISFRIN 759

Qy        767 GVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQI 826
Db        760 GCPVQGVFESFNLDGLFFPVVSFSAGVKVRFLLGGRHGEFKFLPPPGYAPCHEAVLPRER 819

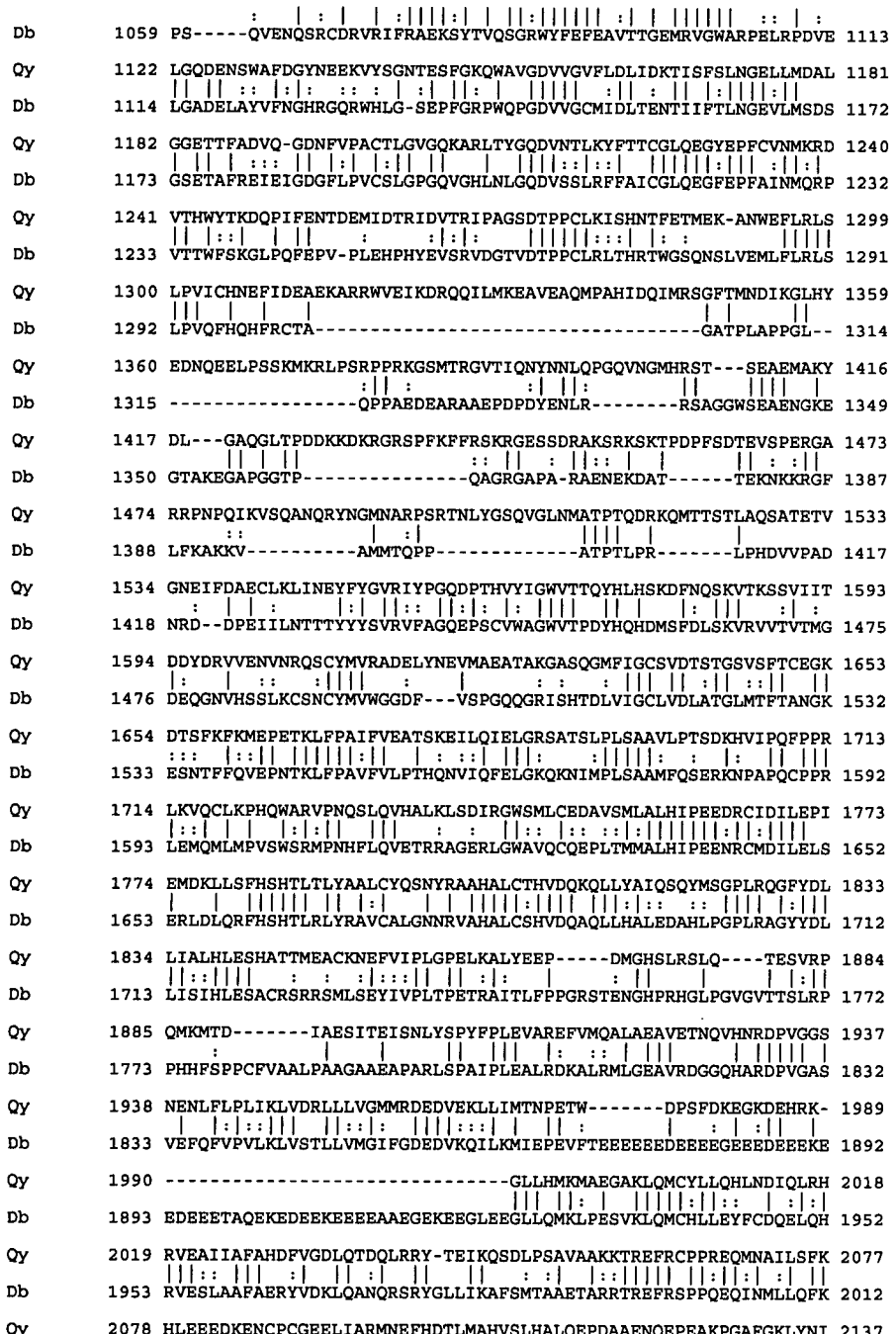
Qy        827 LSLEPCFYFGNLSKRA--LAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHE 884
Db        820 LHLEPIKEYRREGPRGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPHLERIREKLAENIHE 879

Qy        885 MWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYIS 944
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Qy        945 L--DKPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARE 1002
Db        940 MADEKAEDNLKKTKLP-KTYMMSNGYKPAPLDLSHVRLTPAQTTLVDRLAENGHNVWARD 998

Qy       1003 RIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGE 1062
Db        999 RVGQGWSYSAVQDIPARRNPRLVPYRLLDEATKRSNRDSLCQAVRTLLGYGYNIEPPDQE 1058

Qy       1063 QHEALLLEASKQKQAD-FRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMM 1121
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RESULT 3
US-09-424-783-4
; Sequence 4, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seiichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor

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;  FILE REFERENCE: 0652.2000000
;  CURRENT APPLICATION NUMBER: US/09/424,783
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: PCT/EP98/02926
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: DE 197 22 317.6
;  PRIOR FILING DATE: 1997-05-28
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 5037
;   TYPE: PRT
;   ORGANISM: Oryctolagus cuniculus
US-09-424-783-4

  Query Match             40.9%;  Score 6439;  DB 2;  Length 5037;
  Best Local Similarity   44.1%;  Pred. No. 0;
  Matches 1364;  Conservative  529;  Mismatches  902;  Indels  296;  Gaps   63;
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Qy          5 EGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPPD 59
              :||  | |:| ||||:| | | |:||      ::||||||||||| ||||  :: :|:|||
Db          3 DGGEGE-DEVQFLRTDDEVVLQCSATVLKEQLKLCLAAEGFGNRLCFLEPTSNAQNVPPD 61

Qy         60 LSQCVFVIEQALSVRALQELV---TAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLA 116
              |: | | :||:|||||||::     || |: :  | ||||||||:|||||| :| |||:
Db         62 LAICCFTLEQSLSVRALQEMLANTVEAGVESSQ--GGGHRTLLYGHAILLRHAHSRMYLS 119

Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              ||:|| |  |||||||||: : |||||||:|||||||||||||||||||||||::|||
Db        120 CLTTSRSMTDKLAFDVGLQEDATGEACWWTMHPASKQRSEGEKVRVGDDLILVSVSSERY 179

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGG-DECLTIPS 234
              || :  :    |:|||  | |:: |     |      ||| || ||| |||  ||||||
Db        180 LHLSTASGELQVDASFMQTLWNMNP----ICSCCEEGYVTGGHVLRLFHGHMDECLTI-S 234

Qy        235 TWTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVN 294
                  | : :| ||||:| : ||||||||  |  |:|  : |  |:||||:|||||| :
Db        235 AADSDDQRRLVYYEGGAVCTHARSLWRLEPLRISWSGSHLRWGQPLRIRHVTTGRYLALT 294

Qy        295 DQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSET 354
              :  | :|  :| | : :|| |  | ::      :|:| :| | ||||:|  |||  :
Db        295 EDQGLVVVDACKAHTKATSPCFRVSK-EKLDTAPKRDVEGMGPPEIKYGESLCFVQHVAS 353

Qy        355 GLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFT 414
              ||||:| : : |   :| | :|:||||:|| ||| |  :| |:|||: ||:|   : |:
Db        354 GLWLTYAAPDPKALRLG-VLKKKAILHQEGHMDDALFLTRCQQEESQAARMIHSTAGLYN 412

Qy        415 KFINGLETLQENRRHSMFFA--SVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALR 472
              :|| ||::     | |   |  :: :  ::: |:||| ||  | |:::|||||:| |:||
Db        413 QFIKGLDSFSGKPRGSGPPAGPALPIEAVILSLQDLIGYFEPPSEELQHEEKQSKLRSLR 472

Qy        473 NRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIK 532
              ||| ||||||:|:|:|  ||::|| |:    | : ||:|: :||: |   ||:||||::|:
Db        473 NRQSLFQEEGMLSLVLNCIDRLNVYTTAAHFAEY-AGEEAAESWKEIVNLLYELLASLIR 531

Qy        533 GNHTNCAQFANSNRLNWLFSRLGS-QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVI 591
              ||  ||| |  |  |:|: |:|   :||   :|:|:||:||||:||| ||:::: ||| |
Db        532 GNRANCALF--STNLDWVVSKLDRLEAS---SGILEVLYCVLIESPEVLNIIQENHIKSI 586

Qy        592 ISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRP 651
              ||||:|||||: |||||||||||| |||||||:|: | : ||||: |||||  |:::|:|:||
Db        587 ISLLDKHGRNHKVLDVLCSLCVCNGVAVRSNQDLITENLLPGRELLLQTNLINYVTSIRP 646

Qy        652 NIFVGRVEGSAVYRKWYFEVTMDHIEK-TTHMMPHLRIGWANTTGYVPYPGGGEKWGGNG 710
              |||||| ||| | |||||| :| :    |     |||:||| | || |||||| |||||
Db        647 NIFVGRAEGSTQYGKWYFEVMVDEVVPFLTAQATHLRVGWALTEGYSPYPGGGEGWGGNG 706

Qy        711 VGDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRV 770
              |||||||||||| :|:|     ||  |  :  :   ||: | |||:|| |:|  ||  |
Db        707 VGDDLYSYGFDGLHLWTGHVARPV--TSPGQHLLAPEDVVSCCLDLSVPSISFRINGCPV 764

Qy        771 TGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLE 830
              | |  |||:|:||||:| |: :  |||||| ||  ::  | ||:|  |::||:: | ||
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Db        765 QGVFEAFNLDGLFFPVVSFSAGVKVRFLLGGRHGEFKFLPPPGYAPCHEAVLPRERLRLE 824

Qy        831 PCFYFGNLSKRA--LAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAM 888
              |  :   |  | ||     | ||| ||||:|| || ::|:||:|||||||||:||:
Db        825 PIKEYRREGPRGPHLVGPSRCLSHTDFVPCPVDTVQIVLPPHLERIREKLAENIHELWAL 884

Qy        889 NKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISL--D 946
              :|| || ||  |:|  ::|||||  |  ||  |: |::|:: :||||:|||| :: :  :
Db        885 TRIEQGWTYGPVRDDNKRLHPCLVNFHSLPEPERNYNLQMSGETLKTLLALGCHVGMADE 944

Qy        947 KPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQ 1006
              |    ::  :|| : :| ||||||||||||  | |||     |||:|||| ||:|||:|: |
Db        945 KAEDNLKKTKLP-KTYMMSNGYKPAPLDLSHVRLTPAQTTLVDRLAENGHNVWARDRVAQ 1003

Qy       1007 GWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEA 1066
              ||:|   :|    |:| |||| :|:| |::|||:  : |||||  ||| ::||  |
Db       1004 GWSYSAVQDIPARRNPRLVPYRLLDEATKRSNRDSLCQAVRTLLGYGYNIEPPDQEPS-- 1061

Qy       1067 LLLEASKQKQAD-FRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQD 1125
                 :   | : |  | :||||:| | ||:|||||| :| | ||||||  :: | : || |
Db       1062 ---QVENQSRWDRVRIFRAEKSYTVQSGRWYFEFEAVTTGEMRVGWARPELRPDVELGAD 1118

Qy       1126 ENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGET 1185
              | :: |:|:  :: : | :| ||: |  |||||  :|| : || |:||||:||    | ||
Db       1119 ELAYVFNGHRGQRWHLG-SEPFGRPWQSGDVVGCMIDLTENTIIFTLNGEVLMSDSGSET 1177

Qy       1186 TFADVQ-GDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHW 1244
              | ::: || |:| |:|| ||    |  ||||::|::|  ||||||:||| :||:| || |
Db       1178 AFREIEIGDGFLPVCSLGPGQVGHLNLGQDVSSLRFFAICGLQEGFEPFPAINMQRPVTTW 1237

Qy       1245 YTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEK-ANWEFLRLSLPVI 1303
              ::|  | ||          :| |:   ||||||:::| |: :        ||||||||
Db       1238 FSKSLPQFEPVPPE-HPHYEVARMDGTVDTPPCLRLAHRTWGSQNSLVEMLFLRLSLPVQ 1296

Qy       1304 CHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQ 1363
              | |  |                                    | |
Db       1297 FHQHFRCTA----------------------------------GAT------------- 1308

Qy       1364 EELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGL 1423
                    |  ||                 |||          :| |        |:
Db       1309 -----------PLAPP--------------GLQP---------PAEDE-------ARAA 1326

Qy       1424 TPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVS 1483
              ||   :  ||   :  ::  |:      :     || |    | |    | |  :   :
Db       1327 EPDPDYENLRRSAGGWGEAEGGKEGTAKEGTPGGTPQP--GVEAQP---VRAENEKDATT 1381

Qy       1484 QANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETV-GNEIFDAEC 1542
              : |::          |  |: ::    |  |          |  | :   : |  :  | |
Db       1382 EKNKK---------RGFLFKAKKAAMMTQPP------ATPALPRLPHDVVPADNRDDPEI 1426

Qy       1543 LKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVEN 1602
              :     |:| ||:: ||:|: |::|||||  || |  :|: |||    :| : |:   | :
Db       1427 ILNTTTYYYSVRVFAGQEPSCVWVGWVTPDYHQHDMNFDLSKVRAVTVTMGDEQGNVHSS 1486

Qy       1603 VNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKME 1662
              :  :|||   :    |      : :  : ||| || :|| ::||  ||:::  |::|
Db       1487 LKCSNCYMVWGGDF---VSPGQQGRISHTDLVIGCLVDLATGLMTFTANGKESNTFFQVE 1543

Qy       1663 PETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPH 1722
              | ||||||:||  | : ::| |||:    :|||||:  :  |:  || ||||:|| | |
Db       1544 PNTKLFPAVFVLPTHQNVIQFELGKQKNIMPLSAAMFLSERKNPAPQCPPRLEVQMLMPV 1603

Qy       1723 QWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFH 1782
              |:|:||  |||   :  :  ||:: |:| ::|:|||||||:||:|||| |  |  ||
Db       1604 SWSRMPNHFLQVETRRAGERLGWAVQCQDPLTMMALHIPEENRCMDILELSERLDLQRFH 1663

Qy       1783 SHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESH 1842
              |||| || |:|   | | ||||:|||| |||:|::  :: |||| |:|||||::|||||
Db       1664 SHTLRLYRAVCALGNNRVAHALCSHVDQAQLLHALEDAHLPGPLRAGYYDLLISIHLESA 1723

Qy       1843 ATTMEACKNEFVIPLGPELKALYEEPD-------MGHSLRSL-QTESVRPQMKMTD---- 1890
                :  :  :|:::|| || :|:   |          | |  :  | |:||    :
Db       1724 CRSRRSMLSEYIVPLTPETRAITLFPPGRKGGNARRHGLPGVGVTTSLRPPHHFSPPCFV 1783
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Qy       1891 ---IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIK 1947
Db       1784 AALPAAGVAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHARDPVGGSVEFQFVPVLK 1843

Qy       1948 LVDRLLLVGMMRDEDVEKLLIMTNPETW----------DPSFDKEGKDEHRK-------- 1989
Db       1844 LVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEEEEEEEEEEEEEDEEEKEEDEEEEE 1903

Qy       1990 --------------------GLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAH 2028
Db       1904 KEDAEKEEEEAPEGEKEDLEEGLLQMKLPESVKLQMCNLLEYFCDQELQHRVESLAAFAE 1963

Qy       2029 DFVGDLQTDQLRRYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENC 2087
Db       1964 RYVDKLQANQRSRYALLMRAFTMSAAETARRTREFRSPPQEQINMLLHFK--DEADEEDC 2021

Qy       2088 PCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEE 2147
Db       2022 PLPEDIRQDLQDFHQDLLAHCGIQL-----EGEEEEPEEETSLSSRLRSLLETVRLVKKK 2076

Qy       2148 AKAIEE--PPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIR 2205
Db       2077 EEKPEEELPAEEKKPQSLQELVSHMVVRWAQEDYVQSPELVRAMFSLLHRQYDGLGELLR 2136

Qy       2206 ALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPD 2265
Db       2137 ALPRAYTISPSSVEDTMSLLECLGQIRSLLIVQMGPQEENLMIQSIGNIMNNKVFYQHPN 2196

Qy       2266 LIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYF 2325
Db       2197 LMRALGMHETVMEVMVNVLG----------------GGETKE-IRFPKMVTSCCRFLCYF 2239

Qy       2326 CRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLE 2385
Db       2240 CRISRQNQRSMFDHLSYLLENSGIGL---GMQGSTPLDVAAASVIDNNELALALQEQDLE 2296

Qy       2386 KIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRL 2445
Db       2297 KVVSYLAGCGLQSCPMLLAKGYPDIGWNPCGGERYLDFLRFAVFVNGESVEENANVVVRL 2356

Qy       2446 LIRRPECLGPALRGE-GEGLLKAIVDANKMSERIA--------DRRKLREMEQEGDVNFS 2496
Db       2357 LIRKPECFGPALRGEGGSGLLAAIEEAIRISEDPARDGPGVRRDRRR----EHFG----- 2407

Qy       2497 HPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPL 2556
Db       2408 ----EEPPEENRVHLGHAIMSFYAALIDLLGRCAPEMHLIQAGKGEALRIRAILRSLVPL 2463

Qy       2557 EDLQGVLSLRFTLNNPAAGEE----RPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFY 2612
Db       2464 DDLVGIISL--PLQIPTLGKDGALVQPK--MSASFVPDHKASMVLFLDRVYGIENQDFLL 2519

Qy       2613 KLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLL 2672
Db       2520 HVLDVGFLPDMRAAASLDTATFSTTEMALALNRYLCLAVLPLITKCAPLFAGTEHRAIMV 2579

Qy       2673 DATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTV 2732
Db       2580 DSMLHTVYRLSRGRSLTKAQRDVIEDCLMALCRYIRPSMLQHLLRRLVFDVPILNEFAKM 2639

Qy       2733 ALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGK 2792
Db       2640 PLKLLTNHYERCWKYY-CLPTGWANFGVTSEEELHLTRKLFWGIFDSLAHKKYDQELYRM 2698

Qy       2793 ALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLD-NPQYDPQPINTSSVALNNDLNT 2851
Db       2699 AMPCLCAIAGALPPDY-----VDASYSSKAEKKATVDAEGNFDPRPVETLNVIIPEKLDS 2753

Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
Db       2754 FINKFAEYTHEKWAFDKIQNNWSYGENVDEELKTHPMLRPYKTFSEKDKEIYRWPIKESL 2813

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFD----YNPHPVDMT 2967
Db       2814 KAMIAWEWTIEKAREG--EEERTEKKKTRK--------ISQTAQTYDPREGYNPQPPDLS 2863

Qy       2968 NLTLSREMQNMAERLADNAHDIWAKKKKEEL 2998
Db       2864 GVTLSRELQAMAEQLAENYHNTWGRKKKQEL 2894
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RESULT 4
US-09-424-783-3
; Sequence 3, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
; APPLICANT: Hakamata, Yasuhiro
; APPLICANT: Nishimura, Seiichiro
; APPLICANT: Barsoumian, Edward Leon
; TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
; TITLE OF INVENTION: and DNA Molecules Coding Therefor
; FILE REFERENCE: 0652.2000000
; CURRENT APPLICATION NUMBER: US/09/424,783
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/EP98/02926
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: DE 197 22 317.6
; PRIOR FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4872
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-424-783-3

Query Match 40.7%; Score 6413; DB 2; Length 4872;
Best Local Similarity 43.5%; Pred. No. 0;
Matches 1333; Conservative 508; Mismatches 844; Indels 382; Gaps 52;

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Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
Db          2 AEGGEGGEDEIQFLRTEDEVVLQCIATVHKEQRKFCLAAEGLGNRLCFLEPTSEAKFIPP 61

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKGT--GSGHRTLLYGNAILLRHLNSDMYLA 116
Db         62 DLCVCNFVLEQSLSVRALQEMLANTGENGGEGAAQGGGHRTLLYGHAILLRHSFSGMYLT 121

Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
Db        122 CLTTSRSQTDKLAFDVGLREHATGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSERY 181

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
Db        182 LHLSISNGNIQVDASFMQTLWNVHPTCSGSSIEE--GYLLGGHVVRLFHGHDECLTIPST 239

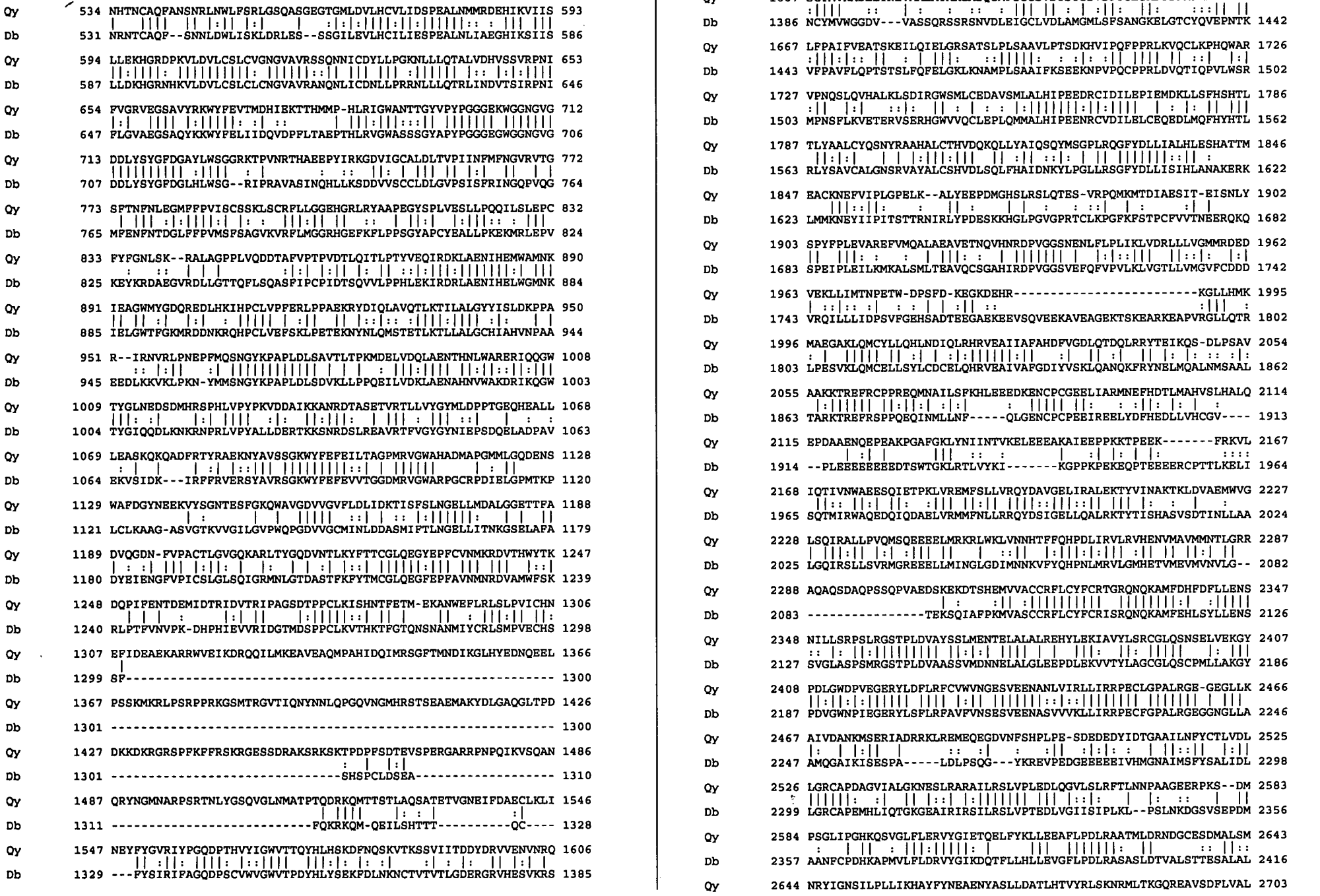
Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
Db        240 DQNDSQHRRIFYEAGGAGTRARSLWRVEPLRISWSGSNIRWGQAFRLRHLTTGHYLALTE 299

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQV--LEDKDLEVIGAPIIKYGDSTVIVQHSE 353
Db        300 DQGLLLQDRGKADTKSTAFSFRPSKETKEKLDSSHKRDIEGMGVPEIKYGDSVCFVQHIA 359

Qy        354 TGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
Db        360 SGLWVTYKAQDAKTSRLGPLKRK-VILHQEGHMDDGLTLQRCQREESQAARIIRNTTALF 418

Qy        414 TKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRN 473
Db        419 SQFVSG-----NNRTAAP--VTLPIEEVLQTLHDLIAYFQPPEEEMQHEDKQNKLRSLKN 471

Qy        474 RQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKG 533
Db        472 RQNLFKEEGMLALVLNCIDRLNIYNSVAHFAG-IAREESGMAWKEVLSLLYKLLAALIRG 530
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Qy 534 NHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIIS 593
Db 531 NRNTCAQF--SNNLDWLISKLDRLES--SSGILEVLHCILIESPEALNLIAEGHIKSIIS 586
Qy 594 LLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNI 653
Db 587 LLDKHGRNHKVLDVLCSLCLCNGVAVRANQNLICDNLLPRRNLLLQTRLINDVTSIRPNI 646
Qy 654 FVGRVEGSAVYRKWYFEVTMDHIEKTTHMMP-HLRIGWANTTGYVPYPGGGEKWGGNGVG 712
Db 647 FLGVAEGSAQYKKWYFELIIDQVDPFLTAEPTHLRVGWASSSGYAPYPGGGEGWGGNGVG 706
Qy 713 DDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTG 772
Db 707 DDLYSYGFDGLHLWSG--RIPRAVASINQHLLKSDDVVSCCLDLGVPSISFRINGQPVQG 764
Qy 773 SFTNFNLEGMPFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPC 832
Db 765 MFENFNTDGLFFPVMSFSAGVKVRFLMGGRHGEFKFLPPSGYAPCYEALLPKEKMRLEPV 824
Qy 833 FYFGNLSK--RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNK 890
Db 825 KEYKRDAEGVRDLLGTTQFLSQASFIPCPIDTSQVVLPPHLEKIRDRLAENIHELWGMNK 884
Qy 891 IEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPA 950
Db 885 IELGWTFGKMRDDNKRQHPCLVEFSKLPETEKNYNLQMSTETLKTLLALGCHIAHVNPAA 944
Qy 951 R--IRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGW 1008
Db 945 EEDLKKVKLPKN-YMMSNGYKPAPLDLSDVKLLPPQEILVDKLAENAHNVWAKDRIKQGW 1003
Qy 1009 TYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALL 1068
Db 1004 TYGIQQDLKNKRNPRLVPYALLDERTKKSNRDSLREAVRTFVGYGYNIEPSDQELADPAV 1063
Qy 1069 LEASKQKQADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENS 1128
Db 1064 EKVSIDK---IRFFRVERSYAVRSGKWYFEFEVVTGGDMRVGWARPGCRPDIELGPMTKP 1120
Qy 1129 WAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFA 1188
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Db 1180 DYEIENGFVPICSLGLSQIGRMNLGTDASTFKFYTMCGLQEGFEPFAVNMNRDVAMWFSK 1239
Qy 1248 DQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETM-EKANWEFLRLSLPVICHN 1306
Db 1240 RLPTFVNVPK-DHPHIEVVRIDGTMDSPPCLKVTHKTFGTQNSNANMIYCRLSMPVECHS 1298
Qy 1307 EFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEEL 1366
Db 1299 SF---------- 1300
Qy 1367 PSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPD 1426
Db 1301 ---------- 1300
Qy 1427 DKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQAN 1486
Db 1301 ----------SHSPCLDSEA---------- 1310
Qy 1487 QRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLI 1546
Db 1311 ----------FQKRKQM-QEILSHTTT----------QC---- 1328
Qy 1547 NEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQ 1606
Db 1329 ---FYSIRIFAGQDPSCVWVGWVTPDYHLYSEKPDLNKNCTVTVTLGDERGRVHESVKRS 1385
Qy 1607 SCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETK 1666
Db 1386 NCYMVWGGDV---VASSQRSSRSNVDLEIGCLVDLAMGMLSFSANGKELGTCYQVEPNTK 1442
Qy 1667 LFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWAR 1726
Db 1443 VFPAVFLQPTSTSLFQFELGKLKNAMPLSAAIFKSEEKNPVPQCPPRLDVQTIQPVLWSR 1502
Qy 1727 VPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTL 1786
Db 1503 MPNSFLKVETERVSERHGWVVQCLEPLQMMALHIPEENRCVDILELCEQEDLMQFHYHTL 1562
Qy 1787 TLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTM 1846
Db 1563 RLYSAVCALGNSRVAYALCSHVDLSQLFHAIDNKYLPGLLRSGFYDLLISIHLANAKERK 1622
Qy 1847 EACKNEFVIPLGPELK--ALYEEPDMGHSLRSLQTES-VRPQMKMTDIAESIT-EISNLY 1902
Db 1623 LMMKNEYIIPITSTTRNIRLYPDESKKHGLPGVGPRTCLKPGFKFSTPCFVVTNEERQKQ 1682
Qy 1903 SPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDED 1962
Db 1683 SPEIPLEILKMKALSMLTEAVQCSGAHIRDPVGGSVEFQFVPVLKLVGTLLVMGVFCDDD 1742
Qy 1963 VEKLLIMTNPETW-DPSFD-KEGKDEHR----------KGLLHMK 1995
Db 1743 VRQILLLIDPSVFGEHSADTEEGAEKEEVSQVEEKAVEAGEKTSKEARKEAPVRGLLQTR 1802
Qy 1996 MAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQS-DLPSAV 2054
Db 1803 LPESVKLQMCELLSYLCDCELQHRVEAIVAFGDIYVSKLQANQKFRYNELMQALNMSAAL 1862
Qy 2055 AAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQ 2114
Db 1863 TARKTREFRSPPQEQINMLLNF-----QLGENCPCPEEIREELYDFHEDLLVHCGV---- 1913
Qy 2115 EPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPEEK-------FRKVL 2167
Db 1914 --PLEEEEEEEDTSWTGKLRTLVYKI-------KGPPKPEKEQPTEEEERCPTTLKELI 1964
Qy 2168 IQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVG 2227
Db 1965 SQTMIRWAQEDQIQDAELVRMMFNLLRRQYDSIGELLQALRKTYTISHASVSDTINLLAA 2024
Qy 2228 LSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRR 2287
Db 2025 LGQIRSLLSVRMGREEELLMINGLGDIMNNKVFYQHPNLMRVLGMHETVMEVMVNVLG-- 2082
Qy 2288 AQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENS 2347
Db 2083 ----------TEKSQIAFPKMVASCCRFLCYFCRISRQNQKAMFEHLSYLLENS 2126
Qy 2348 NILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGY 2407
Db 2127 SVGLASPSMRGSTPLDVAASSVMDNNELALGLEEPDLEKVVTYLAGCGLQSCPMLLAKGY 2186
Qy 2408 PDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE-GEGLLK 2466
Db 2187 PDVGWNPIEGERYLSFLRFAVFVNSESVEENASVVVKLLIRRPECFGPALRGEGGNGLLA 2246
Qy 2467 AIVDANKMSERIADRRKLREMEQEGDVNFSHPLPE-SDEDEDYIDTGAAILNFYCTLVDL 2525
Db 2247 AMQGAIKISESPA-----LDLPSQG---YKREVPEDGEEEEEIVHMGNAIMSFYSALIDL 2298
Qy 2526 LGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKS--DM 2583
Db 2299 LGRCAPEMHLIQTGKGEAIRIRSILRSLVPTEDLVGIISIPLKL--PSLNKDGSVSEPDM 2356
Qy 2584 PSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSM 2643
Db 2357 AANFCPDHKAPMVLFLDRVYGIKDQTFLLHLLEVGFLPDLRASASLDTVALSTTESALAL 2416
Qy 2644 NRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVAL 2703

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Db       2417 NRYICSAVLPLLTRCAPLPAGTEHYTSLIDSTLQTIYRLSKGRSLTKAQRDTIEECLLAI 2476

Qy       2704 TSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSD 2763
Db       2477 CNHLRPSMLQQLLRRLVFDVPQLNDYCKMPLKLLTNHFEQCWKYY-CLPSGWGSYGLAVE 2535

Qy       2764 EEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDY-------SLSKNYDD 2816
Db       2536 EELHLTEKLFWGIFDSLSHKKYDPDLFRMSLPCLSAIAGALPPDYLDTRITATLEK---- 2591

Qy       2817 EFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYG 2876
Db       2592 ------QVSVDADG-NFDPKPINTINFSLPEKLEYIVTKYAEHSHDKWACEKSQSGWKYG 2644

Qy       2877 EGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE-----VDIPSN 2931
Db       2645 ISLDENVKTHPLIRPFKTLTEKEKEIYRWPARESLKTMLAVGWTVERTKEGEALVQLREN 2704

Qy       2932 NRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 2991
Db       2705 EKLRSVSQTSQGN------------SYNPAPLDLSNVVLSRELQGMVEVVAENYHNIWA 2751

Qy       2992 KKKKEEL 2998
Db       2752 KKKKLEL 2758


RESULT 5
US-09-424-783-2
; Sequence 2, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
;  APPLICANT: Hakamata, Yasuhiro
;  APPLICANT:  Nishimura, Seiichiro
;  APPLICANT:  Barsoumian, Edward Leon
;  TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
;  TITLE OF INVENTION:  and DNA Molecules Coding Therefor
;  FILE REFERENCE: 0652.2000000
;  CURRENT APPLICATION NUMBER: US/09/424,783
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: PCT/EP98/02926
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: DE 197 22 317.6
;  PRIOR FILING DATE: 1997-05-28
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 4866
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-424-783-2

  Query Match             40.3%;  Score 6354;  DB 2;  Length 4866;
  Best Local Similarity   43.2%;  Pred. No. 0;
  Matches 1325;  Conservative  508;  Mismatches  848;  Indels  388;  Gaps   52;

Qy          4 AEGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPP 58
Db          2 AEGGEGGEDEIQFLRTEDEVVLQCIATIHKEQRKFCLAAEGLGNRLCFLEPTSEAKYIPP 61

Qy         59 DLSQCVFVIEQALSVRALQELVTAAGSETGKGT--GSGHRTLLYGNAILLRHLNSDMYLA 116
Db         62 DLCVCNFVLEQSLSVRALQEMLANTGENGGEGAAQGGGHRTLLYGHAVLLRHSFSGMYLT 121

Qy        117 CLSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
Db        122 CLTTSRSQTDKLAFDVGLREHATGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSERY 181

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVPGGDVLRFFHGGDECLTIPST 235
Db        182 LHLSVSNGNIQVDASFMQTLWNVHPTCSGSSIEE--GYLLGGHVVRLFHGHDECLTIPST 239

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
Db        240 DQNDSQHRRIFYEAGGAGTRARSLWRVEPLRISWSGSNIRWGQAFRLRHLTTGHYLALTE 299

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLED---KDLEVIGAPIIKYGDSTVIVQHS 352
Db        300 DQGLILQDRAKSDTKSTAFSFRASK-ELKEKLDSSHKRDIEGMGVPEIKYGDSVCFVQHI 358

Qy        353 ETGLWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSL 412
Db        359 ASGLWVTYKAQDAKTSRLGPLKRK-VILHQEGHMDDGLTLQRCQREESQAARIIRNTTAL 417

Qy        413 FTKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALR 472
Db        418 FSQFVSG-----NNRTAAPI--TLPIEEVLQTLQDLIAYFQPPEEEMRHEDKQNKLRSLK 470

Qy        473 NRQDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIK 532
Db        471 NRQNLFKEEGMLALVLNCIDRLNVYNSVAHFAG-IAREESGMAWKEILNLLYKLLAALIR 529

Qy        533 GNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVII 592
Db        530 GNRNNCAQF--SNNLDWLISKLDRLES--SSGILEVLHCILTESPEALNLIAEGHIKSII 585

Qy        593 SLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPN 652
Db        586 SLLDKHGRNHKVLDILCSLCLCNGVAVRANQNLICDNLLPRRNLLLQTRLINDVTSIRPN 645

Qy        653 IFVGRVEGSAVYRKWYFEVTMDHIEKTTHMMP-HLRIGWANTTGYVPYPGGGEKWGGNGV 711
Db        646 IFLGVAEGSAQYKKWYFELIIDQVDPFLTAEPTHLRVGWASSSGYAPYPGGGEGWGGNGV 705

Qy        712 GDDLYSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDV-------IGCALDLTVPIINFM 764
Db        706 GDDLYSYGFDGLHLWSG--RIPRAVASINQHLLRSDDVGKLLPGPRGC------PASHSA 757

Qy        765 FNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQ 824
Db        758 SMGSPCRGCLENFNTDGLFFPVMSFSAGVKVRFLMGGRHGEFKFLPPSGYAPCYEALLPK 817

Qy        825 QILSLEPCFYFGNLSK--RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENI 882
Db        818 EKMRLEPVKEYKRDADGIRDLLGTTQFLSQASFIPCPVDTSQVILPPHLEKIRDRLAENI 877

Qy        883 HEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYY 942
Db        878 HELWGMNKIELGWTFGKIRDDNKRQHPCLVEFSKLPETEKNYNLQMSTETLKTLLTLGCH 937

Qy        943 ISLDKPPAR--IRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWA 1000
Db        938 IAHVNPAAEEDLKKVKLPKN-YMMSNGYKPAPLDLSDVKLLPPQEILVDKLAENAHNVWA 996

Qy       1001 RERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPT 1060
Db        997 KDRIKQGWTYGIQQDLKNKRNPRLVPYALLDERTKKSNRDSLREAVRTFVGYGYNIEPSD 1056

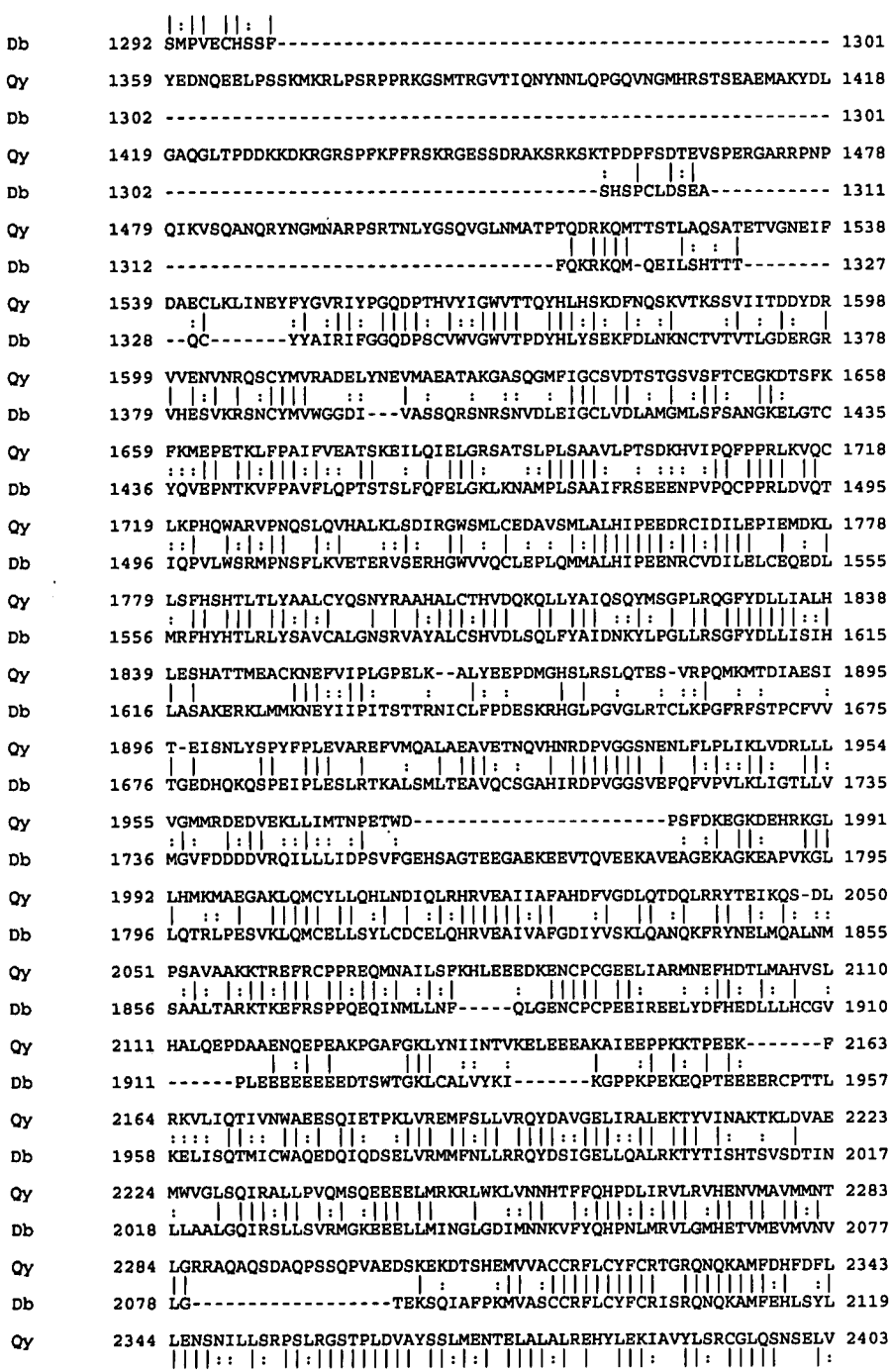
Qy       1061 GEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEPEILTAGPMRVGWAHADMAPGM 1120
Db       1057 QELADSAVEKVSIDK---IRFFRVERSYPVRSGKWYFEPEVVTGGDMRVGWARPGCRPDV 1113

Qy       1121 MLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDA 1180
Db       1114 ELGADDQAFVFEGNRGQRWHQG-SGYFGRTWQPGDVVGCMINLDDASMIFTLNGELLITN 1172

Qy       1181 LGGETTFADVQGDN-FVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKR 1239
Db       1173 KGSELAFADYEIENGFVPICCLGLSQIGRMNLGTDASTFKFYTMCGLQEGFEPFAVNMNR 1232

Qy       1240 DVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETM-EKANWEFLRL 1298
Db       1233 DVAMWFSKRLPTFVNVPK-DHPHIEVMRIDGTMDSPPCLKVTHKTFGTQNSNADMIYCRL 1291

Qy       1299 SLPVICHNEFIDEAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLH 1358
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RESULT 6
US-08-114-555A-8
; Sequence 8, Application US/08114555A
; Patent No. 5854392
; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; APPLICANT: Neve, Rachael L.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF beta-APP-C100
; TITLE OF INVENTION: RECEPTOR (C100-R)
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,555A
; FILING DATE: 30-AUG-1993

```
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  6013-115
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-8864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-114-555A-8

  Query Match             2.1%;  Score 336.5;  DB 1;  Length 240;
  Best Local Similarity   34.7%;  Pred. No. 7.1e-21;
  Matches   82;  Conservative   37;  Mismatches   70;  Indels   47;  Gaps    4;

Qy       1879 TESVRPQMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNR 1931
                 | |:||    :          |  : |      ||  |||  |:  :: | |||     | |
Db          5 TTSLRPPHHFSPPCFVAALPAAGVAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHAR 64

Qy       1932 DPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW----------DPSFDK 1981
                 ||||||  |   |:|::|||   ||::|:  ||||:::| |   || :          :   ::
Db          65 DPVGGSVEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEEEEEEEEEE 124

Qy       1982 EGKDEHRK----------------------------GLLHMKMAEGAKLQMCYLLQHLN 2012
                 | :||  |                                ||| ||: |  ||||| ||::
Db         125 EEEDEEEKEEDEEEEEKEDAEKEEEEAPEGEKEDLEEGLLQMKLPESVKLQMCNLLEYFC 184

Qy       2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQS-DLPSAVAAKKTREFRCPPR 2067
                 | :|:||||:: |||  :|  || :|  ||  : ::  : :|  |::|||||| ||:
Db         185 DQELQHRVESLAAFAERYVDKLQANQRSRYALLMRAFTMSAAETARRTREFRSPPQ 240


RESULT 7
US-08-559-397A-14
; Sequence 14, Application US/08559397A
; Patent No. 6083713
;  GENERAL INFORMATION:
;    APPLICANT:  Manly, Susan P.
;    APPLICANT:  Kozlowski, Michael R.
;    APPLICANT:  Neve, Rachael L.
;    TITLE OF INVENTION:  CLONING AND EXPRESSION OF
;    TITLE OF INVENTION:  BETA APP-C100 RECEPTOR (C100-R)
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036/2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,397A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  6013-135
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-559-397A-14

  Query Match             2.1%;  Score 336.5;  DB 2;  Length 240;
  Best Local Similarity   34.7%;  Pred. No. 7.1e-21;
  Matches   82;  Conservative   37;  Mismatches   70;  Indels   47;  Gaps    4;

Qy       1879 TESVRPQMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNR 1931
                 | |:||    :          |  : |      ||  |||  |:  :: | |||     | |
Db          5 TTSLRPPHHFSPPCFVAALPAAGVAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHAR 64

Qy       1932 DPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW----------DPSFDK 1981
                 ||||||  |   |:|::|||   ||::|:  ||||:::| |   || :          :   ::
Db          65 DPVGGSVEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEEEEEEEEEE 124

Qy       1982 EGKDEHRK----------------------------GLLHMKMAEGAKLQMCYLLQHLN 2012
                 | :||  |                                ||| ||: |  ||||| ||::
Db         125 EEEDEEEKEEDEEEEEKEDAEKEEEEAPEGEKEDLEEGLLQMKLPESVKLQMCNLLEYFC 184

Qy       2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQS-DLPSAVAAKKTREFRCPPR 2067
                 | :|:||||:: |||  :|  || :|  ||  : ::  : :|  |::|||||| ||:
Db         185 DQELQHRVESLAAFAERYVDKLQANQRSRYALLMRAFTMSAAETARRTREFRSPPQ 240


RESULT 8
US-08-114-555A-6
; Sequence 6, Application US/08114555A
; Patent No. 5854392
;  GENERAL INFORMATION:
;    APPLICANT:  Manly, Susan P.
;    APPLICANT:  Kozlowski, Michael R.
;    APPLICANT:  Neve, Rachael L.
;    TITLE OF INVENTION:  CLONING AND EXPRESSION OF beta-APP-C100
;    TITLE OF INVENTION:  RECEPTOR (C100-R)
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/114,555A
;      FILING DATE:  30-AUG-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  6013-115
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-8864/9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
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US-08-114-555A-6

  Query Match             2.1%;  Score 334.5;  DB 1;  Length 240;
  Best Local Similarity   35.6%;  Pred. No. 1.1e-20;
  Matches   84;  Conservative   32;  Mismatches   73;  Indels   47;  Gaps    4;

Qy       1879 TESVRPQMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNR 1931
              | |:||    :         |    |      ||  |||  |:  :: | |||     | |
Db          5 TTSLRPPHHFSPPCFVAALPAAGAAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHAR 64

Qy       1932 DPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW-------DPSFDKEGK 1984
              |||| | |  |:|::|||  ||::|:  ||||:::| |  || :       |   : | :
Db         65 DPVGASVEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEDEEEEGEEE 124

Qy       1985 DEHRK-------------------------------GLLHMKMAEGAKLQMCYLLQHLN 2012
              ||  |                               ||| ||: |  |||||:||::
Db        125 DEEEKEEDEEETAQEKEDEEKEEEEAAEGEKEEGLEEGLLQMKLPESVKLQMCHLLEYFC 184

Qy       2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRY-TEIKQSDLPSAVAAKKTREFRCPPR 2067
              | :|:||||:: ||| :|  || :|  ||   ||   : :|  |::|||||  ||:
Db        185 DQELQHRVESLAAFAERYVDKLQANQRSRYGLLIKAFSMTAAETARRTREFRSPPQ 240


RESULT 9
US-08-559-397A-12
; Sequence 12, Application US/08559397A
; Patent No. 6083713
;  GENERAL INFORMATION:
;    APPLICANT:  Manly, Susan P.
;    APPLICANT:  Kozlowski, Michael R.
;    APPLICANT:  Neve, Rachael L.
;    TITLE OF INVENTION:  CLONING AND EXPRESSION OF
;    TITLE OF INVENTION:  BETA APP-C100 RECEPTOR (C100-R)
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036/2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,397A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  6013-135
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-559-397A-12

  Query Match             2.1%;  Score 334.5;  DB 2;  Length 240;
  Best Local Similarity   35.6%;  Pred. No. 1.1e-20;
  Matches   84;  Conservative   32;  Mismatches   73;  Indels   47;  Gaps    4;

Qy       1879 TESVRPQMKMTD-------IAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNR 1931
              | |:||    :         |    |      ||  |||  |:  :: | |||     | |
Db          5 TTSLRPPHHFSPPCFVAALPAAGAAEAPARLSPAIPLEALRDKALRMLGEAVRDGGQHAR 64

Qy       1932 DPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW-------DPSFDKEGK 1984
              |||| | |  |:|::|||  ||::|:  ||||:::| |  || :       |   : | :
Db         65 DPVGASVEFQFVPVLKLVSTLLVMGIFGDEDVKQILKMIEPEVFTEEEEEDEEEEGEEE 124

Qy       1985 DEHRK-------------------------------GLLHMKMAEGAKLQMCYLLQHLN 2012
              ||  |                               ||| ||: |  |||||:||::
Db        125 DEEEKEEDEEETAQEKEDEEKEEEEAAEGEKEEGLEEGLLQMKLPESVKLQMCHLLEYFC 184

Qy       2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRY-TEIKQSDLPSAVAAKKTREFRCPPR 2067
              | :|:||||:: ||| :|  || :|  ||   ||   : :|  |::|||||  ||:
Db        185 DQELQHRVESLAAFAERYVDKLQANQRSRYGLLIKAFSMTAAETARRTREFRSPPQ 240


RESULT 10
US-09-949-016-8849
; Sequence 8849, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8849
;   LENGTH: 2262
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8849

  Query Match             2.0%;  Score 313.5;  DB 2;  Length 2262;
  Best Local Similarity   23.9%;  Pred. No. 6.1e-17;
  Matches  168;  Conservative  110;  Mismatches  263;  Indels  163;  Gaps   36;

Qy         76 LQELVTAAGSETGKGTGSGHRTLL-----YGNAILLRHLNSDMYLAC-LSTSSSQDKLAF 129
              |::|  ||  | |  | :: ||     | | | | |: |: ||       :  :| |
Db         36 LKKLQHAAELEQ-KQNESENKKLLGEIVKYSNVIQLLHIKSNKYLTVNKRLPALLEKNAM 94

Qy        130 DVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK----EN--- 182
              | |   :  |  |: :||  | |||| : ||| ::|: |   : || :     :|
Db         95 RVSLDA-AGNEGSWFYIHPFWKLRSEGDNIVVGDKVVLMPVNAGQPLHASNIELLDNPGC 153

Qy        183 -EVSIVNASFHVTHWSVQPYGTGISRMKYVGY----VFGGDVLRFFHGGDECLTIPSTWT 237
              ||: || :   | | :  :       |||  |    : ||||:| ||   |       :
Db        154 KEVNAVNCN---TSWKITLF------MKYSSYREDVLKGGDVVRLFHAEQEKFLTCDEYE 204

Qy        238 KDGGQNI----VVYEGGSVMSQARSLWRLELA-RTKWAGGFINWYHPMRIRHITTGRYLG 292
              |   |:|    : :  :  : :::|| :|:       ||   |    | :|: || ||
Db        205 KK--QHIFLRTTLRQSATSATSSKALWEIEVVHHDPCRGGAGQWNSLFRFKHLATGNYLA 262

Qy        293 V-------NDQNE----------------------LY-LVS----------REEATTAS 311
                    : |||                      :| |||           :|||
Db        263 AELNPDYRDAQNEGKNVRDGVPPTSKKKRQAGEKIMYTLVSVPHGNDIASLFELDATTLQ 322

Qy        312 CAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSYKSY----ETKK 367
              | ||                          :| | ::|  |  |::  |     : ::
Db        323 RADCLVPR----------------------NSYVRLRHLCTNTWVTSTSIPIDTDEER 358

Qy        368 KGVGKV------EEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLE 421
                : |:      |:|:|      : :  |  : :      |  ::|           ||
Db        359 PVMLKIGTCQTKEDKEAFAIVSVPLSEVRDLLDFANDANKVLATTVKKLE-------NG-- 409

Qy        422 TLQENRRHSMFFASVNLGEMVMCLEDLINYFAQ-PDEDMEHEE----KQNKFRALRNRQD 476
```

```
Db        410 TITQNERRF----------VTKLLEDLIFFVADVPNNGQEVLDVVITKPN-----RERQK 454

Qy        477 LFQEEGILNL---ILEAIDKINVITSQGFLAGFL-AGDESGQSWEMISGYLYQLLAAIIK 532
Db        455 LMREQNILAQVFGILKAPFKEK--AGEGSMLRLEDLGDQRYAPYKYMLRLCYRVL----- 507

Qy        533 GNHTNCAQFANSNRLNWLFSRLGSQASGEGTGML--DVLHCVLIDSPEALNM-MRDEHIK 589
Db        508 -RHSQQDYRKNQEYIAKNFCVMQSQI---GYDILAEDTITALLHNNRKLLEKHITAKEIE 563

Qy        590 VIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLL-PGK-NLLLQTALVDHVS 647
Db        564 TFVSLLRRN-REPRFLDYLSDLCVSNTTAIPVTQELICKFMLSPGNADILIQTKVVSMQA 622

Qy        648 S--VRPNIFVGRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIG 689
Db        623 DNPMESSILSDDIDDEEVWLYWIDSNKEPHGKAIRHLAQEAKEG 666
```

RESULT 11
PCT-US96-01735-1
; Sequence 1, Application PC/TUS9601735
; GENERAL INFORMATION:
; APPLICANT: Marks, Andrew R.
; TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01735
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/386,039
; FILING DATE: 09-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kole, Lisa B
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A30042 - 165/30555
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2628
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2713 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
PCT-US96-01735-1

Query Match 1.8%; Score 289; DB 4; Length 2713;
Best Local Similarity 23.2%; Pred. No. 1.3e-14;
Matches 176; Conservative 106; Mismatches 306; Indels 172; Gaps 37;

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Qy         15 SFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLE-NIADKNIPP-DLSQCVFVI----- 67
Db          7 SFLHIGD-ICSLYAEGSTNGFISTLGLVDDRCVVQPETGDLNNPPKKFRDCLFKLCPMNR 65

Qy         68 --------------EQALSVRALQELVTAAGSETGKGTGSGHRTLL-----YGNAILLR 107
Db         66 YSAQKQFWKAAKPGANSTTDAVLLNKLHHAADLEK-KQNETENRKLLGTVIQYGNVIQLL 124

Qy        108 HLNSDMYLAC-LSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLI 166
Db        125 HLKSNKYLTVNKRLPALLEKNAMRVTLDE-AGNEGSWFYIQPFYKLRSIGDSVVIGDKVV 183

Qy        167 LVSVATERYLHTTKE--------NEVSIVNASFHVTHWSVQPYGTGISRMKYV----GYV 214
Db        184 LNPVNAGQPLHASSHQLVDNPGCNEVNSVNCN---TSWKI------VLFMKWSDNKDDIL 234

Qy        215 FGGDVLRFFHGGDE-CLTIPSTWTKDGGQNIVVYEGG----SVMSQARSLWRLELAR-TK 268
Db        235 KGGDVVRLFHAEQEKFLTCDEHRKK---QHVFLRTTGRQSATSATSSKALWEVEVVQHDP 291

Qy        269 WAGGFINWYHPMRIRHITTGRYLGVN-----------------DQNELYLVSREEATTA 310
Db        292 CRGGAGYWNSLFRFKHLATGHYLAAEVDPDFEEECLEFQPSVDPDQD----ASRSRLRNA 347

Qy        311 SCAFCLRQEK----------DDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLS 359
Db        348 -------QEKMVYSLVSVPEGNDISSIFELDPTTLRGGDSLVPRNSYVRLRHLCTNTWV- 399

Qy        360 YKSYETKKKGVGKVEEKQAILH------EEGKMDDG----------LDFSRSQEEESRT 402
Db        400 ----HSTNIPIDKEEEKPVMLKIGTSPVKEDKEAFGIVPVSPAEVRDLDFAND------A 449

Qy        403 ARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHE 462
Db        450 SKVL---GSIAGKLEKG--TITQNERRS----------VTKLLEDLV-YFVTGGTNSGQD 493

Qy        463 EKQNKF-RALRNRQDLFQEEGILNLILEAIDKINVITSQG-FLAGFLAGDESGQSWEMIS 520
Db        494 VLEVVFSKPNRERQKLMREQNILKQIFKLLQAPFTDCGDGPMLRLEELGDQRHAPFRHIC 553

Qy        521 GYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEAL 580
Db        554 RLCYRVLRHSQQDYRKNQEYIA--KQFGFMQKQIGYDVLAE-----DTITALLHNNRKLL 606

Qy        581 NMMRDEH-----IKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKN 635
Db        607 ----EKHITAAEIDTFVSLVRKN-REPRFLDYLSDLCVSMNKSIPVTQELICKAVLNPTN 661

Qy        636 --LLLQTALV------DHVSSVRPNIFVGRVEGSAVYRKW 667
Db        662 ADILIETKLVLSRPEFEGVSSTGENALEAGEDEEEVWLFW 701
```

RESULT 12
US-09-385-222A-4
; Sequence 4, Application US/09385222A
; Patent No. 6465211
; GENERAL INFORMATION:
; APPLICANT: RIKEN;
; APPLICANT: Katsuhiko Mikoshiba
; TITLE OF INVENTION: High affinity IP3 binding polypeptide
; FILE REFERENCE: PH-657US
; CURRENT APPLICATION NUMBER: US/09/385,222A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: JP98/242207
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2749
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-385-222A-4

```
  Query Match             1.8%;  Score 279;  DB 2;  Length 2749;
  Best Local Similarity   23.2%;  Pred. No. 1e-13;
  Matches  167;  Conservative  100;  Mismatches  306;  Indels  148;  Gaps   34;

Qy         15 SFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLE-NIADKNIPP-DLSQCVFVI----- 67
              |||   | :|          ::  |  :  | ::    | | ||     |:| :
Db          7 SFLHIGD-ICSLYAEGSTNGFISTLGLVDDRCVVQPEAGDLNNPPKKFRDCLFKLCPMNR 65

Qy         68 --------------EQALSVRALQELVTAAGSETGKGTGSGHRTLL-----YGNAILLR 107
                           | :|  ||  |  |   : :| ||      ||| | |
Db         66 YSAQKQFWKAAKPGANSTTDAVLLNKLHHAADLEK-KQNETENRKLLGTVIQYGNVIQLL 124

Qy        108 HLNSDMYLAC-LSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLI 166
              || |: ||       :  :| |  | | : :  |  |: : |  | || |: | :|| ::
Db        125 HLKSNKYLTVNKRLPALLEKNAMRVTLDE-AGNEGSWFYIQPFYKLRSIGDSVVIGDKVV 183

Qy        167 LVSVATERYLHTTKE--------NEVSIVNASFHVTHWSVQPYGTGISRMKYV----GYV 214
              |  |   : || :          |||: || :   | | :      :  ||:       :
Db        184 LNPVNAGQPLHASSHQLVDNPGCNEVNSVNCN---TSWKI------VLFMKWSDNKDDIL 234

Qy        215 FGGDVLRFFHGGDE-CLTIPSTWTKDGGQNIVVYEGG----SVMSQARSLWRLELAR-TK 268
              ||||:| ||   |  ||       |   |:: :   |    :  : :::|| :|: :
Db        235 KGGDVVRLFHAEQEKFLTCDEHRKK---QHVFLRTTGRQSATSATSSKALWEVEVVQHDP 291

Qy        269 WAGGFINWYHPMRIRHITTGRYLGVN-----------------DQNELYLVSREEATTA 310
              ||   |    | :|: || ||                     ||:     ||     |
Db        292 CRGGAGYWNSLFRFKHLATGHYLAAEVDPDFEEECLEFQPSVDPDQD----ASRSRLRNA 347

Qy        311 SCAFCLRQEK-----------DDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLS 359
                  |||           :|   : |     : |   :   :| | ::|  |  |:
Db        348 -------QEKMVYSLVSVPEGNDISSIFELDPTTLRGGDSLVPRNSYVRLRHLCTNTWV- 399

Qy        360 YKSYETKKKGVGKVEEKQAILH------EEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
                :   : | |||  :|       :| |  :          | |         | :
Db        400 ----HSTNIPIDKEEEKPVMLKIGTSPLKEDK--EAFAIVPVSPAEVRDLDFANDASKVL 453

Qy        414 TKFINGLE--TLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKF-RA 470
                 ||  |: :| | |          :   ||||: ||     :  :  :  | :
Db        454 GSIAGKLEKGTITQNERRS----------VTKLLEDLV-YFVTGGTNSGQDVLEVVFSKP 502

Qy        471 LRNRQDLFQEEGILNLILEAIDKINVITSQG-FLAGFLAGDESGQSWEMISGYLYQLLAA 529
              | || | :|: ||  | : :          |  |      ||:    :  |     |::|
Db        503 NRERQKLMREQNILKQIFKLLQAPFTDCGDGPMLRLEELGDQRHAPFRHICRLCYRVLRH 562

Qy        530 IIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEH-- 587
                :    |     |   :  ::  ::|      |      | :  :| :: : |    ::|
Db        563 SQQDYRKNQEYIA--KQFGFMQKQIGYDVLAE-----DTITALLHNNRKLL----EKHIT 611

Qy        588 ---IKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKN--LLLQTAL 642
                  |   :||: |: |:|: || |  |||     ::  :|  ||  :|   |  :|::| |
Db        612 AAEIDTFVSLVRKN-REPRFLDYLSDLCVSMNKSIPVTQELICKAVLNPTNADILIETKL 670

Qy        643 V 643
              |
Db        671 V 671
```

```
RESULT 13
US-09-385-222A-2
; Sequence 2, Application US/09385222A
; Patent No. 6465211
; GENERAL INFORMATION:
;  APPLICANT:   RIKEN;
;  APPLICANT:  Katsuhiko Mikoshiba
;  TITLE OF INVENTION:  High affinity IP3 binding polypeptide
;  FILE REFERENCE:  PH-657US
;  CURRENT APPLICATION NUMBER: US/09/385,222A
;  CURRENT FILING DATE:  1999-08-26
;  PRIOR APPLICATION NUMBER:  JP98/242207
;  PRIOR FILING DATE:  1998-08-27
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 604
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-385-222A-2

  Query Match             1.4%;  Score 222;  DB 2;  Length 604;
  Best Local Similarity   23.4%;  Pred. No. 6.6e-10;
  Matches  131;  Conservative   71;  Mismatches  231;  Indels  128;  Gaps   27;

Qy         15 SFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLE-NIADKNIPP-DLSQCVFVI----- 67
              |||   | :|          ::  |  :  | ::    | | ||     |:| :
Db          7 SFLHIGD-ICSLYAEGSTNGFISTLGLVDDRCVVQPEAGDLNNPPKKFRDCLFKLCPMNR 65

Qy         68 --------------EQALSVRALQELVTAAGSETGKGTGSGHRTLL-----YGNAILLR 107
                           | :|  ||  |  |   : :| ||      ||| | |
Db         66 YSAQKQFWKAAKPGANSTTDAVLLNKLHHAADLEK-KQNETENRKLLGTVIQYGNVIQLL 124

Qy        108 HLNSDMYLAC-LSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLI 166
              || |: ||       :  :| |  | | : :  |  |: : |  | || |: | :|| ::
Db        125 HLKSNKYLTVNKRLPALLEKNAMRVTLDE-AGNEGSWFYIQPFYKLRSIGDSVVIGDKVV 183

Qy        167 LVSVATERYLHTTKE--------NEVSIVNASFHVTHWSVQPYGTGISRMKYV----GYV 214
              |  |   : || :          |||: || :   | | :      :  ||:       :
Db        184 LNPVNAGQPLHASSHQLVDNPGCNEVNSVNCN---TSWKI------VLFMKWSDNKDDIL 234

Qy        215 FGGDVLRFFHGGDE-CLTIPSTWTKDGGQNIVVYEGG----SVMSQARSLWRLELAR-TK 268
              ||||:| ||   |  ||       |   |:: :   |    :  : :::|| :|: :
Db        235 KGGDVVRLFHAEQEKFLTCDEHRKK---QHVFLRTTGRQSATSATSSKALWEVEVVQHDP 291

Qy        269 WAGGFINWYHPMRIRHITTGRYLGVN-----------------DQNELYLVSREEATTA 310
              ||   |    | :|: || ||                     ||:     ||     |
Db        292 CRGGAGYWNSLFRFKHLATGHYLAAEVDPDFEEECLEFQPSVDPDQD----ASRSRLRNA 347

Qy        311 SCAFCLRQEK-----------DDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLS 359
                  |||           :|   : |     : |   :   :| | ::|  |  |:
Db        348 -------QEKMVYSLVSVPEGNDISSIFELDPTTLRGGDSLVPRNSYVRLRHLCTNTWV- 399

Qy        360 YKSYETKKKGVGKVEEKQAILH------EEGKMDDGLDFSRSQEEESRTARVIRKCSSLF 413
                :    : | |||  :|       :| |  :          | |         | :
Db        400 ----HSTNIPIDKEEEKPVMLKIGTSPLKEDK--EAFAIVPVSPAEVRDLDFANDASKVL 453

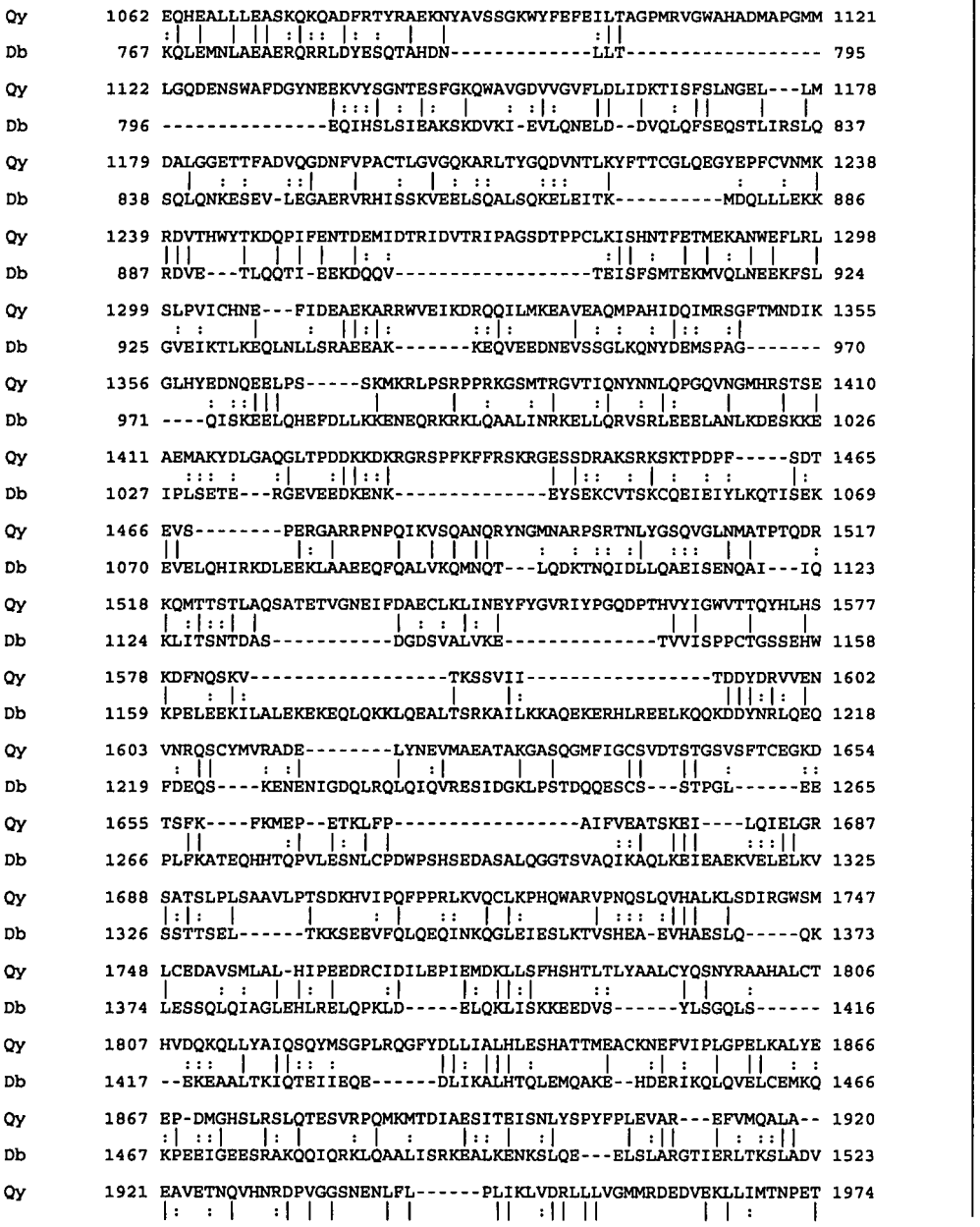
Qy        414 TKFINGLE--TLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKF-RA 470
                 ||  |: :| | |          :   ||||: ||     :  :  :  | :
Db        454 GSIAGKLEKGTITQNERRS----------VTKLLEDLV-YFVTGGTNSGQDVLEVVFSKP 502

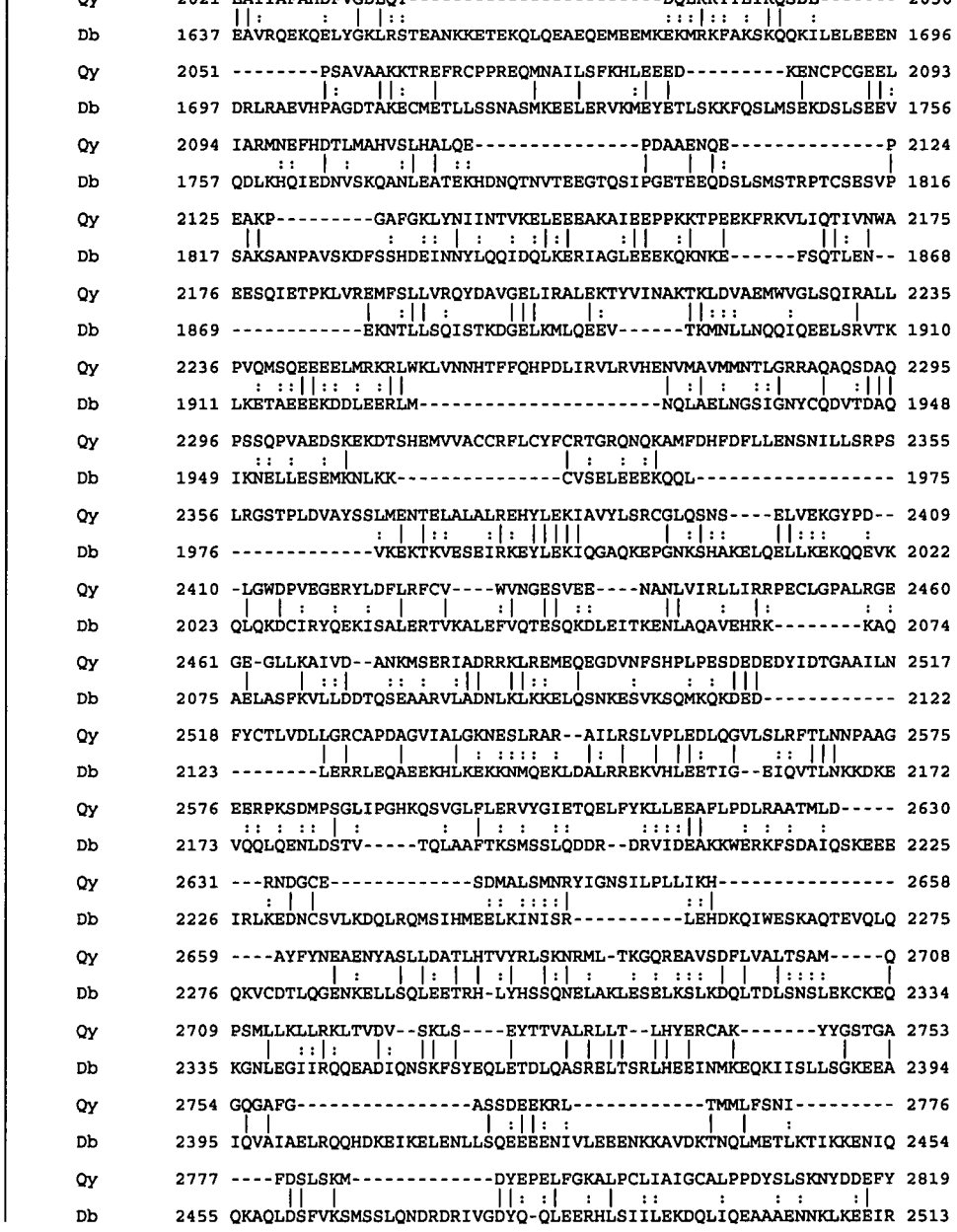
Qy        471 LRNRQDLFQEEGILNLILEAI 491
              | || | :|: ||  | : :
Db        503 NRERQKLMREQNILKQIFKLL 523
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```
RESULT 14
US-09-949-016-6507
; Sequence 6507, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6507
;   LENGTH: 3259
;   TYPE: PRT
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; ORGANISM: Human
US-09-949-016-6507

Query Match 1.3%; Score 198; DB 2; Length 3259;
Best Local Similarity 17.4%; Pred. No. 2.3e-06;
Matches 405; Conservative 370; Mismatches 800; Indels 746; Gaps 102;





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Qy       2820 GKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQ-KFSEHYH----DAWASRKIENGWV 2874
Db       2514 GLRSHMDDLNS---ENAKLDAELIQYREDLNQVITIKDSQQKQLLEVQLQQNKELENKYA 2570

Qy       2875 -YGEGWSDSQKTHPRL-KPYNMLNDYEKERYKEPVRESLKALLA--------------IG 2918
Db       2571 KLEEKLKESEEANEDLRRSFNALQEEKQDLSKE--IESLKVSISQLTRQVTALQEEGTLG 2628

Qy       2919 WSVEHSEVDIPSNN--------RSSMRR-----------QSKSGGRPPEIVTDSATPFDY 2959
Db       2629 --LYHAQLKVKEEEVHRLSALPSSSQKRIAELEEELVCVQKEAAKKVGEIEDKLKKELKH 2686

Qy       2960 NPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000
Db       2687 LHHDAGI----MRNETETAEERVAELARDLVEMEQKLLMVT 2723


RESULT 15
US-09-150-867-1
; Sequence 1, Application US/09150867
; Patent No. 6645748
; GENERAL INFORMATION:
;  APPLICANT: Wood, Kenneth W.
;  APPLICANT: Sakowicz, Roman
;  APPLICANT: Goldstein, Lawrence S.B.
;  APPLICANT: Cleveland, Don W.
;  APPLICANT: The Regents of the University of California
;  TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
;  TITLE OF INVENTION: Chromosome Congression
;  FILE REFERENCE: 18557C-000110US
;  CURRENT APPLICATION NUMBER: US/09/150,867
;  CURRENT FILING DATE: 1998-09-10
;  EARLIER APPLICATION NUMBER: US 60/058,645
;  EARLIER FILING DATE: 1997-09-11
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 2954
;   TYPE: PRT
;   ORGANISM: Xenopus sp.
;   FEATURE:
;   OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E)
;   OTHER INFORMATION: member of the kinesin superfamily of microtubule
;   OTHER INFORMATION: motor proteins
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (1)..(472)
;   OTHER INFORMATION: kinesin like motor domain
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (473)..(2752)
;   OTHER INFORMATION: rod domain
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (2753)..(2954)
;   OTHER INFORMATION: tail domain
US-09-150-867-1

  Query Match             1.3%;  Score 197.5;  DB 2;  Length 2954;
  Best Local Similarity   17.3%;  Pred. No. 2.1e-06;
  Matches  452;  Conservative  425;  Mismatches  983;  Indels  757;  Gaps  119;

Qy        296 QNELYLVSREEATTASCAFC------------LRQEKDDQKQVLEDKDLEVIGAP---II 340
Db        530 ENQLQYLPKDSGDMAECRKASFEKEITSLQQQLQSKEEEKKELVQSFELKIAELEEQLSV 589

Qy        341 KYGDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILHEEG----------KMDDGL 390
Db        590 KAKNLEMVTNSREHSINAEVQTDVEKE----VVRKEMSVLGDSGYNASNSDLQDSSVDGK 645

Qy        391 DFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSM----FFASVNLGEMVMCLE 446

Db        646 RLSSSHDECIEHRKMLEQKIVDLEEFIENLNKKSENDKQKSSEQDFMESIQLCEAIMA-- 703

Qy        447 DLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQGFLAGF 506
Db        704 ---------------EKANALEELALMRDNFD-----NIILEN---------------- 726

Qy        507 LAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGEGTGML 566
Db        727 ----------ETLKREIADLERSLKENQETN-----------EFEILEKETQKEHEAQL 764

Qy        567 DVLHCV-----LIDSPEALNMMRDEHIKVIISLLEKH---------------------- 598
Db        765 --IHEIGSLKKLVENAEMYNQNLEEDLETKTKLLKEQEIQLAELRKRADNLQKKVRNFDL 822

Qy        599 ----GRDPKVLDVLCSL--CVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPN 652
Db        823 SVSMGDSEKLCEEIFQLKQSLSDAEAVTRDAQKECSF-LRSENLELKEKMED-----TSN 876

Qy        653 IFVGRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVG 712
Db        877 WYNQKEKAASLFEKQLETEKSNYKKMEADLQKELQSAF-NEINYL----------NG-- 922

Qy        713 DDLYSYGFDGAYLWSGGRKTP---VNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVR 769
Db        923 -----------LLAG--KVPRDLLSRVELE----KKVSEFSKQLEKALEEKNALENEVT 964

Qy        770 VTGSFTNFNLEGMFFP-VISC----SSKLSCRFLL---GGEHGRLRYAAPEGYSPLVESL 821
Db        965 CLSEY-------KFLPNEVECLKNQISKASEEIMLLKQEGEHSASIISKQE----IIMQE 1013

Qy        822 LPQQILSLEPCFYFGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAEN 881
Db       1014 QSEQILQL-------------------TDEVTHTQSKV---QQTEEQYLEM--KKMHDD 1048

Qy        882 IHEMWAMNKIEAGWMYGDQREDL----------------------HKIHPCLVPFERLPP 919
Db       1049 LFEKYIRNKSEA--------EDLLREMENLKGTMESVEVKIADTKHELEETIRDKEQL-L 1099

Qy        920 AEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNEPFMQSNGYKPAPLD--LSA 977
Db       1100 HEKKYFFQ-AMQTIFPITPL----SDSLPPSKL----------VEGNSQDPIEINDYHNL 1144

Qy        978 VTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDA-IKK 1036
Db       1145 IALATERNNIMVCLETERNSL--KEQV----------IDLNTQLQSLQAQSIEKSDLQK 1191

Qy       1037 ANRDTASETVRTL----LVYGYMLDPPTG-EQHEALLLEASKQKQADFRTYRAE-KNYAV 1090
Db       1192 PKQDLEEGEVKLLLEMELLKGHLTDSQLSIEKLQLENLEVTEKLQ----TLQEEMKNITI 1247

Qy       1091 SSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQ 1150
Db       1248 ERNELQTNFEDLKAEHDSLKQDLSENIEQSIETQDELRAAQEELREQKQL---VDSFRQQ 1304

Qy       1151 W-------------AVGDVVGVFLDLIDKTISFSLNGE-----LLMDALGGETTF----- 1187
Db       1305 LLDCSVGISSPNHDAVANQEKVSLGEVNSLQSEMLRGERDELQTSCKALVSELELLRAHV 1364

Qy       1188 ADVQGDNFVPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTK 1247
Db       1365 KSVEGENLEITKKLNGLEKEILGKSEESEVLK-----SMLENLKEDNNKLKEQAEEYSSK 1419

Qy       1248 D-----QPIFENTDEMIDTRIDV--TRIPAGSDTPPCLKI-SHNTFETMEKANWEFL--R 1297
Db       1420 ENQFSLEEVFSGSQKLVD-EIEVLKAQLKAAEER---LEIKDRDYFELVQTANTNLVEGK 1475

Qy       1298 LSLPVICHNEFIDEAEKARRWVEIK------DRQQILMKEAVEAQMPAH-----IDQIMR 1346
Db       1476 LETPLQADHE-EDSIDRRSEEMEIKVLGEKLERNQYLLERLQEEKLELSNKLEILQKEME 1534

Qy       1347 SGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHR 1406
Db       1535 TSVLLKD-------DLQQKLESLLSENIILKE------NIDTTLKHHSDTQA----QLQK 1577
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Qy       1407 STSEAEMAK-YDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDT 1465
Db       1578 TQQELQLAKNLAIAASDNCP-------------ITQEKETSADCVHPLEEK-------I 1616

Qy       1466 EVSPERGARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTL 1525
Db       1617 LLLTEELHQKTNEQEKLLH------------EKNELEQAQVELK----CEVEHLMKSMIE 1660

Qy       1526 AQSATETVGNEIFDAE--CLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQS 1583
Db       1661 SKSSLESLQHEKHDTEQQLLALKQQM-----------------QVVTQ--------EKK 1694

Qy       1584 KVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTST 1643
Db       1695 ELQQTHEHLTAEVDHLKENI-----------ELGLNFKNEAQQKTTKEQCLLNENKELEQ 1743

Qy       1644 GSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEILQ--IELGRSATSLPLSAAVLPT 1701
Db       1744 SQHRLQCEIEELMKSLK-DKESAL-------ETLKESEQKVINLNQEMEMVMLEMEELKN 1795

Qy       1702 SDKHVIPQFPPRLKVQ---------CLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDA 1752
Db       1796 SQRTVIAE---RDQLQDDLRESVEMSIETQDDLRKAQEALQQQKDKVQELTSQISVLQEK 1852

Qy       1753 VSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQ 1812
Db       1853 ISLL-------------------------------------------------------ENQ 1859

Qy       1813 LLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPELKALYEEPDMGH 1872
Db       1860 MLYNVATVKETLSERDDLNQSKQHLFSEIETLSLSLKEKEF------------------- 1900

Qy       1873 SLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRD 1932
Db       1901 ALEQAEKDKADAARKTIDITEKISNI-------------EEQLLQQATNLKET--LYERE 1945

Qy       1933 PVGGSNENLFLPLIKLVDRL----LLVGMM---RDEDVEKLLIMTNPETWDPSFDKEGKD 1985
Db       1946 SLIQCKEQLALNTEHLRETLKSKDLALGKMEQERDEAANKVIALTEKMS-------SLEE 1998

Qy       1986 EHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEI 2045
Db       1999 QINENVTTLKEGEGEK--ETFYLQRPSKQQ---------------SSSQMEELRE--SL 2038

Qy       2046 KQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIA-RMNEFHD-- 2102
Db       2039 KTKDLQLEEAEKEISE---ATNEIKNLTAKISSLEEEILQNASILNEAVSERENLRHSKQ 2095

Qy       2103 ---TLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVK-------ELEEEAKAIE 2152
Db       2096 QLVSELEQLSL-TLKSRDHAFAQSKREKDEAVNKIASLAEEIKILTKEMDEFRDSKESLQ 2154

Qy       2153 EPPKKTPEEKFR-KVLIQTIVNWAEESQIETPKLVREM------FSLLVRQYDAVGELIR 2205
Db       2155 EQSSHLSEELCTYKTELQMLKQQKEDINNKLAEKVKEVDELLQHLSSLKEQLDQIQMELR 2214

Qy       2206 ALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQ-------------MSQEEEELMRKRL 2251
Db       2215 N-EKLRNYELCEKMDIMEKEISVLRLMQNEPQQEEDDVAERMDILESRNQEIQELMEKIS 2273

Qy       2252 WKLVNNHTFFQ--HPDLIRVLRVHE----NVMAVMMNTLGR------------RAQAQS- 2292
Db       2274 AVYSEQHTLLSSLSSELQKETEAHKHCMLNIKESLSSTLSRSFGSLQTEHVKLNTQLQTL 2333

Qy       2293 ----DAQPSSQPVAEDSK-----EKDTSHE--------MVVACCRFLCYFCRTGRQ---- 2331
Db       2334 LNKFKVVYRTAAVKEDHSLIKDYEKDLAAEQKRHDELRLQLQCLE------QHGRKWSDS 2387

Qy       2332 -NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVY 2390
Db       2388 ASEELKFCEIEFLNE---------------------LLFKKANIIQSVQDDFSE-VQVF 2424

Qy       2391 LSRCGLQSNSELV-EKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANL--VIRLLI 2447
Db       2425 LNQVGSTLQEELEHKKGF--MQWLEEFGDLHVDAKKLSEGMQ----QENRRIASTIQLLT 2478

Qy       2448 RRPECLGPALRGEGEGLLKAIVDA----------NKMSERIADRRK-----LREMEQEGD 2492
Db       2479 KR---------------LKAVVQSKIQREITVYLNQFEAKLQEKKEQNKELMRRMEHHG- 2522

Qy       2493 VNFSHPLPESDEDEDYIDTGAAILNFYCTLVD----LLGRCAPDAGVIALGKNESLRAR- 2547
Db       2523 -----PSASVMEEEN-----ARLLGILKTVQDESKKLQSRIKMLENELNLVKDDAMHKGE 2572

Qy       2548 --AILRSLVPLEDLQGVLS---LRFTL---NNPAAGE--ERPKSDMPSGLIPGHKQSVGL 2597
Db       2573 KVAILQDKLLSRNAEAELNAMQVKLTKKQDNLQAAMKEIENLQKMVAKGAVP-YKEEIDN 2631

Qy       2598 FLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDG 2634
Db       2632 LKTKVVKIEMEKIKYSKATDQEIAYLKSC-LEDKEEG 2667
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Search completed: April 14, 2006, 01:43:55
Job time : 95 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 14, 2006, 01:44:08 ; Search time 42 Seconds
(without alignments)
3034.945 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Perfect score: 15748
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Scoring table: BLOSUM62
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Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6440.5	40.9	4868	7	US-11-044-111-24	Sequence 24, Appl
2	2983	18.9	3375	7	US-11-044-111-23	Sequence 23, Appl
3	2709.5	17.2	1056	7	US-11-044-111-22	Sequence 22, Appl
4	643	4.1	237	7	US-11-044-111-11	Sequence 11, Appl
5	636.5	4.0	240	7	US-11-044-111-10	Sequence 10, Appl
6	623.5	4.0	240	7	US-11-044-111-9	Sequence 9, Appli
7	614	3.9	237	7	US-11-044-111-12	Sequence 12, Appl
8	603	3.8	239	7	US-11-044-111-5	Sequence 5, Appli
9	603	3.8	239	7	US-11-044-111-25	Sequence 25, Appl
10	576.5	3.7	212	7	US-11-044-111-6	Sequence 6, Appli
11	576.5	3.7	212	7	US-11-044-111-26	Sequence 26, Appl
12	285	1.8	2671	6	US-10-876-787-6	Sequence 6, Appli
13	199	1.3	2668	7	US-11-124-368A-215	Sequence 215, App
14	198.5	1.3	2665	7	US-11-124-368A-214	Sequence 214, App
15	187.5	1.2	1249	6	US-10-506-454-486	Sequence 486, App
16	186	1.2	576	7	US-11-240-769-70	Sequence 70, Appl
17	186	1.2	5024	6	US-10-793-626-2964	Sequence 2964, Ap
18	183.5	1.2	2228	6	US-10-511-096-2	Sequence 2, Appli
19	183.5	1.2	2230	6	US-10-511-096-4	Sequence 4, Appli
20	183.5	1.2	2250	6	US-10-511-096-6	Sequence 6, Appli
21	183.5	1.2	2252	6	US-10-511-096-8	Sequence 8, Appli
22	172	1.1	5406	6	US-10-995-561-774	Sequence 774, App
23	166.5	1.1	1976	7	US-11-069-834-54	Sequence 54, Appl
24	164.5	1.0	3803	6	US-10-995-561-773	Sequence 773, App
25	164.5	1.0	3960	6	US-10-995-561-771	Sequence 771, App
26	164.5	1.0	5335	6	US-10-995-561-777	Sequence 777, App
27	164.5	1.0	5415	6	US-10-995-561-779	Sequence 779, App
28	164.5	1.0	5464	6	US-10-995-561-775	Sequence 775, App
29	163	1.0	2101	6	US-10-857-780-23	Sequence 23, Appl
30	160.5	1.0	2304	6	US-10-330-773-310	Sequence 310, App
31	159.5	1.0	1976	7	US-11-069-834-52	Sequence 52, Appl
32	158.5	1.0	5935	6	US-10-995-561-776	Sequence 776, App
33	158	1.0	1960	7	US-11-069-834-48	Sequence 48, Appl
34	157.5	1.0	630	7	US-11-196-400-5	Sequence 5, Appli
35	157.5	1.0	1404	6	US-10-878-556A-169	Sequence 169, App
36	151.5	1.0	1960	6	US-10-530-171-17	Sequence 17, Appl
37	151.5	1.0	1960	7	US-11-069-834-50	Sequence 50, Appl
38	151.5	1.0	8746	7	US-11-098-686-10232	Sequence 10232, A
39	150.5	1.0	2348	6	US-10-450-224A-2	Sequence 2, Appli
40	150.5	1.0	4384	6	US-10-821-234-1120	Sequence 1120, Ap
41	149	0.9	1562	7	US-11-052-554A-211	Sequence 211, App
42	149	0.9	1992	7	US-11-069-834-58	Sequence 58, Appl
43	146	0.9	1786	7	US-11-196-400-3	Sequence 3, Appli
44	145.5	0.9	957	7	US-11-051-720-1438	Sequence 1438, Ap
45	145	0.9	860	7	US-11-019-711-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-11-044-111-24
; Sequence 24, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 4868
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-11-044-111-24

Query Match 40.9%; Score 6440.5; DB 7; Length 4868;
Best Local Similarity 43.7%; Pred. No. 0;
Matches 1341; Conservative 496; Mismatches 845; Indels 387; Gaps 49;

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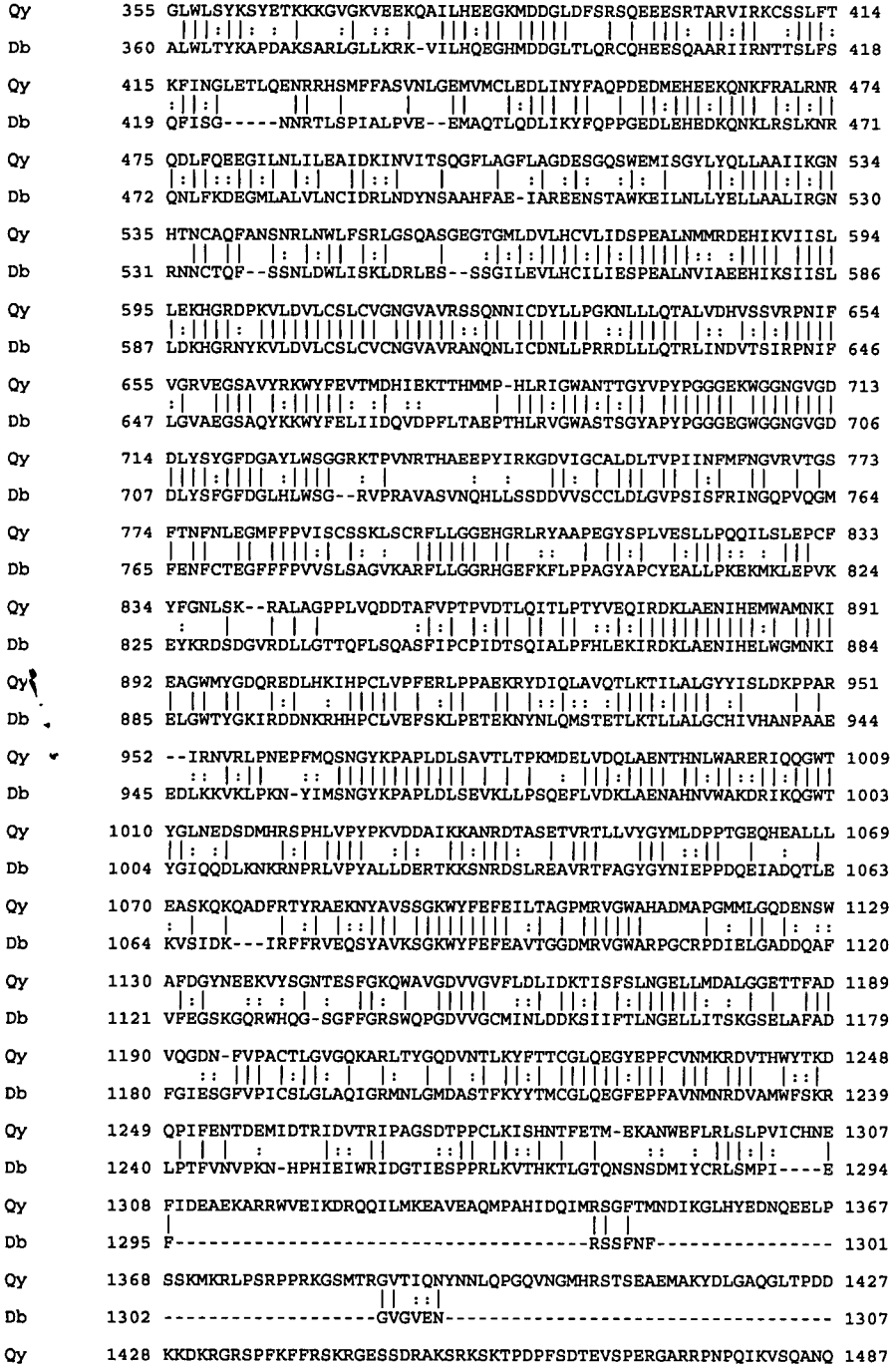
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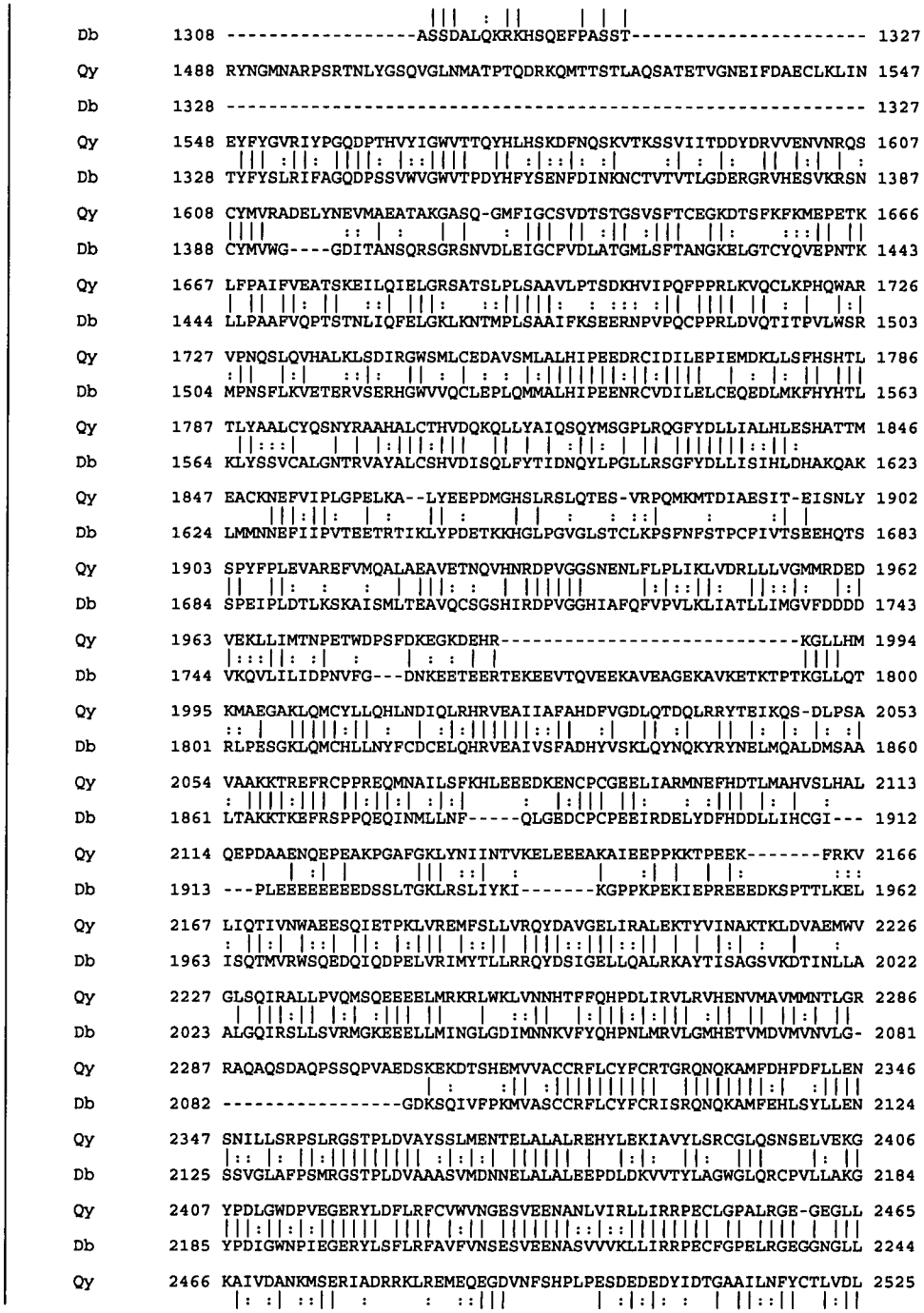
Qy        118 LSTSSSQ-DKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYL 176
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Db        122 LTSSRSQTDKLAFDVGLRENAAGEACWWTIHPASKQRSEGEKVRIGDDLILVSVSSERYL 181

Qy        177 HTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTW 236
              | :  |    |:|||  | |:| |  :| :  :  ||: || |:||||| |||||||||
Db        182 HLSMSNGSIQVDASFMQTLWNVHPTCSGSNITE--GYLLGGHVVRFFHGHDECLTIPSTD 239

Qy        237 TKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQ 296
              .  | |  |:|| |    :|||||:|  |  |:|  | |  | |:||||| || :||
Db        240 QNDSQQKKVLYETGGAGVRARSLWRVEPLRISWSGSNIRWGQPFRLRHITTGMYLALNDD 299

Qy        297 NELYLVSREEATTASCAFCLRQEKD--DQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSET 354
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Qy       2586 GLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNR 2645

Db       2357 NFCPDHKAPMVLFLDRVYGIKDQSFLLHLLEVGFLPDLRASASLDTVSLSTTEAALALNR 2416

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Qy       2990 WAKKKKEEL 2998

Db       2749 WAKKKKMEL 2757


RESULT 2
US-11-044-111-23
; Sequence 23, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
;   LENGTH: 3375
;   TYPE: PRT
;   ORGANISM: Meleagris gallopavo
US-11-044-111-23

  Query Match           18.9%;  Score 2983;  DB 7;  Length 3375;
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Qy       1831 YDLLIALHLESHATTMEACKNEFVIPL--------------GPELKALYEEPDMGHSLRS 1876

Db         306 YDLLLAVHLEQGVRARASMSTEFIVPMDEASKRISLFPAGGGGDVK-VPGPPGVGLS--- 361

Qy       1877 LQTESVRPQMKMTDIAESI----TEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRD 1932

Db         362 ---ACLRPR---PHFAEPCFVRPPDGRALLGPSIPLRALGRRAIRMLREAVAGGGPHARD 415

Qy       1933 PVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRK--- 1989

Db         416 PVGGGVEFQLVPVLKLVSALLAVGALRDPEVRKVLRMIEPRVFGGGEEEEEEEERRRRK 475

Qy       1990 --------------------------------GLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017

Db         476 AVEAGEEEEEVDEEEEVDEEEDEEEEEDGPEEGLLQMKLPESVKLQMCNLLQFFCDQELQ 535

Qy       2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQS-DLPSAVAAKKTREFRCPPREQMNAILSF 2076

Db         536 HRVEAIVAFSERHVERLQRDQRRRYGRLMGAVTMSAAETARRTREFRSPPQEQINMLLQY 595

Qy       2077 KHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYN 2136

Db         596 K--GGADEEDCPVPPDIRGELLQFHSDLLAHCGIE-LQ----GEEEEEEEDASLRQRLLA 648

Qy       2137 IINTV------KELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMF 2190

Db         649 LVQRVVGRQQKEEEEEEATSPEPPVPRTLQE----LISHTMVHWAQESFIQSPELVRSMF 704

Qy       2191 SLLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKR 2250

Db         705 SLLHRQYDGLGELVRALPKAYTISAHSVPDTTALLECLGQIRSLLIVQMGPEEENLMIQS 764

Qy       2251 LWKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDT 2310

Db         765 IGNIMNNKVFYQHPNLMRALGMHETVMQVMVSVLG----------------GGETKE-IR 807

Qy       2311 SHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLM 2370

Db         808 FPKMVTNCCRFLCYFCRISRQNQRSMFDHLGYLLENSSIGL---GMQGSTPLDVAAASVI 864

Qy       2371 ENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWV 2430

Db         865 DNNELALALKEQDLEKVVTYLASCGLQSCPMLLSKGYPDIGWNPCGGERYLDFLRFAVFV 924

Qy       2431 NGESVEENANLVIRLLIRRPECLGPALRGE-GEGLLKAIVDANKMSERIA----DRRKLR 2485

Db         925 NGESVEENANVVVRLLIRRPECFGPALRGEGGSGLLAAIEDAIKISEDPARDGPTVKKER 984

Qy       2486 EMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLR 2545

Db         985 RREIFG--------AEEPHEENRVHLGNAIMSFYAASIDLLGRCAPEMHLIQAGKGEALR 1036

Qy       2546 ARAILRSLVPLEDLQGVLSLRFTLNNPAAGEE----RPKSDMPSGLIPGHKQSVGLFLER 2601

Db         1037 IRAILRSLVPLDDLVGVISL--PLQIPAFGKDGNVVQPR--MAASFVPDHKAPMVLFLDR 1092

Qy       2602 VYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYF 2661

Db         1093 VYGIETQQPLLHVLEVGFLPDMRPAASLDTAAFSTTKMALALNRYLCVPVLPLITKCAPL 1152

Qy       2662 YNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTV 2721

Db         1153 FAGTEHRAIMVDSMLHTIYRLSRGRALTKAQRDAIEECLMALCRYIRPSMLQHLLRRLVF 1212
```

```
Qy       2722 DVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLS 2781
Db       1213 DVPILNEFAKMPLKLLTNHYERCWKYY-CLPSGWPNYGVSSEEELHLTRKLFWGIFESLA 1271

Qy       2782 KMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLD-NPQYDPQPINT 2840
Db       1272 HKKFDPELYKLAMPCLCAIAGALPPDY-----VDASYSSKTEKKASVDAEGNFDPKPVET 1326

Qy       2841 SSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEK 2900
Db       1327 LNVIIPEKLDGFINKYAEFTHEKWAFDKIQNNWTYGETVDEEAKTHPMLRPYKTFSEKDK 1386

Qy       2901 ERYKEPVRESLKALLAIGWSVEHS-EVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFD- 2958
Db       1387 EIYRWPIKESLKAMLAWEWMVEKAREGDEEKAEKKKTRKISQS----------AQATYDP 1436

Qy       2959 ---YNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEEL 2998
Db       1437 SHGYNPQPVDLSGVTLSRELQAMAEQLAENYHNTWGRKKKQEL 1479
```

RESULT 3
US-11-044-111-22
; Sequence 22, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 1056
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-11-044-111-22

Query Match 17.2%; Score 2709.5; DB 7; Length 1056;
Best Local Similarity 50.9%; Pred. No. 3.5e-188;
Matches 546; Conservative 186; Mismatches 302; Indels 39; Gaps 22;

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Qy          5 EGGASEQDDVSFLRTEDMVCLSCTAT----GERVCLAAEGFGNRHCFLENIAD-KNIPPD 59
Db          3 DGG---EGDVQFLRTDDEVVLQCTTTLLKEQLKLCLAAEGFGNRPCFLEPTSNAQNVPPD 59

Qy         60 LSQCVFVIEQALSVRALQELVTAAGSETGK--GTGSGHRTLLYGNAILLRHLNSDMYLAC 117
Db         60 LAVCCFVLEQSLSVRALQEML-ANCAESGRESSQGGGHRTLLYGHAILLRHSHSGMYLSC 118

Qy        118 LSTSSS-QDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYL 176
Db        119 LTTSRSVTDKLAFDVGLQKDAAGEACWWTLHPASKQRSEGEKVRVGDDIILVSVSSERYL 178

Qy        177 HTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGG-DECLTIPST 235
Db        179 HLSTASGELQADASFMQTLWNMNPICSGAEE----GYVTGGHVLRLFHGHMDECLSTSPP 234

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
Db        235 EQGDERSSVVSYEGGAVCTHARSLWRLEPLRISWSGSHLRWGQPFRVRHVTSGRYLALSE 294

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355
Db        295 ERGLVVVEAAAAGTRAAAFCFRASK-EKLEAGTKRDVEGMGPPEIKYGESLCFVQHAASG 353

Qy        356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415
Db        354 LWLTYAAADTKALRLG-LMKRRPILHQEGHMDDALSLSRSQGEESQAARMIYSTAGLYGS 412

Qy        416 FINGLETL-QENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNR 474
Db        413 FIRSLDALSSRGRGGGAGNAALPIAAVILSLRDLIAYFRAPHTELQHEQRQNRLRSLRRR 472

Qy        475 QDLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGN 534
Db        473 QDLFQQEGMISLVLNCIDRLNVYSTAAHFAEF-AGEEAAAAWKEIVNLLYELLASLIRGN 531

Qy        535 HTNCAQFANSNRLNWLFSRLGS-QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIIS 593
Db        532 RTNCALF--STNLDWLVSKLDRLEAS---SGILEVLYCVLIESPEVLNIIQENHIKSIIS 586

Qy        594 LLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNI 653
Db        587 LLDKHGRNHKVLNVLCSLCVCNAVAVRSNQNLITENLLPRRDLLLQTGPVSYVSSIRPNI 646

Qy        654 FVGRVEGSAVYRKWYFEVTMDHIEKTTHMMP-HLRIGWANTTGYVPYPGGGEKWGGNGVG 712
Db        647 LLGTHEGSTQYPRWYFEVAVDHVEPFVTAQPTHLRVGWAMAEGYSPYPGGGEGWGAYGAG 706

Qy        713 DDLYSYGFDGAYLWSGG--RKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRV 770
Db        707 DDLYSFAFDGLHLWAGGVPRAAPSPQQHILAP----GDVVSCCLDLSVPTISSRLNGSPV 762

Qy        771 TGSFTNFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLE 830
Db        763 LGMFEKFNRDALFSPVVSFSAGVRLRFLLGGRHGDFQFLPPPGYSPCAEALLPRERLRLE 822

Qy        831 PC-FYFGN-LSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAM 888
Db        823 PIKAYRGDGPPPHCLLGPTKALPHTAFTPCPVDTAQIVLPPHLERIREKLAENIHELWAL 882

Qy        889 NKIEAGWMYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISL--D 946
Db        883 TRIEQGWTYGPIHDDAEQLHPCLLDPHSLPEPERNYNLQMSGETLKTLLALGCHVGMADE 942

Qy        947 KPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQ 1006
Db        943 KAEENLRKIKLP-KTYTMRNGYKPAPLDLAHVRLTPAQLTLVDRLAENAHNVWARDRVQQ 1001

Qy       1007 GWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPP 1059
Db       1002 GRTYSIVQDIKNKRNPRLVPYNLLDERTKKTNRDSLCEAVRTLIGYGYNIEPP 1054
```

RESULT 4
US-11-044-111-11
; Sequence 11, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-11-044-111-11

Query Match 4.1%; Score 643; DB 7; Length 237;
Best Local Similarity 54.1%; Pred. No. 6.6e-39;
Matches 132; Conservative 49; Mismatches 55; Indels 8; Gaps 5;

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Qy        379 ILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNL 438
Db          1 ILHQEGHMDDALSLSRSQREESQAARMIYSTAGLFNIFIKGLDSLNGKNKPSKPI-SLPL 59
```

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Qy        439 GEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVIT 498
              :|: |:||| ||  |:|:::||||| | |:|:|||:|||||||:: :|: ||::|| :
Db         60 DMVVLTLQDLIGYFQHPEEELQHEEKQTKLRSLKNRQNLFQEEGIISQVLDCIDRLNVYS 119

Qy        499 SQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGS-Q 557
              :    | | ||:|: :||: |   ||:|||::|:|| :||| |  || |:|: |:|   :
Db        120 TAAHFAEF-AGEEAAESWKEIVNLLYELLASLIRGNRSNCALF--SNNLDWVVSKLDRLE 176

Qy        558 ASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGV 617
              ||   :|:|:||:||||:||| ||:::  ||| |||||:||||: |||||||||| |||
Db        177 AS---SGILEVLYCVLIESPEVLNIIKKNHIKSIISLLDKHGRNHKVLDVLCSLCVCNGV 233

Qy        618 AVRS 621
              ||||
Db        234 AVRS 237


RESULT 5
US-11-044-111-10
; Sequence 10, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-11-044-111-10

  Query Match             4.0%;  Score 636.5;  DB 7;  Length 240;
  Best Local Similarity   53.3%;  Pred. No. 2e-38;
  Matches  131;  Conservative   49;  Mismatches   57;  Indels    9;  Gaps    5;

Qy        379 ILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSMFFA--SV 436
              |||:|| ||| |  :| |:|||: ||:|   : |:  || ||::     | |   | ::
Db          1 ILHQEGHMDDALSLTRCQQEESQAARMIYSTAGLYNHFIKGLDSFSGKPRGSGAPAGTAL 60

Qy        437 NLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINV 496
              |  ::: |:||| ||  | |:::|||||:| |:|||| ||||||:|:|:|  ||::||
Db         61 PLEGVILSLQDLIGYFEPPSEELQHEEKQSKLRSLRNRQSLFQEEGMLSLVLNCIDRLNV 120

Qy        497 ITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGS 556
              |:    | | ||:|: :||: |   ||::||::|:||  ||| |  || |:|| |:|
Db        121 YTTAAHFAEF-AGEEAAESWKEIVNLLYEILASLIRGNRANCALF--SNNLDWLVSKLDR 177

Qy        557 -QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGN 615
               :||   :|:|:||:||||:||| ||:::  ||| |||||:||||: |||||||||| |
Db        178 LEAS---SGILEVLYCVLIESPEVLNIIQENHIKSIISLLDKHGRNHKVLDVLCSLCVCN 234

Qy        616 GVAVRS 621
              ||||||
Db        235 GVAVRS 240


RESULT 6
US-11-044-111-9
; Sequence 9, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-044-111-9

  Query Match             4.0%;  Score 623.5;  DB 7;  Length 240;
  Best Local Similarity   51.6%;  Pred. No. 1.8e-37;
  Matches  127;  Conservative   52;  Mismatches   58;  Indels    9;  Gaps    5;

Qy        379 ILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHS--MFFASV 436
              :|||:|| ||| |  :| |:|||: ||:|   : |: :||  |::       | |     ::
Db          1 MLHQEGHMDDALSLTRCQQEESQAARMIHSTNGLYNQFIKSLDSFSGKPRGSGPPAGTAL 60

Qy        437 NLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINV 496
              :  ::: |:||| ||  | ||::|||||:| |:|||| ||||||:|:::|  ||::||
Db         61 PIEGVILSLQDLIIYFEPPSEDLQHEEKQSKLRSLRNRQSLFQEEGMLSMVLNCIDRLNV 120

Qy        497 ITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGS 556
              |:    | | ||:|: :||: |   ||:|||::|:|| :||| |  | |:|| |:|
Db        121 YTTAAHFAEF-AGEEAAESWKEIVNLLYELLASLIRGNRSNCALF--STNLDWLVSKLDR 177

Qy        557 -QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGN 615
               :||   :|:|:||:||||:||| ||:::: ||| |||||:||||: |||||||||| |
Db        178 LEAS---SGILEVLYCVLIESPEVLNIIQENHIKSIISLLDKHGRNHKVLDVLCSLCVCN 234

Qy        616 GVAVRS 621
              ||||||
Db        235 GVAVRS 240


RESULT 7
US-11-044-111-12
; Sequence 12, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Makaira nigricans
US-11-044-111-12

  Query Match             3.9%;  Score 614;  DB 7;  Length 237;
  Best Local Similarity   51.2%;  Pred. No. 8.5e-37;
  Matches  125;  Conservative   54;  Mismatches   57;  Indels    8;  Gaps    5;

Qy        379 ILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNL 438
              |||:|| ||| |  :||| ||:: ||:|   : || :|| ||:||   :  |    |: :
Db          1 ILHKEGHMDDALTVARSQTEEAQAARMIYSTTGLFNQFIKGLDTL-SGKNKSANPPSLPM 59

Qy        439 GEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVIT 498
              :|: |:||| ||  |  ::|||:|| | |:|:|||:||||||:: |:|: :|::||
Db         60 DTVVLSLQDLIFYFRPPGHELEHEDKQFKLRSLKNRQNLFQEEGMITLVLDCVDRLNVYN 119

Qy        499 SQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGS-Q 557
              :    : : ||:|: :||: |   ||:|||::|:||  ||| | ::  |:|| |:|   :
Db        120 TAAHFSEY-AGEEAAESWKEIVNLLYELLASLIRGNRANCALFCDN--LDWLVSKLDRLE 176

Qy        558 ASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGV 617
              ||   :|:|:||:||||:||| ||:::: ||| |||||:||||: |||||||||| |||
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Db        177 AS---SGILEVLYCVLIESPEVLNIIQENHIKSIISLLDKHGRNHKVLDVLCSLCVCNGV 233

Qy        618 AVRS 621
              ||||
Db        234 AVRS 237


RESULT 8
US-11-044-111-5
; Sequence 5, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Meleagris gallopavo
US-11-044-111-5

  Query Match             3.8%;  Score 603;  DB 7;  Length 239;
  Best Local Similarity   50.6%;  Pred. No. 5.4e-36;
  Matches  124;  Conservative   50;  Mismatches   63;  Indels    8;  Gaps    5;

Qy        379 ILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETL-QENRRHSMFFASVN 437
              |||:|| ||| |  |||| |||: ||:|   : |:  ||  |: |    |       |::
Db          1 ILHQEGHMDDALSLSRSQGEESQAARMIYSTAGLYGSFIRSLDALSSRGRGGGAGNAALP 60

Qy        438 LGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVI 497
              :  ::: | ||| ||  |  :::||::||: |:|| ||||||:||:::|:|  ||::||
Db         61 IAAVILSLRDLIAYFRAPHTELQHEQRQNRLRSLRRRQDLFQQEGMISLVLNCIDRLNVY 120

Qy        498 TSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGS- 556
              ::    | | ||:|:  :|: |   ||:|||::|:|| |||| |  |  |:|| |:|
Db        121 STAAHFAEF-AGEEAAAAWKEIVNLLYELLASLIRGNRTNCALF--STNLDWLVSKLDRL 177

Qy        557 QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNG 616
              :||   :|:|:||:||||:||| ||:::: ||| |||||:|||: |||||||||| |
Db        178 EAS---SGILEVLYCVLIESPEVLNIIQENHIKSIISLLDKHGRNHKVLDVLCSLCVCNA 234

Qy        617 VAVRS 621
              |||||
Db        235 VAVRS 239


RESULT 9
US-11-044-111-25
; Sequence 25, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Meleagris gallopavo
US-11-044-111-25

  Query Match             3.8%;  Score 603;  DB 7;  Length 239;
  Best Local Similarity   50.6%;  Pred. No. 5.4e-36;
  Matches  124;  Conservative   50;  Mismatches   63;  Indels    8;  Gaps    5;

Qy        379 ILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETL-QENRRHSMFFASVN 437
              |||:|| ||| |  |||| |||: ||:|   : |:  ||  |: |    |       |::
Db          1 ILHQEGHMDDALSLSRSQGEESQAARMIYSTAGLYGSFIRSLDALSSRGRGGGAGNAALP 60

Qy        438 LGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVI 497
              :  ::: | ||| ||  |  :::||::||: |:|| ||||||:||:::|:|  ||::||
Db         61 IAAVILSLRDLIAYFRAPHTELQHEQRQNRLRSLRRRQDLFQQEGMISLVLNCIDRLNVY 120

Qy        498 TSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGS- 556
              ::    | | ||:|:  :|: |   ||:|||::|:|| |||| |  |  |:|| |:|
Db        121 STAAHFAEF-AGEEAAAAWKEIVNLLYELLASLIRGNRTNCALF--STNLDWLVSKLDRL 177

Qy        557 QASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNG 616
              :||   :|:|:||:||||:||| ||:::: ||| |||||:|||: |||||||||| |
Db        178 EAS---SGILEVLYCVLIESPEVLNIIQENHIKSIISLLDKHGRNHKVLDVLCSLCVCNA 234

Qy        617 VAVRS 621
              |||||
Db        235 VAVRS 239


RESULT 10
US-11-044-111-6
; Sequence 6, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
;   LENGTH: 212
;   TYPE: PRT
;   ORGANISM: Meleagris gallopavo
US-11-044-111-6

  Query Match             3.7%;  Score 576.5;  DB 7;  Length 212;
  Best Local Similarity   49.2%;  Pred. No. 3.7e-34;
  Matches  120;  Conservative   43;  Mismatches   48;  Indels   33;  Gaps    5;

Qy        379 ILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNL 438
              |||:|| ||| |  |||| |||: ||:|   : |:  ||
Db          1 ILHQEGHMDDALSLSRSQGEESQAARMIYSTAGLYGSFIR---------------------- 40

Qy        439 GEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVIT 498
                    | ||| ||  |  :::||::||: |:|| ||||||:||:::|:|  ||::|| :
Db         41 ------LRDLIAYFRAPHTELQHEQRQNRLRSLRRRQDLFQQEGMISLVLNCIDRLNVYS 94

Qy        499 SQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGS-Q 557
              :    | | ||:|:  :|: |   ||:|||::|:|| |||| |  |  |:|| |:|   :
Db         95 TAAHFAEF-AGEEAAAAWKEIVNLLYELLASLIRGNRTNCALF--STNLDWLVSKLDRLE 151

Qy        558 ASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGV 617
              ||   :|:|:||:||||:||| ||:::: ||| |||||:|||: |||||||||| | |
Db        152 AS---SGILEVLYCVLIESPEVLNIIQENHIKSIISLLDKHGRNHKVLDVLCSLCVCNAV 208

Qy        618 AVRS 621
              ||||
Db        209 AVRS 212


RESULT 11
US-11-044-111-26
; Sequence 26, Application US/11044111
; Publication No. US20050272362A1
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; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
;   LENGTH: 212
;   TYPE: PRT
;   ORGANISM: Meleagris gallopavo
US-11-044-111-26

  Query Match             3.7%;  Score 576.5;  DB 7;  Length 212;
  Best Local Similarity   49.2%;  Pred. No. 3.7e-34;
  Matches  120;  Conservative   43;  Mismatches   48;  Indels   33;  Gaps    5;

Qy        379 ILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNL 438
              |||:|| ||| |  |||| |||: ||:|   : |:  ||
Db          1 ILHQEGHMDDALSLSRSQGEESQAARMIYSTAGLYGSFIR------------------- 40

Qy        439 GEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVIT 498
                  | ||| ||  |  :::||::||: |:|| ||||||:||:::|:|  ||::|| :
Db         41 ------LRDLIAYFRAPHTELQHEQRQNRLRSLRRRQDLFQQEGMISLVLNCIDRLNVYS 94

Qy        499 SQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGS-Q 557
              :   | | ||:|:  :|: |   ||:|||::|:|| |||| |  |  |:|| |:|   :
Db         95 TAAHFAEF-AGEEAAAAWKEIVNLLYELLASLIRGNRTNCALF--STNLDWLVSKLDRLE 151

Qy        558 ASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGV 617
              ||   :|:|:||:||||:||| ||:::: ||| |||||:||||: |||||||||| | |
Db        152 AS---SGILEVLYCVLIESPEVLNIIQENHIKSIISLLDKHGRNHKVLDVLCSLCVCNAV 208

Qy        618 AVRS 621
              ||||
Db        209 AVRS 212


RESULT 12
US-10-876-787-6
; Sequence 6, Application US/10876787
; Publication No. US20050287535A1
; GENERAL INFORMATION:
;  APPLICANT: McGrath, Kevin P.
;  APPLICANT:  Kimberly-Clark Worldwide, Inc.
;  TITLE OF INVENTION: BIOMARKERS FOR WOUND HEALING
;  FILE REFERENCE: 1443.156US1
;  CURRENT APPLICATION NUMBER: US/10/876,787
;  CURRENT FILING DATE:  2004-06-24
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 2671
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-876-787-6

  Query Match             1.8%;  Score 285;  DB 6;  Length 2671;
  Best Local Similarity   18.0%;  Pred. No. 5.3e-11;
  Matches  431;  Conservative  314;  Mismatches  829;  Indels  820;  Gaps  101;

Qy         31 GERVCLAAEGFGN----------RHCFLENIAD--KNIPPDLSQCVFVI----------- 67
              |: | | ||| |           | :| |    |  |     |:| :
Db         11 GDIVSLYAEGSVNGFISTLGLVDDRCVVEPAAGDLDNPPKKFRDCLFKVCPMNRYSAQKQ 70

Qy         68 -----------EQALSVRALQELVTAAGSETGKGTGSGHR----TLLYGNAILLRHLNSD 112
                        |:   |  ||:|  ||  |  :      :    : ||: | | |: |:
Db         71 YWKAKQTKQDKEKIADVVLLQKLQHAAQMEQKQNDTENKKVHGDVVKYGSVIQLLHMKSN 130

Qy        113 MYLAC-LSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVA 171
```

```
              ||      :  :| | | |   :  | | : |  | || |: | ||| :||  |
Db        131 KYLTVNKRLPALLEKNAMRVTLDA-TGNEGSWLFIQPFWKLRSNGDNVVVGDKVILNPVN 189

Qy        172 TERYLHTTKE--------NEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFF 223
              : || :           ||: || :   | | :  :      :: |  : ||||:| |
Db        190 AGQPLHASNYELSDNAGCKEVNSVNCN---TSWKINLFMQFRDHLEEV--LKGGDVVRLF 244

Qy        224 HGGDECLTIPSTWTKDGGQ-----NIVVYEGGSVMSQARSLWRLELA-RTKWAGGFINWY 277
              |  |      | :  |:        : :  :  : : :|| :|:       ||  :|
Db        245 HAEQEKFL---TCDEYKGKLQVFLRTTLRQSATSATSSNALWEVEVVHHDPCRGGAGHWN 301

Qy        278 HPMRIRHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGA 337
                | :|: || ||   ::|  |   : :|:    |   | :  ::    |    ::
Db        302 GLYRFKHLATGNYLAA-EENPSY---KGDASDPKAAGMGAQGRTGRRNAGEKIKYCLVAV 357

Qy        338 PIIKYG----------------------DSTVIVQHSETGLW---------------- 357
              |   :|                     :| | ::|  |  |
Db        358 P---HGNDIASLFELDPTTLQKTDSFVPRNSYVRLRHLCTNTWIQSTNVPIDIEEERPIR 414

Qy        358 LSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFI 417
              |   :  ||       |:|:|       : :  |   : :  |  |  : | :  |
Db        415 LMLGTCPTK-------EDKEAFAIVSVPVSEIRDLDFANDASSMLASAVEKLNEGFIS-- 465

Qy        418 NGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDL 477
                  | :||           ::  ||||: : :    : ::       :  | || |
Db        466 ------QNDRRF-----------VIQLLEDLVFFVSDVPNNGQNVLDIMVTKPNRERQKL 508

Qy        478 FQEEGILNLILEAIDKINVITSQGFLAGFLA-----GDESGQSWEMISGYLYQLLAAIIK 532
              :|: ||  :   | |:       |   | |       |:   :: :    |::|    :
Db        509 MREQNILKQVF-GILKVPFREKGG--EGPLVRLEELSDQKNAPYQHMFRLCYRVLRYSQE 565

Qy        533 GNHTNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHI---- 588
              |    |   :  : |::|      |      | :  :| :: : |    ::||
Db        566 DYRKNQEHIA--KQFGMMQSQIGYDILAE-----DTITALLHNNRKLL----EKHITKTE 614

Qy        589 -KVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKN--LLLQTAL--- 642
              :  :||: |: |:|: || |  ||| | :|:  :|  ||  :|  ||  :|::| |
Db        615 VETFVSLVRKN-REPRFLDYLSDLCVSNHIAIPVTQELICKCVLDPKNSDILIRTELRPV 673

Qy        643 ----------------------------VDHVSSVRPNIFVGRV-----EGSAVYRKWYF 669
                                           |  |||      |      |    | ::
Db        674 KEMAQSHEYLSIEYSEEEVWLTWTDKNNEHHEKSVRQLAQEARAGNAHDENVLSYYRYQL 733

Qy        670 E-----------VTMDHIEKT----------------------THMMPHLRIG------ 689
              :           : :| | :                           |:| |: :
Db        734 KLFARMCLDRQYLAIDEISQQLGVDLIFLCMADEMLPFDLRASFCHLMLHVHVDRDPQEL 793

Qy        690 ----------------------------------WANTTGYVPYPGGGEKWGGNGVGD 713
                                               :|||  :|      | :  | | :
Db        794 VTPVKFARLWTEIPTAITIKDYDSNLNASRDDKKNKFANTMEFV------EDYLNNVVSE 847

Qy        714 ---------------------DLYSYGFDG-------------------------AYLW 726
                                  :|  :||                          ||
Db        848 AVPFANEEKNKLTFEVVSLAHNLIYFGPYSFSELLRLTRTLLGIIDCVQGPPAMLQAYED 907

Qy        727 SGGRKT-----------------------------------PVNRTHAEEPYIRKGDVI 750
              ||:                                    |::|:  ||      |::
Db        908 PGGKNVRRSIQGVGHMMSTMVLSRKQSVFSAPSLSAGASAAEPLDRSKFEE----NEDIV 963

Qy        751 GCALDLTV-PIINFMFNGVRV--------------------------------TGSFTN 776
                | :  |: |: | ||:                                 :  |
Db        964 VMETKLKILEILQFILN-VRLDYRISYLLSVFKKEFVEVFPMQDSGADGTAPAFDSTTAN 1022

Qy        777 FNLEGM------FFPVISCSSKLSCRFLLGGEHGR-----LRYAAPEGYSPLVESLLPQQ 825
              ||: :       | |   || |     :  | ||      | :     |:|||   | |
Db       1023 MNLDRIGEQAEAMFGVGKTSSMLE----VDDEGGRMFLRVLIHLTMHDYAPLVSGAL--Q 1076

Qy        826 ILSLEPCFYFPGNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEM 885
              :|     | : |:|  |          |:  :: : : ::::|  : ::  |:
Db       1077 LL-------FKHFSQRQEAMHTFKQVQLLISAQDVENYKV-IKSELDRLRTMVEKS--EL 1126

Qy        886 WAMNK-------IEAGWMYG------DQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQT 932
              |  |       :|||          |:   ||            || ||  :     |
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Db       1127 WVDKKGSGKGEEVEAGTAKDKKERPTDEEGFLH-----------PPGEKSSE---NYQI 1171

Qy        933 LKTILALGYYISLDKPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLA 992

Db       1172 VKGILE-----RLNKMCGVGEQMRKKQQRLLKNMDAHKVMLDLLQIPY-DKGDAKMMEIL 1225

Qy        993 ENTHNLWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVY 1052

Db       1226 RYTHQF-----LQKFCAGNPGNQALLHKHLHLFLTPGLLEA----------ETMQHIFLN 1270

Qy       1053 GYMLDPPTGE---QHEALLLEASKQ--KQADF--RTYRAEKNYAVSSGKWYFEFEILTAG 1105

Db       1271 NYQLCSEISEPVLQHFVHLLATHGRHVQYLDFLHTVIKAEGKY-VKKCQDMIMTELTNAG 1329

Qy       1106 PMRVGWAHADMAPGMMLGQDENSWAFDGYNEEK--VYSGNTESFGKQWAVGDVVGVFLDL 1163

Db       1330 DDVVVFYNDKASLAHLL--DMMKAARDGVEDHSPLMY------------------HISL 1368

Qy       1164 IDKTISFSLNGELLMDALGGETTFADVQGDNFVPA-----------CTLGVGQKARLTYG 1212

Db       1369 VD----------LLAACAEGKNVYTEIKCTSLVPLEDVVSVVTHEDCITEV----KMAYV 1414

Qy       1213 QDVNTLKYFTTCGLQEGY---------EPFCVNMKRDVTHWYTKDQPIFENTDEMIDTRI 1263

Db       1415 NFVNHCYVDTEVEMKEIYTSNHIWTLFENFTLDMARVCS---KREKRVADPTLEKYVLSV 1471

Qy       1264 DVTRIPAGSDTP----------------------------PCLKISH--------NTFET 1287

Db       1472 VLDTINAFFSSPFSENSTSLQTHQPVVVQLLQSTTRLLECPWLQQQHKGSVEACIRTLAM 1531

Qy       1288 MEKANWEFLRLSLPVICHNEFIDEAE------------------------KARRWVE--- 1320

Db       1532 VAKGRAILLPMDLDAHISSMLSSGASCAAAAQRNASSYKATTRAFPRVTPTANQWDYKNI 1591

Qy       1321 IKDRQQIL------MKEAVEAQMPAHID-----------------QIMRSGFTMNDIKGL 1357

Db       1592 IEKLQDIITALEERLKPLVQAELSVLVDVLHWPELLFLEGSEAYQRCESGGFLSKLIQ-- 1649

Qy       1358 HYED---NQEELPSSKMKRLPSRPPRK------GSMTRGVTIQNYNNLQPGQVNGMHRST 1408

Db       1650 HTKDLMESEEKLCIKVLRTLQQMLVKKTKYGDRGNQLRKMLLQNY--LQ------NRKST 1701

Qy       1409 SEAEMAKYDLGAQGLTPD--------DKKDKRGRSPF-----------KFFRSKRGESSD 1449

Db       1702 SRGDLP--DPIGTGLDPDWSAIAATQCRLDKEGATKLVCDLITSTKNEKIFQESIGLAIH 1759

Qy       1450 RAKSRKSKTPDPPSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLN 1509

Db       1760 LLDGGNTEIQKSFHNLMMSDKKSER----FFKV-----LHDRMKRAQQETK---STVAVN 1807

Qy       1510 M----ATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVY 1565

Db       1808 MNDLGSQPHEDREPVDPTTKGRVASFSIPGS---------SSRYSLGPSLRRGHEVS--- 1855

Qy       1566 IGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDR----VVENVNRQSCYMVRADELYNEVM 1621

Db       1856 -------------ERVQSSEMGTSVLIMQPILRFLQLLCENHNRDLQNFLR--------- 1893

Qy       1622 AEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEIL 1681

Db       1894 ----------------------------CQNNKTNYNLVCE-------------TLQFL 1911

Qy       1682 QIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKP---HQWARVPNQSLQVH--- 1735

Db       1912 DIMCGSTTGGLGLLGLYINEDNVGLVIQTLETLTEYCQGPCHENQTCIVTHESNGIDIIT 1971

Qy       1736 ALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQ 1795

Db       1972 ALILNDI---SPLCK----------------------YRMDLVLQLKDNASKLLLAL-ME 2005

Qy       1796 SNYRAAHA--LCTHVDQKQLLYAIQSQYMS---------GPLRQGFYDLLIALHLESHAT 1844

Db       2006 SRHDSENAERILISLRPQELVDVIKKAYLQEEERENSEVSPREVGHNIYILALQLSRH-- 2063

Qy       1845 TMEACKNEFVIPLGPELKALYEEPDMG-HSLRSLQTESVRPQMKMTDIAESITE 1897

Db       2064 ------NKQLQHLLKPVKRIQEEEAEGISSMLSLNNKQLSQMLKSSAPAQEEEE 2111


RESULT 13
US-11-124-368A-215
; Sequence 215, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  James J. Devlin
;  APPLICANT:  May Luke
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Vascular Diseases, Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001524
;  CURRENT APPLICATION NUMBER: US/11/124,368A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,845
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/625,936
;  PRIOR FILING DATE: 2004-11-09
;  NUMBER OF SEQ ID NOS: 21112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 215
;   LENGTH: 2668
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-124-368A-215

  Query Match             1.3%;  Score 199;  DB 7;  Length 2668;
  Best Local Similarity   17.1%;  Pred. No. 9.6e-05;
  Matches  354;  Conservative  340;  Mismatches  780;  Indels  602;  Gaps   81;

Qy       1235 VNMKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE 1294

Db        455 INLLRREIDESVCSESDVFSNT---LDTLSEIEWNPA-------------TKLLNQENIE 497

Qy       1295 FLRLSLPVICHNEFID----EAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFT 1350

Db        498 SELNSLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTKK--DQEMQLIHE 555

Qy       1351 MNDIKGL------HYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGM 1404

Db        556 ISNLKNLVKHAEVYNQDLENEL-SSKVELLREKEDQIKKLQEYIDSQKLENIKMDLSYSL 614

Qy       1405 HRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSD 1464

Db        615 ESIEDPKQMKQTLFDAETVALDAKRES------APLRSENLELKEKMKELATTYKQMEND 668

Qy       1465 TEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTST 1524

Db        669 IQ---------------------------------LYQSQL--------EAKKKMQVD- 685

Qy       1525 LAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYI-----GWVTTQYHLHSKD 1579

Db        686 ------------LEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGKITDLQKELNKE 732

Qy       1580 FNQSKVTKSSVIITDDYDRVVENVNR---------QSCYMVRA--DELYNEVMAEATAKG 1628

Db        733 VEENEALREEVILLSELKSLPSEVERLRKEIQDKSEELHIITSEKDKLFSEVVHK---ES 789

Qy       1629 ASQGMF--IGCSVD----------TSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEA 1675

Db        790 RVQGLLEEIGKTKDDLATTQSNYKSTDQEFQNFKTLHMDFEQKYKMVLEEN-------ER 842

Qy       1676 TSKEILQI---------ELGRSATSLPLSAAVLPTSDKHV------IPQFPPRL------ 1714

Db        843 MNQEIVNLSKEAQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLENRDST 902

Qy       1715 ------------KVQ-------------CLKPHQWARVPNQSLQVHALKL-SDIRGWS 1746
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Db        903 LQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQ------ESLQIERDQLKSDI---- 952

Qy       1747 MLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRAAH---- 1802

Db        953 ---HDTVNM---NIDTQEQLRNALESLKQ------HQETINTLKSKISEEVSRNLHMEEN 1000

Qy       1803 ---------ALCTHVDQKQLLYAIQSQYMSGPLRQG--------FYDLL-----IALHLE 1840

Db       1001 TGETKDEFQQKMVGIDKKQDLEAKNTQTLTADVKDNEIIEQQRKIFSLIQEKNELQQMLE 1060

Qy       1841 SHATTMEACKN------EFVIP-------LGPELK------------ALYEEPDMGHS-- 1873

Db       1061 SVIAEKEQLKTDLKENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSRTCD 1120

Qy       1874 ---------------LRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFVMQA 1918

Db       1121 RLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIENL----------------- 1163

Qy       1919 LAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNP----ET 1974

Db       1164 ------KNELKNKE----------LTLEHMETERLELAQKLNENYEEVKSITKERKVLKE 1207

Qy       1975 WDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDL 2034

Db       1208 LQKSFETE--RDHLRGYIREIEATGLQTKEELKIAH---IHLKEHQETI----------- 1251

Qy       2035 QTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELI 2094

Db       1252 --DELRRSVSEKTAQIINTQDLEKS-------HTKLQEEIPVLHEEQELLPNVKEVSETQ 1302

Qy       2095 ARMNEFH----------DTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKEL 2144

Db       1303 ETMNELELLTEQSTTKDSTTLARIEMERLRLNEKFQESQEEIK--SLTKERDNLKTIKEA 1360

Qy       2145 -----EEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREM-------FSL 2192

Db       1361 LEVKHDQLKEHIRETLAKIQESQSKQ---EQSLNMKEKDN-ETTKIVSEMEQFKPKDSAL 1416

Qy       2193 LVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLW 2252

Db       1417 LRIEIEMLG-LSKRLQESH----DEMKSVAKEKDDLQRLQEVL-----QSESDQLKENIK 1466

Qy       2253 KLVNNH------------TFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSD-AQPSSQ 2299

Db       1467 EIVAKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQLEAINDKLQNKIQ 1526

Qy       2300 PV------------------------AEDSKEKDTSHEMVVACCRFLCYFCRTGRQN-- 2332

Db       1527 EIYEKEEQFNIKQISEVQEKVNELKQFKEHRKAKDSALQSIESKMLELTNRLQESQEEIQ 1586

Qy       2333 ------------QKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSL----------- 2369

Db       1587 IMIKEKEEMKRVQEALQIERDQLKENTKEIVAK--MKESQEKEYQFLKMTAVNETQEKMC 1644

Qy       2370 --------------------MENTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPD 2409

Db       1645 EIEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERDDLRSVEETLK----- 1699

Qy       2410 LGWDPVEGERYLDFLRFCVWVNGESVEENANL-VIRLLIRRPECLGPALRGEGEGLLKAI 2468

Db       1700 -----VERDQLKENLRETITRLIKDLEKQEELKIVHMHLKEHQETIDKLRGIVSEKTNEI 1754

Qy       2469 VDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGR 2528

Db       1755 SNMQKDLEHSNDALKAQDLKIQEELRIAH--MHLKEQQETIDKLRGIVS---EKTDKLSN 1809

Qy       2529 CAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLI 2588

Db       1810 MQKDLE----NSNAKLQEKVI-------QELKANEHQLITLKKDVNETQKKVSEMEQLKK 1858

Qy       2589 PGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIG 2648

Db       1859 QIKDQSLTLSKLEIENLNLAQKLHENLEE------MKSVMKERDNLRRVEETLKLERD-- 1910

Qy       2649 NSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALT-SAM 2707

Db       1911 ------QLKESLQETKARD--------LEIQQELKTARMLSKEHKETVDKLREKISEKTI 1956

Qy       2708 QPSMLLKLLRKLTVDV-SKLSEYTTVALRLLTL------------HYERCAKYYGSTGAG 2754

Db       1957 QISDIQKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKINEMEQLKKQF------ 2010

Qy       2755 QGAFGASSDEEKRLTM--------MLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPP 2806

Db       2011 ---------EAQNLSMQSVRMDNFQLTKKLHESLE----EIRIVAKERDELRRIKESL-- 2055

Qy       2807 DYSLSKNYDDEFYG--KEQAAGDLDNPQYDP---------QPINTSSVALNNDLNTIVQK 2855

Db       2056 -----KMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQHLTESLREKCSRIKELLKR 2110

Qy       2856 FSE---HYH-----------DAWASRKIENGWVYGEGWSDSQKTHPRLKPYNM--LNDYE 2899

Db       2111 YSEMDDHYECLNRLSLDLEKEIEFQKELSMRYVLSYVTKIKEEQHESINKFEMDFIDEVE 2170

Qy       2900 KERYKEPVRESLKALLAIGWSVEH--SEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPF 2957

Db       2171 KQ----------KELLI---KIQHLQQDCDVPSRELRDLKLNQNMDLHIEEILKD----F 2213

Qy       2958 DYNPHPVDMTN----LTLSREMQNMAERLADNAHDI 2989

Db       2214 SESEFPSIKTEFQQVLSNRKEMTQFLEEWLNTRFDI 2249


RESULT 14
US-11-124-368A-214
; Sequence 214, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  James J. Devlin
;  APPLICANT:  May Luke
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Vascular Diseases, Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001524
;  CURRENT APPLICATION NUMBER: US/11/124,368A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,845
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/625,936
;  PRIOR FILING DATE: 2004-11-09
;  NUMBER OF SEQ ID NOS: 21112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 214
;   LENGTH: 2665
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-124-368A-214

  Query Match             1.3%;  Score 198.5;  DB 7;  Length 2665;
  Best Local Similarity   16.9%;  Pred. No. 0.0001;
  Matches  369;  Conservative  359;  Mismatches  777;  Indels  675;  Gaps   86;

Qy       1235 VNMKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWE 1294

Db        455 INLLREIDESVCSESDVFSNT---LDTLSEIEWNPA-------------TKLLNQENIE 497

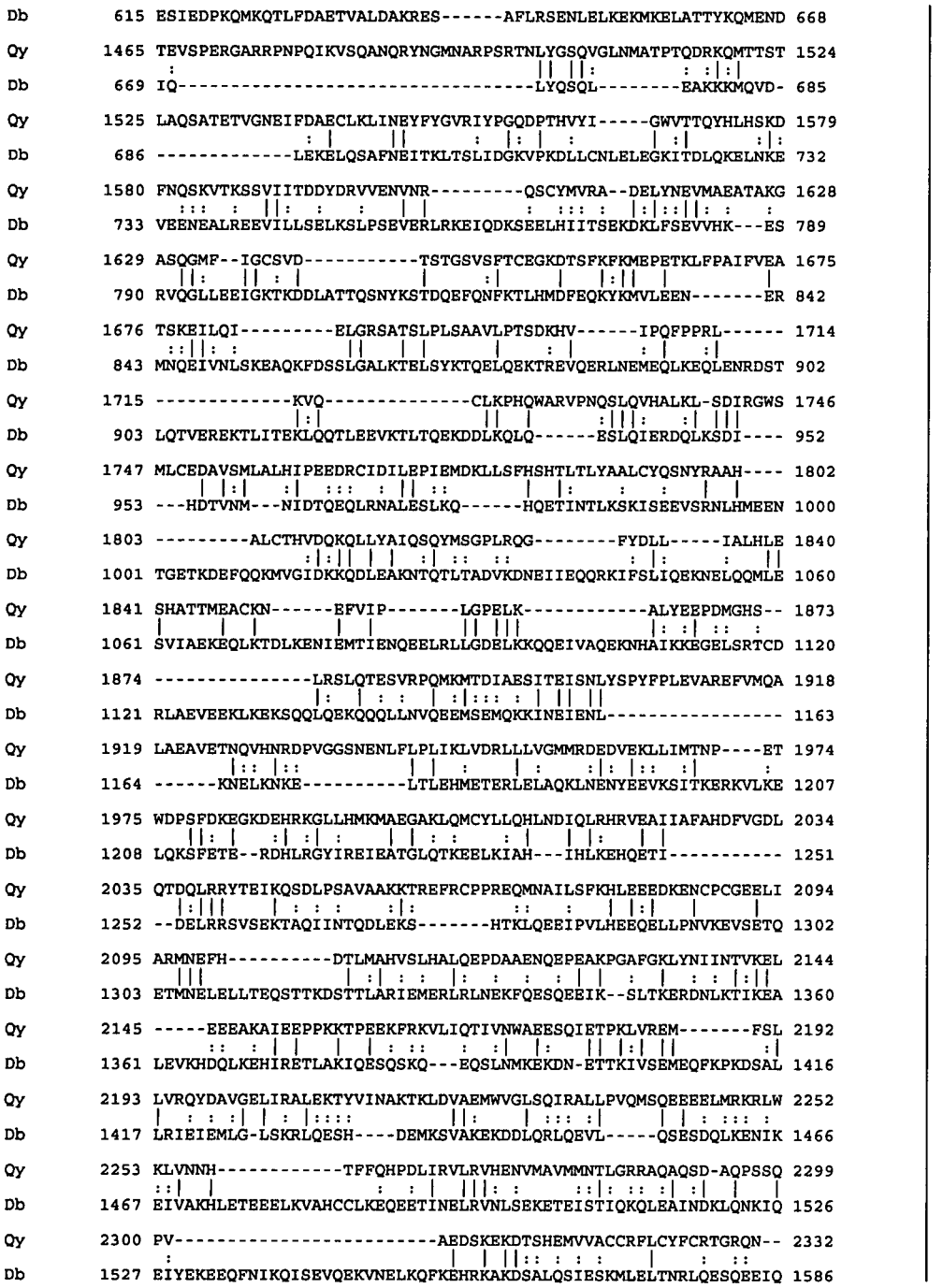
Qy       1295 FLRLSLPVICHNEFID----EAEKARRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFT 1350

Db        498 SELNSLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTKK--DQEMQLIHE 555

Qy       1351 MNDIKGL------HYEDNQEELPSSKMKRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGM 1404

Db        556 ISNLKNLVKHAEVYNQDLENEL-SSKVELLREKEDQIKKLQEYIDSQKLENIKMDLSYSL 614

Qy       1405 HRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSD 1464
```



RESULT 15
US-10-506-454-486
; Sequence 486, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G

```
;  APPLICANT:  Kozyavkin, Sergei A
;  TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
;  TITLE OF INVENTION:  Methanopyrus Kandleri AV19 and Monophyly of Archael Methanogens
;  TITLE OF INVENTION:  and Methods of Use Thereof
;  FILE REFERENCE: FID001
;  CURRENT APPLICATION NUMBER: US/10/506,454
;  CURRENT FILING DATE:  2004-08-31
;  PRIOR APPLICATION NUMBER: PCT/US03/06664
;  PRIOR FILING DATE: 2003-03-04
;  PRIOR APPLICATION NUMBER: 60/361,742
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 1722
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 486
;   LENGTH: 1249
;   TYPE: PRT
;   ORGANISM: Methanopyrus kandleri
US-10-506-454-486

  Query Match             1.2%;  Score 187.5;  DB 6;  Length 1249;
  Best Local Similarity   19.0%;  Pred. No. 0.00017;
  Matches  276;  Conservative  178;  Mismatches  455;  Indels  541;  Gaps   71;

Qy       1584 KVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTST 1643
Db         42 KITGSKTTVARVLPAKKEDVGKG---IVRMDKY------ERQNAGASVGEPV--EVDRAE 90

Qy       1644 GSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRS--------------- 1688
Db         91 EKVAKRVE--------LMPTERVVVP---VQAGLKEEVEEELTREHEQDILEQIKRYLRS 139

Qy       1689 -ATSLPLSAA---VLP------TSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALK 1738
Db        140 RAQQTPIPATHRDVIPLEVQGKTIAGHVLIKFPPDSLLVVGIEPED-ATVIGPETEI---- 194

Qy       1739 LSDIRGWSMLCEDAVSMLALHIPEE--------DRCIDILE-----PIEMDKLLSFHSHT 1785
Db        195 --EVKPYS---EDLAK--AAEIPDVTYDDIGGLDREIELIREYVELPLKRPELLK----- 242

Qy       1786 LTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATT 1845
Db        243 -----------------ELGIKPPKGVLLY--------GPPGTGKTLLAKAVANE----- 272

Qy       1846 MEACKNEFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPY 1905
Db        273 ---CGAKFYSINGPEIMSKY------------------------YGESEARIREVF--- 301

Qy       1906 FPLEVAREFV--------MQALA-EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVG 1956
Db        302 ---EEARKNAPAIIYIDEIDAIAPKRGETGEVERR---------VVAQLLTLMD-----G 344

Qy       1957 MMRDEDVEKLLIMTNPETWDPS------FDKE-----GKDEHRKGLLHMKMAEGAKLQMC 2005
Db        345 LSEDERVVVLASTNRPDDIDPALRRPGRFDKEIEIGVPDKEGRKEILQI----------- 393

Qy       2006 YLLQHLNDIQLRHRV--EAIIAFAHDFVG-DLQT------------------------D 2037
Db        394 ----HTRDMPLADDVDLDKLAELTHGFTGADLEALCKSAGLKALRRAIRKIGAKLAEKGE 449

Qy       2038 QLRRYTEIKQSDLPS----AVAAKKTREFRCPPREQMNAILSFKHLEEEDKENC------ 2087
Db        450 KEEREVAVKVSELSDEELMEVLEKGLDRARIPEEKKRALRRVLREAEEEEKEEVAYTDAL 509

Qy       2088 ----------PCGEELIARMNEFHDTLMAHVSLHALQE-----PDAAENQEPEAKPGAFG 2132
Db        510 DKVLEAEELPEIREELKVTMRDFMEAL-KEIEPSALREVIVEVPDVS------------- 555

Qy       2133 KLYNIINTVKELEEEAKAIEEPPKKTPE--EKF-----------------RKVLIQTIVN 2173
Db        556 --WDDVGGLEDVKQELKEAVEYPLKYPEVYEKLGTRPPKGILLYGPPGTGKTLLAKAVAN 613

Qy       2174 WAEES--QIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQI 2231

Db        614 ESDANFIAVRGPEVLSKW----------VGESIPGDE--------------VVWAKVDGE 649

Qy       2232 RALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQ 2291
Db        650 AKLIPIEDLYE--------LWK-----------------------------EGRDVEV- 670

Qy       2292 SDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILL 2351
Db        671 --AALTEEGVVWSSVDRVARHRRRTGLVKII---TRTGRE-VIVTEDHSVFTVRDGKI-- 722

Qy       2352 SRPSLRGSTPLDVAYSSLMENTELALALR---------------EHYLEKIAVYLSRCGL 2396
Db        723 ----------VDVPTSELSEGDWIVLPARLPAGDSDEIDGIKIDEDLAFLLGLYVAEGSL 772

Qy       2397 QSNS-------------ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVE---ENAN 2440
Db        773 TNQKDAVRIHNKDPEVIEEIDRIVREKGW---EGRYYESDHSY--WIKSRKLRQLCEKLG 827

Qy       2441 LVIR------LLIRRPECLGPALRG--EGEGLL-------KAIVDANKMSERIADR---- 2481
Db        828 TKAREKRLGPLLSLKPELLAAALRGYYTGDGSFSVKPHGRSAIIEATTVSKRLADELLVA 887

Qy       2482 --------RKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDA 2533
Db        888 LQILDIVARRYECDDTKGSTRYRVMITKSE-------------YIRTFVEKVGFAQSE- 932

Qy       2534 GVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLI--PGH 2591
Db        933 ------KNERIR-------------KFLAERKWT---------RGRSDIPTELIGSPYT 963

Qy       2592 KQSVGLFLERVY---GIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA---LSMNR 2645
Db        964 YVEVEYISDRVAADGGLMKAE-----LEHLYFDKIKEIVPLDRDDEYVYDVVEVKLGHNF 1018

Qy       2646 YIGNSIL-------------------PLLIKHAYFYNEAENYASLLDATL--HTVYRLSK 2684
Db       1019 VGGQGVLLHNSEKKIREIFQKARQTAPCVI----FFDEIDAIAPKRGTEVGGSRVTERIV 1074

Qy       2685 NRMLTKGQR-EAVSD-FLVALT--------SAMQPSMLLKLLRKLTVDVSKLSEYTTVAL 2734
Db       1075 NQLLTEMDGIEATEDVFVIAATNRPDIIDEALLRPGRFDRIVYVPPPDEEAMKEIVKIHT 1134

Qy       2735 RLLTL----------------HYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFD 2778
Db       1135 RDMPLAEDLTVDDIVEILRRREREEDAKY---TGADIEAVCMEA------AMLALREVLD 1185

Qy       2779 SLSKMDYEPE 2788
Db       1186 ELERIEKESE 1195

Search completed: April 14, 2006, 01:49:33
Job time : 55 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 14, 2006, 01:28:13 ; Search time 313 Seconds
(without alignments)
4211.298 Million cell updates/sec

Title: US-10-668-767-128_COPY_1_3000
Perfect score: 15748
Sequence: 1 MAEAEGGASEQDDVSFLRTE.....RLADNAHDIWAKKKKEELVT 3000

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	15748	100.0	5128	8	ADM68884	Adm68884 Heliothis
2	15693.5	99.7	5134	8	ADM68886	Adm68886 Heliothis
3	15655.5	99.4	5142	8	ADM68900	Adm68900 Heliothis
4	15550.5	98.7	5142	8	ADM68758	Adm68758 Heliothis
5	15475	98.3	5100	8	ADM68902	Adm68902 Heliothis
6	12738	80.9	5127	8	ADM68764	Adm68764 Peregrinu
7	12516.5	79.5	5127	8	ADM68878	Adm68878 Drosophil
8	12489.5	79.3	5113	8	ADM68877	Adm68877 Drosophil
9	12465.5	79.2	5127	8	ADM68876	Adm68876 Drosophil
10	12460.5	79.1	5109	8	ADM68766	Adm68766 Drosophil
11	12445	79.0	5104	8	ADM68762	Adm68762 Periplane
12	12384	78.6	5107	4	ABB65257	Abb65257 Drosophil
13	12354	78.4	5112	8	ADM68881	Adm68881 Drosophil
14	12338	78.3	5126	8	ADM68880	Adm68880 Drosophil
15	12338	78.3	5126	8	ADM68812	Adm68812 Drosophil
16	12327	78.3	5101	8	ADM68760	Adm68760 Myzus per
17	12311	78.2	5112	8	ADM68882	Adm68882 Drosophil
18	12295	78.1	5126	8	ADM68879	Adm68879 Drosophil
19	12178.5	77.3	4868	8	ADM68813	Adm68813 Mosquito
20	7210	45.8	5071	8	ADM68814	Adm68814 Nematode
21	6986.5	44.4	5317	8	ADM68815	Adm68815 Sea urchi
22	6828	43.4	5107	8	ADN23724	Adn23724 Bacterial
23	6778	43.0	4968	8	ADM68817	Adm68817 Rabbit ry
24	6769	43.0	4767	4	ABB11532	Abb11532 Human rya
25	6769	43.0	4967	8	ADM68818	Adm68818 Human rya
26	6758	42.9	4967	8	ADM68816	Adm68816 Mouse rya
27	6566.5	41.7	3647	7	ADJ70630	Adj70630 Human hea
28	6445.5	40.9	5035	2	AAR25450	Aar25450 MH mutant
29	6443	40.9	5038	8	ADQ18491	Adq18491 Human sof
30	6443	40.9	5038	9	ADY19486	Ady19486 PRO polyp
31	6443	40.9	5081	4	ABG04969	Abg04969 Novel hum
32	6442.5	40.9	5032	7	ADJ68220	Adj68220 Human hea
33	6440	40.9	5081	4	ABB11480	Abb11480 Human rya
34	6411.5	40.7	5072	2	AAR11510	Aar11510 Ryanodine
35	6370.5	40.5	4771	4	AAU02939	Aau02939 Angiotens
36	6356	40.4	4899	4	ABG12314	Abg12314 Novel hum
37	6356	40.4	4899	7	ADF60293	Adf60293 Human con
38	6356	40.4	4934	4	ABG23346	Abg23346 Novel hum
39	6354	40.3	4866	2	AAW77410	Aaw77410 Human rya
40	6293	40.0	4987	2	AAR10834	Aar10834 Rianodin
41	4416	28.0	2000	9	ADY15562	Ady15562 PRO polyp
42	942	6.0	374	4	AAB70482	Aab70482 Ryanodine
43	722.5	4.6	616	4	ABG23345	Abg23345 Novel hum
44	712	4.5	1232	4	ABG03701	Abg03701 Novel hum
45	698.5	4.4	599	4	ABG23343	Abg23343 Novel hum

ALIGNMENTS

RESULT 1
ADM68884
ID ADM68884 standard; protein; 5128 AA.
XX
AC ADM68884;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor protein SEQ ID NO:128.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism.
XX
OS Heliothis virescens.
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR N-PSDB; ADM68883.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 15; SEQ ID NO 128; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant

CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 5128 AA;

Query Match 100.0%; Score 15748; DB 8; Length 5128;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200

Qy       1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260

Qy       1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320

Qy       1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380

Qy       1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440

Qy       1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500

Qy       1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560

Qy       1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620

Qy       1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680

Qy       1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740

Qy       1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800
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Db       1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800

Qy       1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860

Qy       1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFVMQALA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFVMQALA 1920

Qy       1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980

Qy       1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040

Qy       2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100

Qy       2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160

Qy       2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220

Qy       2221 VAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 VAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280

Qy       2281 MNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 MNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340

Qy       2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400

Qy       2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460

Qy       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520

Qy       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580

Qy       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640

Qy       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700

Qy       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760

Qy       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820

Qy       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVYGEGWS 2880

Qy       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940

Qy       2941 KSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 KSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000
```

RESULT 2
ADM68886
ID ADM68886 standard; protein; 5134 AA.
XX
AC ADM68886;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor protein SEQ ID NO:130.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism.
XX
OS Heliothis virescens.
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR N-PSDB; ADM68885.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 15; SEQ ID NO 130; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing

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CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 5134 AA;

  Query Match             99.7%;  Score 15693.5;  DB 8;  Length 5134;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2992;  Conservative    4;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSSQDKPAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KSYETKKEGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              |||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db        661 SAVYRKWYFEVTMDHIEKTTHMIPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDDLTVPIINFMFNGVRVTGSFTNFNLE 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDDLTVPIINFMFNGVRVTGSFTNFNLE 780

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200

Qy       1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260

Qy       1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320

Qy       1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLPSRPPR 1380

Qy       1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 KGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFF 1440

Qy       1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 RSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTN 1500

Qy       1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 LYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQD 1560

Qy       1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 PTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEV 1620

Qy       1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 MAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEI 1680

Qy       1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 LQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLS 1740

Qy       1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1741 DIRGWSMLCEDAVSMLALHIPEEDRCIDILELIEMDKLLSFHSHTLTLYAALCYQSNYRA 1800

Qy       1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPE 1860

Qy       1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFVMQALA 1920
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       1861 LKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVVREFVMQALA 1920

Qy       1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 EAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPSFD 1980
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Qy       1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 KEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQLR 2040

Qy       2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 RYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMNEF 2100

Qy       2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 HDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKKTPE 2160

Qy       2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 EKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKTKLD 2220

Qy       2221 VAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 VAGMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVMAVM 2280

Qy       2281 MNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340
             ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db       2281 MNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQNQKAMFDHF 2340

Qy       2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 DFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCGLQSNS 2400

Qy       2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGPALRGE 2460

Qy       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAILNFYC 2520

Qy       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAGEERPK 2580

Qy       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 SDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGCESDMA 2640

Qy       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 LSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREAVSDFL 2700

Qy       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 VALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQGAFGA 2760

Qy       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 SSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYDDEFYG 2820

Qy       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKPSEHYHDAWASRKIENGWVYGEGWS 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 KEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKPSEHYHDAWASRKIENGWVYGEGWS 2880

Qy       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 DSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQS 2940

Qy       2941 KSGGRPPEIV-TDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELV 2999
             |||||||||| ||||||:||||||||||||||||||||||||||||||||||||||||||||
Db       2941 KSGGRPPEIVQTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELV 3000

Qy       3000 T 3000
             |
Db       3001 T 3001
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RESULT 3
ADM68900
ID   ADM68900 standard; protein; 5142 AA.
XX
AC   ADM68900;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Heliothis virescens ryanodine receptor protein SEQ ID NO:144.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism.
XX
OS   Heliothis virescens.
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
DR   N-PSDB; ADM68899.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Claim 15; SEQ ID NO 144; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 5142 AA;

  Query Match             99.4%;  Score 15655.5;  DB 8;  Length 5142;
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 2988; Conservative 5; Mismatches 7; Indels 9; Gaps 2;

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Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLNSDMYL 115
              |||||||||||||||||||||||||||     |||||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKENLGKGTGSGHRTLLYGNAILLRHLNSDMYL 120

Qy        116 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 180

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 240

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 300

Qy        296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 QNELYLVSREEATTASCAFCLRQEKGDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 360

Qy        356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 420

Qy        416 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 475
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 480

Qy        476 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 535
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        481 DLFQEEGILNLILEAIVKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 540

Qy        536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 595
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 600

Qy        596 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 655
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 660

Qy        656 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 715
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 720

Qy        716 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 775
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 780

Qy        776 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 835
              |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        781 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRHAAPEGYSPLVESLLPQQILSLEPCFYF 840

Qy        836 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 900

Qy        896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 960

Qy        956 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1015
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        961 RLPNEPFMQSNGYKPAPLDLGAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1020

Qy       1016 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1075
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1021 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1080

Qy       1076 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1140

Qy       1136 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1200

Qy       1196 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1255
              |||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db       1201 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMERDVTHWYTKDQPIFENT 1260

Qy       1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1315
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1320

Qy       1316 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1375
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1380

Qy       1376 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1435
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1440

Qy       1436 PFKPFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1500

Qy       1496 PSRTNLYGSQVGLN----MATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
              |||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||
Db       1501 PSRTNLYGSQVGLNSNAQMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1560

Qy       1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1620

Qy       1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1680

Qy       1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1740

Qy       1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
              |||||||||||||||||||||||||||||||||||:|||| ||||||||||||||||||||
Db       1741 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCMDILELIEMDKLLSFHSHTLTLYAA 1800

Qy       1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1860

Qy       1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVV 1920

Qy       1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1980

Qy       1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 PETWDPSFDKGGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2040

Qy       2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2100

Qy       2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2151
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2160
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```
Qy       2152 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2220

Qy       2212 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2280

Qy       2272 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQ 2331
             ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db       2281 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQ 2340

Qy       2332 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 NQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2400

Qy       2392 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2460

Qy       2452 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2520

Qy       2512 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2580

Qy       2572 PAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDR 2631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 PAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDR 2640

Qy       2632 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2700

Qy       2692 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2760

Qy       2752 GAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLS 2811
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 GAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLS 2820

Qy       2812 KNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2871
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 KNYDGEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2880

Qy       2872 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2940

Qy       2932 NRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 2991
             ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db       2941 NRSSMRRQSKSGGRPPEIVTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 3000

Qy       2992 KKKKEELVT 3000
             |||||||||
Db       3001 KKKKEELVT 3009
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RESULT 4
ADM68758
ID   ADM68758 standard; protein; 5142 AA.
XX
AC   ADM68758;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Heliothis virescens ryanodine receptor protein SEQ ID NO:2.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism.
XX
OS   Heliothis virescens.
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
DR   N-PSDB; ADM68757.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Claim 15; SEQ ID NO 2; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 5142 AA;

  Query Match             98.7%;  Score 15550.5;  DB 8;  Length 5142;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 2966;  Conservative   12;  Mismatches   22;  Indels    9;  Gaps    2;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGPGNRHCFLENIADKNIPPDL 60
              |||||||||||||| |||||||:|||||||||||||| ||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSILRTEDMVCMSCTATGERVCLAAEGLGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLNSDMYL 115
              |||||||||||||||||||||||||||     ||||||:|||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKENLGKGTGSGYRTLLYGNAILLRHLNSDMYL 120
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Qy       116 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
Db       121 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVAIERY 180

Qy       176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
Db       181 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 240

Qy       236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
Db       241 WTKDGGQNIVVYKGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 300

Qy       296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355
Db       301 QNELYLVSREEPTTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 360

Qy       356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415
Db       361 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDLSRSQEEESMTARVIRKCSSLFTK 420

Qy       416 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 475
Db       421 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLTNYFAQPDEDMEHEEKQNKFRALRNRQ 480

Qy       476 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 535
Db       481 DLFQEEGILNLILEAIDKINVVTSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 540

Qy       536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 595
Db       541 TNCAQFANSNRFNWLFSRLGSQASGEGTGMLDVLHCILIDSPEALNMMRDEHIKVIISLL 600

Qy       596 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 655
Db       601 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 660

Qy       656 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 715
Db       661 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 720

Qy       716 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 775
Db       721 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 780

Qy       776 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 835
Db       781 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 840

Qy       836 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895
Db       841 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 900

Qy       896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955
Db       901 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 960

Qy       956 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1015
Db       961 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVGQLAENTHNLWARERIQQGWTYGLNED 1020

Qy      1016 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1075
Db      1021 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1080

Qy      1076 QADFRTYRAEKNYAVSSGKWYFEPEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1135
Db      1081 QADFRTYRAEKNYAVSSGKWYFEPEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1140

Qy      1136 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1195
Db      1141 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1200

Qy      1196 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1255
Db      1201 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1260

Qy      1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1315
Db      1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1320

Qy      1316 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1375
Db      1321 RRWVEIKDRQRILMKEAVEAQMSAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1380

Qy      1376 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1435
Db      1381 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1440

Qy      1436 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495
Db      1441 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1500

Qy      1496 PSRTNLYGSQVGLN----MATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db      1501 PSRTNLYGSQVGLNSNAQMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1560

Qy      1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db      1561 GVRIYPGQDPTHMYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1620

Qy      1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db      1621 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1680

Qy      1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db      1681 SVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1740

Qy      1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db      1741 LQVHALKLSGIRGWXMLCEDAVSMLALHIPEEDRCIDILELIEMDKLLSFHSHTLTLYAA 1800

Qy      1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db      1801 LCYQSNYRAAHALCSHADQKQLLYAIQSQYMSGPLRQGFYDLLTALHLESHATTMEACKN 1860

Qy      1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
Db      1861 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVV 1920

Qy      1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
Db      1921 REFVMQALAEAVETNQVHNWDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1980

Qy      1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
Db      1981 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEATIAFAHDFV 2040

Qy      2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
Db      2041 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNVILSFKHLEEEDKENCPCGE 2100

Qy      2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2151
Db      2101 ELIARMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAI 2160

Qy      2152 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2211
Db      2161 EEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTY 2220

Qy      2212 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2271
Db      2221 VINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLR 2280

Qy      2272 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQ 2331
```

```
Db       2281 VHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQ 2340

Qy       2332 NQKAMFDHFDFDLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 NQKAMFDHFDFDLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYL 2400

Qy       2392 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 SRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPE 2460

Qy       2452 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2511
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDT 2520

Qy       2512 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNN 2580

Qy       2572 PAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDR 2631
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       2581 PAAGEERPKSDMPSGLIPGHKQSVGLFLGRVYGIETQELFYKLLEEAFLPDLRAATMLDR 2640

Qy       2632 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 NDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKG 2700

Qy       2692 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 QREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGST 2760

Qy       2752 GAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLS 2811
             ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:||
Db       2761 GAGQGAFGASSDEEKRLTMMLFSSIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYTLS 2820

Qy       2812 KNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2871
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 KNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIEN 2880

Qy       2872 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2931
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSN 2940

Qy       2932 NRSSMRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 2991
             |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 NRSSMGRQSKSGGRPPEIVTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWA 3000

Qy       2992 KKKKEELVT 3000
             |||||||||
Db       3001 KKKKEELVT 3009


RESULT 5
ADM68902
ID   ADM68902 standard; protein; 5100 AA.
XX
AC   ADM68902;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Heliothis virescens ryanodine receptor protein SEQ ID NO:146.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism.
XX
OS   Heliothis virescens.
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
DR   N-PSDB; ADM68901.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Claim 15; SEQ ID NO 146; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 5100 AA;

  Query Match             98.3%;  Score 15475;  DB 8;  Length 5100;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 2958;  Conservative    4;  Mismatches    5;  Indels   38;  Gaps    3;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60

Qy         61 SQCVFVIEQALSVRALQELVTAAGSET-----GKGTGSGHRTLLYGNAILLRHLNSDMYL 115
              |||||||||||||||||||||||||||     |||||||||||||||||||||||||||||
Db         61 SQCVFVIEQALSVRALQELVTAAGSETGKENLGKGTGSGHRTLLYGNAILLRHLNSDMYL 120

Qy        116 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACLSTSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERY 180

Qy        176 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LHTTKENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPST 240

Qy        236 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WTKDGGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVND 300
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Qy       296 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 355
Db       301 QNELYLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETG 360

Qy       356 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 415
Db       361 LWLSYKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTK 420

Qy       416 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 475
Db       421 FINGLETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQ 480

Qy       476 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 535
Db       481 DLFQEEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNH 540

Qy       536 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 595
Db       541 TNCAQFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLL 600

Qy       596 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 655
Db       601 EKHGRDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFV 660

Qy       656 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 715
Db       661 GRVEGSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDL 720

Qy       716 YSYGFDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 775
Db       721 YSYGLDGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFT 780

Qy       776 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 835
Db       781 NFNLEGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYF 840

Qy       836 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 895
Db       841 GNLSKRALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGW 900

Qy       896 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 955
Db       901 MYGDQREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNV 960

Qy       956 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1015
Db       961 RLPNEPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNED 1020

Qy      1016 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1075
Db      1021 SDMHRSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQK 1080

Qy      1076 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1135
Db      1081 QADFRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYN 1140

Qy      1136 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1195
Db      1141 EEKVYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNF 1200

Qy      1196 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1255
Db      1201 VPACTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENT 1260

Qy      1256 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1315
Db      1261 DEMIDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKA 1320

Qy      1316 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1375
Db      1321 RRWVEIKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLHYEDNQEELPSSKMKRLP 1380

Qy      1376 SRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1435
Db      1381 SRPPRKGSMTR-----------GQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRS 1428

Qy      1436 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNAR 1495
Db      1429 PFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQSNAQ------- 1481

Qy      1496 PSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRI 1555
Db      1482 -------------MATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRI 1527

Qy      1556 YPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADE 1615
Db      1528 YPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIIIDDYDRVVENVNRQSCYMVRADE 1587

Qy      1616 LYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEA 1675
Db      1588 LYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEA 1647

Qy      1676 TSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVH 1735
Db      1648 TSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVH 1707

Qy      1736 ALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQ 1795
Db      1708 ALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILELIEMDKLLSFHSHTLTLYAALCYQ 1767

Qy      1796 SNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVI 1855
Db      1768 SNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVI 1827

Qy      1856 PLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVAREFV 1915
Db      1828 PLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVVREFV 1887

Qy      1916 MQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW 1975
Db      1888 MQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETW 1947

Qy      1976 DPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQ 2035
Db      1948 DPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQ 2007

Qy      2036 TDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIA 2095
Db      2008 TDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIA 2067

Qy      2096 RMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPP 2155
Db      2068 RMNEFHDTLMAHVSLHALQEPDAAENQEPEAKPGAFGKLYNIINTVKELEEEAKAIEEPP 2127

Qy      2156 KKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINA 2215
Db      2128 KKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINA 2187

Qy      2216 KTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHEN 2275
Db      2188 KTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHEN 2247

Qy      2276 VMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2335
Db      2248 VMAVMMNTLGRRAQAQSDAQPSSQPVAEDNKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2307

Qy      2336 MFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2395
Db      2308 MFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2367

Qy      2396 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2455
Db      2368 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2427

Qy      2456 ALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAI 2515
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Db       2428 ALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDVNFSHPLPESDEDEDYIDTGAAI 2487

Qy       2516 LNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAG 2575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2488 LNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNPAAG 2547

Qy       2576 EERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGC 2635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2548 EERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRNDGC 2607

Qy       2636 ESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREA 2695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2608 ESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQREA 2667

Qy       2696 VSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQ 2755
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2668 VSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTGAGQ 2727

Qy       2756 GAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYD 2815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2728 GAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSKNYD 2787

Qy       2816 DEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVY 2875
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2788 DEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENGWVY 2847

Qy       2876 GEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSS 2935
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2848 GEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNNRSS 2907

Qy       2936 MRRQSKSGGRPPEIVTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKK 2995
             ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db       2908 MRRQSKSGGRPPEIVTDSATPFNYNPHPVDMTNLTLSREMQNMAERLADNAHDIWAKKKK 2967

Qy       2996 EELVT 3000
             |||||
Db       2968 EELVT 2972
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RESULT 6
ADM68764
ID   ADM68764 standard; protein; 5127 AA.
XX
AC   ADM68764;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Peregrinus maidis ryanodine receptor protein SEQ ID NO:8.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism.
XX
OS   Unidentified.
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
DR   N-PSDB; ADM68763.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Claim 15; SEQ ID NO 8; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 5127 AA;
```

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  Query Match             80.9%;  Score 12738;  DB 8;  Length 5127;
  Best Local Similarity   80.5%;  Pred. No. 0;
  Matches 2446;  Conservative  236;  Mismatches  278;  Indels   78;  Gaps   24;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||::||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADSEGG-SEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              | |||||||||||||||||||||| |||||||||||||||||| |||||||| ||
Db         60 STCVFVIEQALSVRALQELVTAAGSEEGKGTGSGHRTLLYGNAILLRHQNSDMYLACSST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:||||||:||||||||||:||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

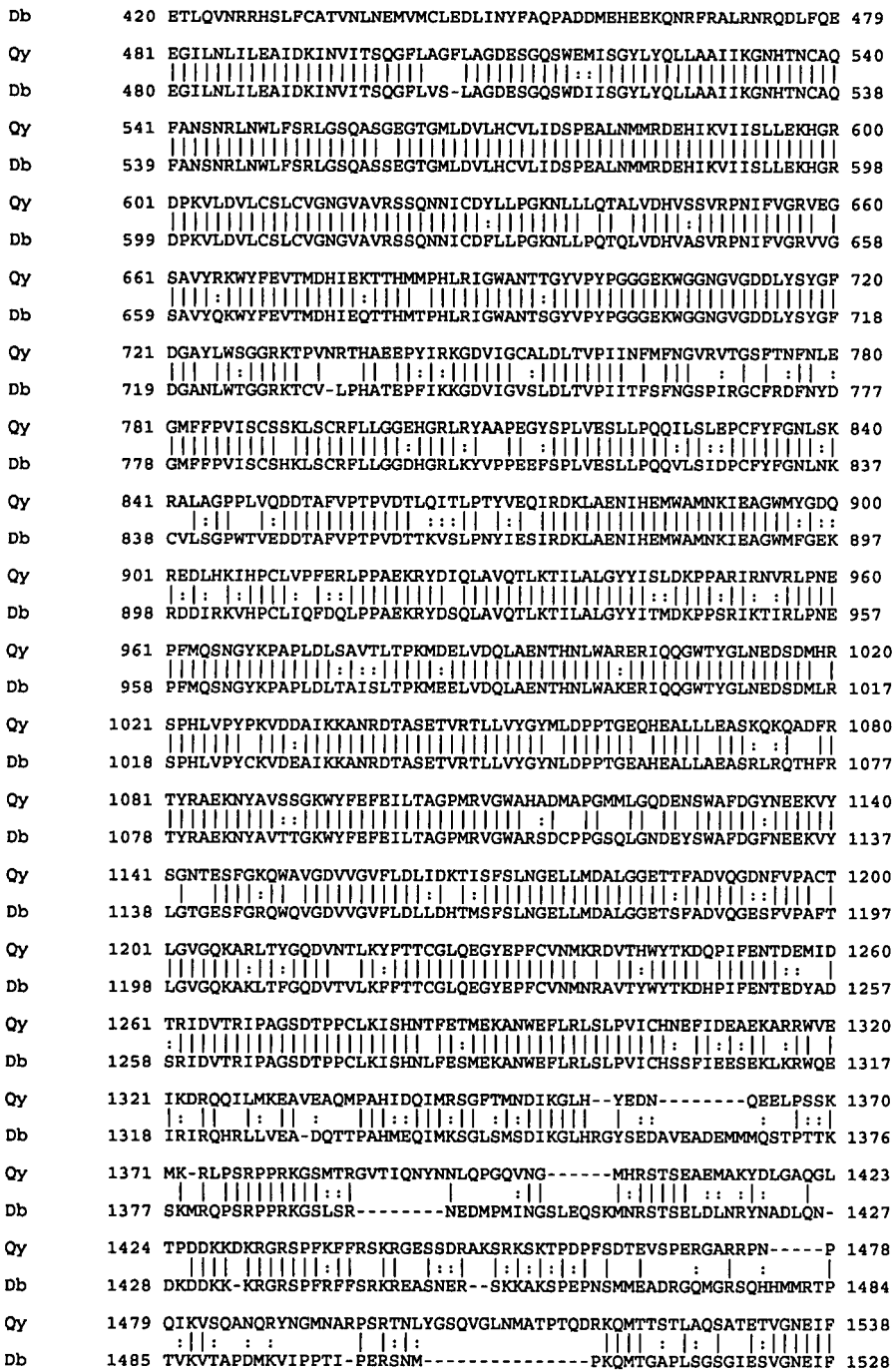
Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||::||||||||||||||||||||||||||||||||||||||||||||||||||||||::
Db        180 ENDLSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWSEAP 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||: |||:
Db        240 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHLTTGRYLGVNENNELH 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              |: |:|||||  |||||||||||| ||||||||||||||||||:||||||||||:|
Db        300 LIVRDEATTALSAFCLRQEKDDQKVVLEDKDLEVIGAPIIKYGDSTVLVQHSETGLWLTY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              ||||||||||||||||:||||||||||||||||||||||||||||||:|  ||
Db        360 KSYETKKKGVGKVEEKQAVLHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTQFXRGL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| ||||:| |:||| |||||||||||||||| :|||||||||:||||||||||||||
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Db 420 ETLQVNRRHSLFCATVNLNEMVMCLEDLINYFAQPADDMEHEEKQNRFRALRNRQDLFQE 479
Qy 481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db 480 EGILNLILEAIDKINVITSQGFLVS-LAGDESGQSWDIISGYLYQLLAAIIKGNHTNCAQ 538
Qy 541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db 539 FANSNRLNWLFSRLGSQASSEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598
Qy 601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db 599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLPQTQLVDHVASVRPNIFVGRVVG 658
Qy 661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db 659 SAVYQKWYFEVTMDHIEQTTHMTPHLRIGWANTSGYVPYPGGGEKWGGNGVGDDLYSYGF 718
Qy 721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db 719 DGANLWTGGRKTCV-LPHATEPFIKKGDVIGVSLDLTVPIITFSFNGSPIRGCFRDFNYD 777
Qy 781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db 778 GMFFPVISCSHKLSCRFLLGGDHGRLKYVPPEEFSPLVESLLPQQVLSIDPCFYFGNLNK 837
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 838 CVLSGPWTVEDDTAFVPTPVDTTKVSLPNYIESIRDKLAENIHEMWAMNKIEAGWMFGEK 897
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 898 RDDIRKVHPCLIQFDQLPPAEKRYDSQLAVQTLKTILALGYYITMDKPPSRIKTIRLPNE 957
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db 958 PFMQSNGYKPAPLDLTAISLTPKMEELVDQLAENTHNLWAKERIQQGWTYGLNEDSDMLR 1017
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1018 SPHLVPYCKVDEAIKKANRDTASETVRTLLVYGYNLDPPTGEAHEALLAEASRLRQTHFR 1077
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1078 TYRAEKNYAVTTGKWYFEFEILTAGPMRVGWARSDCPPGSQLGNDEYSWAFDGFNEEKVY 1137
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPACT 1200
Db 1138 LGTGESFGRQWQVGDVVGVFLDLLDHTMSFSLNGELLMDALGGETSFADVQGESFVPAFT 1197
Qy 1201 LGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMID 1260
Db 1198 LGVGQKAKLTFGQDVTVLKFFTTCGLQEGYEPFCVNMNRAVTYWYTKDHPIFENTEDYAD 1257
Qy 1261 TRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVE 1320
Db 1258 SRIDVTRIPAGSDTPPCLKISHNLFESMEKANWEFLRLSLPVICHSSFIEESEKLKRWQE 1317
Qy 1321 IKDRQQILMKEAVEAQMPAHIDQIMRSGFTMNDIKGLH--YEDN--------QEELPSSK 1370
Db 1318 IRIRQHRLLVEA-DQTTPAHMEQIMKSGLSMSDIKGLHRGYSEDAVEADEMMMQSTPTTK 1376
Qy 1371 MK-RLPSRPPRKGSMTRGVTIQNYNNLQPGQVNG------MHRSTSEAEMAKYDLGAQGL 1423
Db 1377 SKMRQPSRPPRKGSLSR--------NEDMPMINGSLEQSKMNRSTSELDLNRYNADLQN- 1427
Qy 1424 TPDDKKDKRGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPN-----P 1478
Db 1428 DKDDKK-KRGRSPFRFFSRKREASNER--SKKAKSPEPNSMMEADRGQMGRSQHHMMRTP 1484
Qy 1479 QIKVSQANQRYNGMNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIF 1538
Db 1485 TVKVTAPDMKVIPPTI-PERSNM----------PKQMTGAPLSGSGIESVGNEIF 1528
Qy 1539 DAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDR 1598
Db 1529 DGECLKLINEYFYGVRIFPGQDPTHVYVGWVTTQYHFFANEFNQSKVRKVTVHTLDEFSR 1588
Qy 1599 VVENVNRQSCYMVRADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFK 1658
Db 1589 VNESVDRQSCYMVRSDELFNEVTNDSSGKGASQGMFIGCFVDAATGYISFTCEGKETSHK 1648
Qy 1659 FKMEPETKLFPAIFVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQC 1718
Db 1649 FKMEPETKLFPAIFVEATSKEILQIELGRTSTTLPLSAAVLQNSERHVNPQFPPRLKVQC 1708
Qy 1719 LKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKL 1778
Db 1709 LKPHQWARVPNVSLQVHALKLSDIRGWSMLCEDPMSMLALHIPEEDRSIDILELIEMEKL 1768
Qy 1779 LSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALH 1838
Db 1769 LSFHAHTLTLYAALCFQSNYRAAHTLCSHVDEKQLLYAIRSDYMSGPLRQGFYDLLIALH 1828
Qy 1839 LESHATTMEACKNEFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIA------ 1892
Db 1829 LESHAYTMEVCKNEFIIPIGQELKDVYEDPEMCHSLRSLKTESVLPTMKMTDKADEPSPS 1888
Qy 1893 ESITEISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRL 1952
Db 1889 EVVDNIRSLYSPQFPLDVVRDFVMAALDEAVQINQLHNRDPVGGSNENYFLPLLKLVDRL 1948
Qy 1953 LLVGMMRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLN 2012
Db 1949 LLVGMLRDGDVMKLLIMFSPETWDTAFEKDGKDEHRKGLLTMKMAEGAKLQMCYLLHHLY 2008
Qy 2013 DIQLRHRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNA 2072
Db 2009 DIQLRHRVEAIISFSVDFVGDLQSDQLRRYIEIKQSDLPSAIAAKKTREFRCPPREQMNA 2068
Qy 2073 ILSFKHLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAE-NQEPEAKPGAF 2131
Db 2069 ILGFKNLEEGDIENCPCGDELRERLNSFHEKLMHKVSLLALQEPSEEEASAEEVKKPNAL 2128
Qy 2132 GKLYNIINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFS 2191
Db 2129 NRLYNFINAVKELEETPQIEEEPEKKTPEEIFRKVLISTIVKWAEETQIESPKLVREMFS 2188
Qy 2192 LLVRQYDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRL 2251
Db 2189 LLVRQYDTVGELIRALGKTYVINSKTKDDAALMWVGLSQIRALLPVQMSQEEEGLMRERL 2248
Qy 2252 WKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAEDSKEKDTS 2311
Db 2249 WKLVNNHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAPQAGQEGEPVAKEKDTS 2308
Qy 2312 HEMVVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLME 2371
Db 2309 HEMVVACCRFLCYFCRTSRQNQKAMFDHFAFLLENSNILLSRPSLRGSTPLDVAYSSLME 2368
Qy 2372 NTELALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVN 2431
Db 2369 NTELALALREHYLEKIAIYLSRCGLQSNSELIEKGYPDLGWDPVEGERYLDFLRFCVWVN 2428
Qy 2432 GESVEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEG 2491
Db 2429 GESVEENANLVIRLLIRRPGCLGPALRGEGEGLLRAIVDANKMSERIADRRKVMD-EPEG 2487
Qy 2492 D---VNFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARA 2548
Db 2488 TTMVMHFEHPLPESDDDEDYIDTGAAILAFYCTLVDLLGRCAPDSSVIAQGKNESLRARA 2547
Qy 2549 ILRSLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQ 2608
Db 2548 ILRSLVPLEDLQGVLSLKFTLQNPAAGEERPKSDMPSGLIPGHKQSVVLFLERVYGIETQ 2607

```
Qy       2609 ELFYKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENY 2668
             |||::|||||||||||||||||||||| |||||:|||||||||||||| |: |||||:||
Db       2608 ELFFRLLEEAFLPDLRAATMLDRNDGSESDMALAMNRYIGNSILPLLITHSKFYNEADNY 2667

Qy       2669 ASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSE 2728
             |||||||||||||||||||||||||||||||||||:||||||||||||||||||||:|
Db       2668 ASLLDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSSMQPSMLLKLLRKLTVDVSKLTE 2727

Qy       2729 YTTVALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPE 2788
             |||||||||||:|||||||||| ||| :|:||||||||||||||||||||||:||
Db       2728 YTTVALRLLTLHYDRCAKYYGSTG-GQGLYGSSSDEEKRLTMMLFSNIFDSLSKMDYDPE 2786

Qy       2789 LFGKALPCLIAIGCALPPDYSLSKNYDDEFYG-KEQAAGDLDNPQYDPQPINTSSVALNN 2847
             |||||||| |||||||||||||||||| ||  ::  ||  | | |:|||||| || |||
Db       2787 LFGKALPCLTAIGCALPPDYSLSKNYDDELYGARDSQAGPSDGP-YNPQPINTHSVVLNN 2845

Qy       2848 DLNTIVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDY-----EKER 2902
             |||||||||||||||||||:|||| ||: ||||||||||||||||||     |:||
Db       2846 DLNTIVQKFSEHYHDAWASRKLENGWTYGDQWSDSQKTHPRLKPYNMLNDYVEPSIERER 2905

Qy       2903 YKEPVRESLKALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEIVTDSATPFDYNPH 2962
             ||||||||:||||||||:|||| |:|  :| |:|||||     |  : ||:|||:|:|:
Db       2906 YKEPVRESIKALLAIGWTVEHSEADVPLTSRGSIRRQSK-----PNAMVDSSTPFNYHPN 2960

Qy       2963 PVDMTNLTLSREMQNMAERLADNAHDIWAKKKKEELVT 3000
             |:|||||| |||||||||||:|||||||||||||:|
Db       2961 PIDMTNLTLGREMQNMAERLAENAHDIWAKKKKEELIT 2998
```

RESULT 7
ADM68878

```
ID   ADM68878 standard; protein; 5127 AA.
XX
AC   ADM68878;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Drosophila melanogaster ryanodine receptor protein SEQ ID NO:122.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism.
XX
OS   Drosophila melanogaster.
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Disclosure; SEQ ID NO 122; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 5127 AA;
```

Query Match 79.5%; Score 12516.5; DB 8; Length 5127;
Best Local Similarity 78.8%; Pred. No. 0;
Matches 2387; Conservative 263; Mismatches 312; Indels 67; Gaps 21;

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Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||| |||||||||||||| |||||||||||||||||||||||||||||:||||
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:||||||:||||||||||:||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||||| |||||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |||||||||:|:|||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

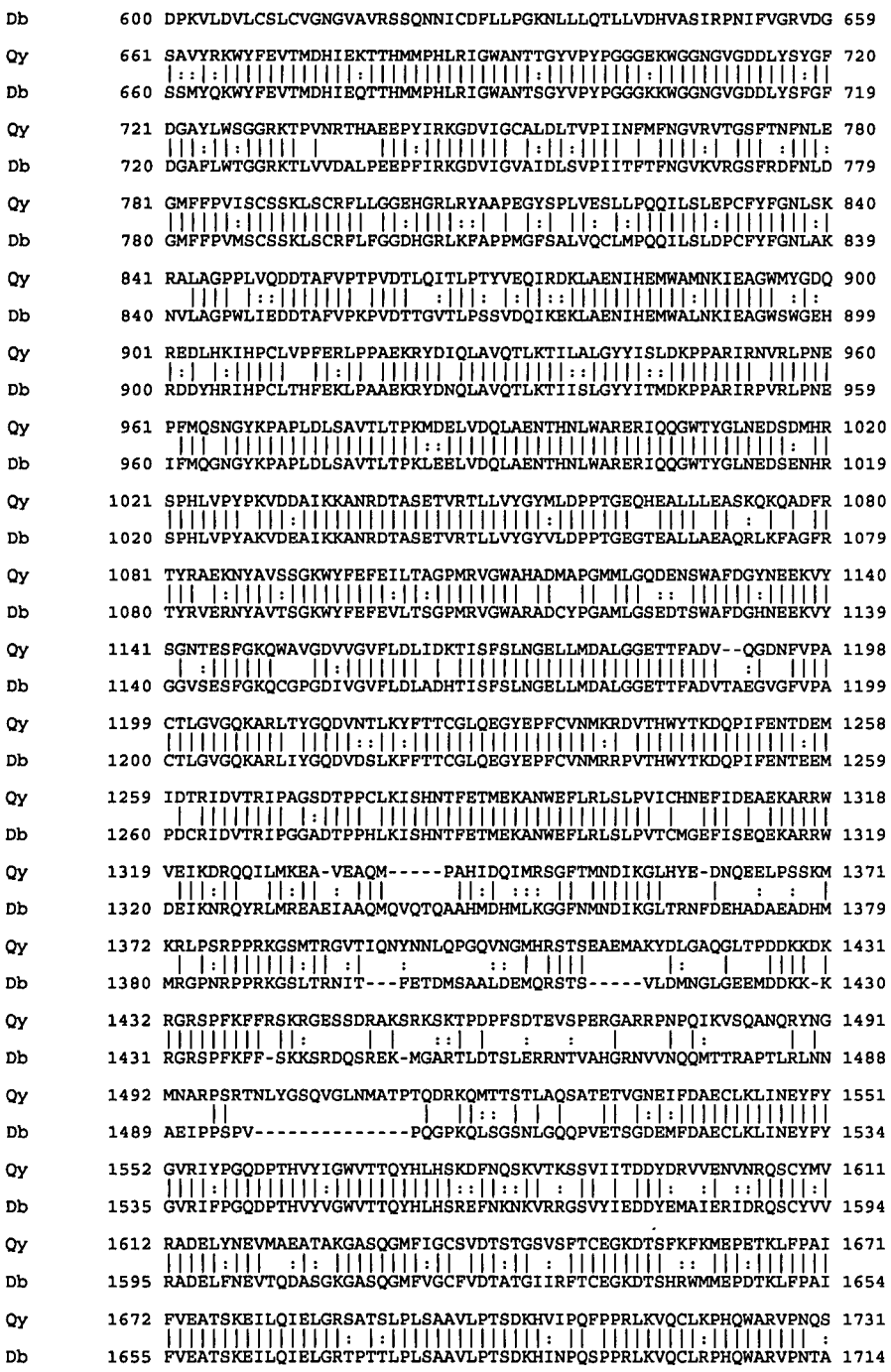
Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||||||||||||||| ||||||||||:|||||||||:||  |
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| |||||:||  ||| ||||||||||||:||::|||||||:||||||||||||
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||:|||||||||:|||||||| |||||:||||::|| ||||||||||||||||||||||
Db        480 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              |||||||||||||||||| ||:|||||||||||||||||||||||||||||||||||||
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              |||||||||||||||||||||||||:|||||||||| |||||:|:|||||||||:|
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Db 600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659
Qy 661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db 660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719
Qy 721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db 720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779
Qy 781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db 780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db 960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNEEKVY 1139
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db 1140 GGVSESFGKQCGPGDIVGVFLDLADHTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1199
Qy 1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db 1200 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1259
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db 1260 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1319
Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1431 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1488
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1489 AEIPPSPV--------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1534
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
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Db 1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
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Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
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Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDI----------AESITE 1897
Db 1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPD 1894
Qy 1898 ISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957
Db 1895 IDQLYSPKFPLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1954
Qy 1958 MRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017
Db 1955 LTDEDVQRLLVMIDPETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLR 2014
Qy 2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db 2015 HRVESIIAFSHDFVGDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFK 2074
Qy 2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYN 2136
Db 2075 NLEPDDQDNCTCGLELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYN 2134
Qy 2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196
Db 2135 FINTVKELEEGPKEVEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQ 2194
Qy 2197 YDAVGELIRALEKTYVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2256
Db 2195 YDTVGELVRALEKTYVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2254
Qy 2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEM 2314
Db 2255 NATFFQHPDLIRILRVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEM 2313
Qy 2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374
Db 2314 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTE 2373
Qy 2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434
Db 2374 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2433
Qy 2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493
Db 2434 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2492
Qy 2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551
Db 2493 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILR 2552
Qy 2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611
Db 2553 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2612
Qy 2612 YKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASL 2671
Db 2613 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2672
Qy 2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731
Db 2673 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2732
Qy 2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791
Db 2733 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2791

```
Qy       2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851
             ||||||||||||||||||||||| |:::||::  |    | ||| | ||:|::| |:||||:
Db       2792 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2849

Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911
              :|||||||||||||||::| || ||:  ||: : ||||||||||::||:|||::|||| |
Db       2850 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2909

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969
              | ||||||:||||||::  |:| | |||||     |:|    :  :||:||||||||:||
Db       2910 KGLLAIGWTVEHSEVEVALNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2964

Qy       2970 TLSREMQNMAERLADNAHDIWAKKKKEEL 2998
              |||||||||||||:|:|||||||| |||
Db       2965 TLSREMQNMAERLAENSHDIWAKKKNEEL 2993
```

RESULT 8
ADM68877
ID ADM68877 standard; protein; 5113 AA.
XX
AC ADM68877;
XX
DT 17-JUN-2004 (first entry)
XX
DE Drosophila melanogaster ryanodine receptor protein SEQ ID NO:121.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism.
XX
OS Drosophila melanogaster.
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Disclosure; SEQ ID NO 121; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 5113 AA;

Query Match 79.3%; Score 12489.5; DB 8; Length 5113;
Best Local Similarity 78.8%; Pred. No. 0;
Matches 2376; Conservative 271; Mismatches 315; Indels 53; Gaps 20;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||| |||||||||||||||| ||||||||||||||||||||||||||||||:||||
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:||||||:||||||||:|||||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||||| ||||||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |||||||||:|:|||||||||:||||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||||||||||||| |||||||||:|||||||||||:|| |
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| ||||:||  ||| |||||||||||:||::|||||||:|||||||||||||
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||:|||||||||:|||||||| |||||:||||::|| |||||||||||||||||||||||
Db        480 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539

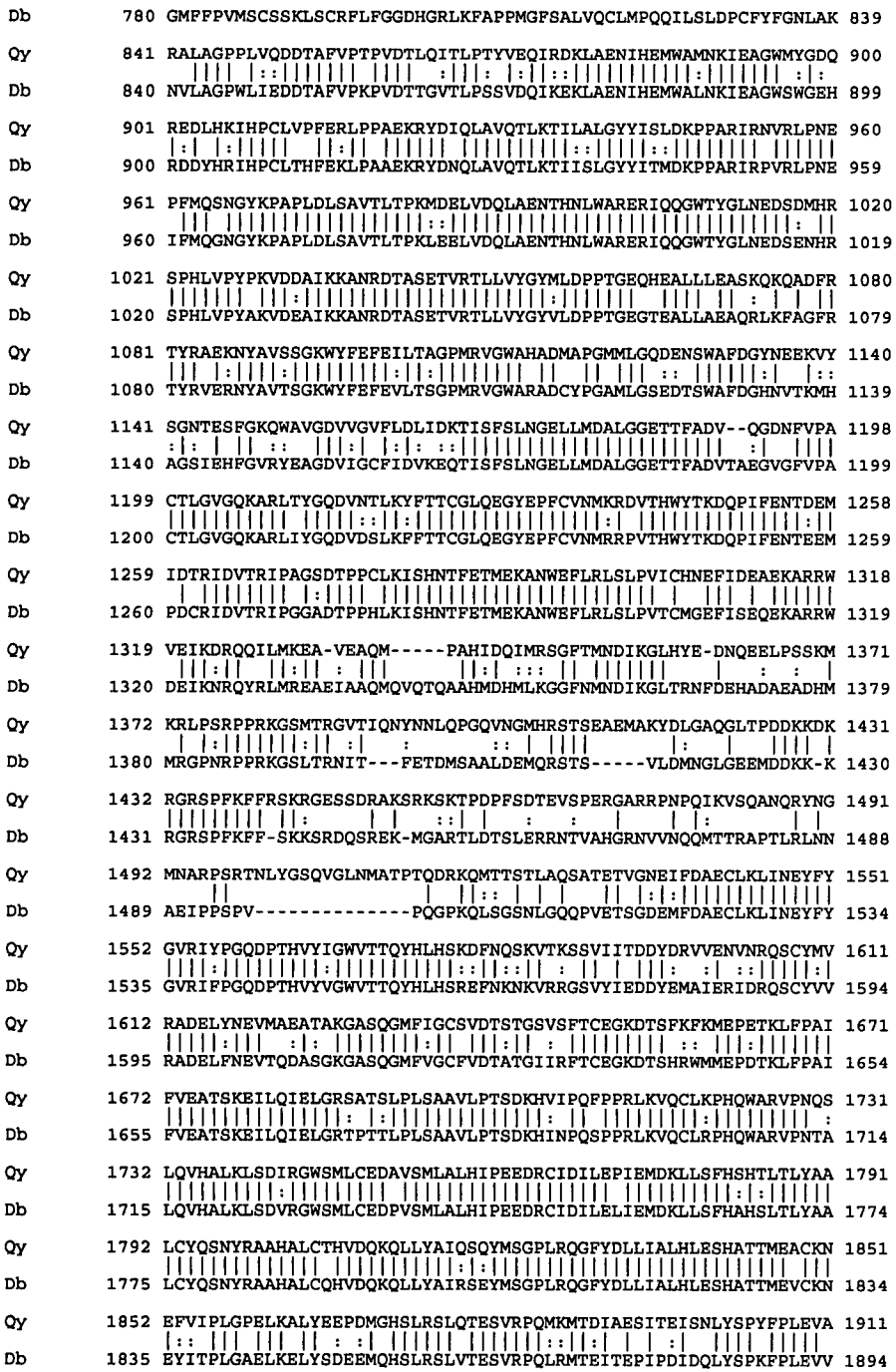
Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              |||||||||||||||||| ||:|||||||||||||||||||||||||||||||||||||
Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              |||||||||||||||||||||||:|||||||||| ||||:|:|||||||:|
Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              |::|:|||||||||||:|||||||||||:|||||||||:|||||||||||||||||:||
Db        660 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 719

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              |||:||:||||| |      |||:|||||||  |:||:|||| | ||||:| ||| :|||:
Db        720 DGAFLWTGGRKTLVVDALPEEPPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||:|||||||||| ||:||||::| | |:| ||: |:|||||||:|||||||:|
```


Db 780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db 960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
Db 1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079
Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMH 1139
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db 1140 AGSIEHFGVRYEAGDVIGCFIDVKEQTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1199
Qy 1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db 1200 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1259
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db 1260 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1319
Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1320 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1379
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1380 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1430
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1431 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1488
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1489 AEIPPSPV--------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1534
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1535 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1594
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1595 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1654
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1655 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1714
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
Db 1715 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1774
Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
Db 1775 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1834
Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
Db 1835 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITEPIPDIDQLYSPKFPLEVV 1894
Qy 1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
Db 1895 RQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGVLTDEDVQRLLVMID 1954
Qy 1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
Db 1955 PETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLRHRVESIIAFSHDFV 2014
Qy 2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
Db 2015 GDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFKNLEPDDQDNCTCGL 2074
Qy 2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYNIIINTVKELEEEAKA 2150
Db 2075 ELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYNFINTVKELEEGPKE 2134
Qy 2151 IEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKT 2210
Db 2135 VEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQYDTVGELVRALEKT 2194
Qy 2211 YVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVL 2270
Db 2195 YVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNATFFQHPDLIRIL 2254
Qy 2271 RVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEMVVACCRFLCYFCRT 2328
Db 2255 RVHENVMAVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRT 2313
Qy 2329 GRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2388
Db 2314 GRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2373
Qy 2389 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIR 2448
Db 2374 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGESVEENANLVIRLLIR 2433
Qy 2449 RPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDED 2505
Db 2434 RPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEED 2492
Qy 2506 EDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL 2565
Db 2493 EDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILRSLVPLEDLQGVLSL 2552
Qy 2566 RFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRA 2625
Db 2553 KFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRT 2612
Qy 2626 ATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKN 2685
Db 2613 ATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASLLDATLHTVYRLSKN 2672
Qy 2686 RMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745
Db 2673 RMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHFDRCA 2732
Qy 2746 KYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALP 2805
Db 2733 KYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALP 2791
Qy 2806 PDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWA 2865
Db 2792 PDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWA 2849
Qy 2866 SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE 2925
Db 2850 SRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSE 2909
Qy 2926 VDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNLTLSREMQNMAERLA 2983
Db 2910 VEVALNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNLTLSREMQNMAERLA 2964

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Qy       2984 DNAHDIWAKKKKEEL 2998
              :|:|||||||| |||
Db       2965 ENSHDIWAKKKNEEL 2979


RESULT 9
ADM68876
ID   ADM68876 standard; protein; 5127 AA.
XX
AC   ADM68876;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Drosophila melanogaster ryanodine receptor protein SEQ ID NO:120.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism.
XX
OS   Drosophila melanogaster.
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Disclosure; SEQ ID NO 120; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 5127 AA;

  Query Match             79.2%;  Score 12465.5;  DB 8;  Length 5127;
  Best Local Similarity   78.4%;  Pred. No. 0;
  Matches 2375;  Conservative  272;  Mismatches  315;  Indels   67;  Gaps   21;

Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||| |||||||||||||||| |||||||||||||||||||||||||||||:||||
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:|||||:|||||||||:||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||| ||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |||||||||:|:|||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||||||||||||| ||||||||||:|||||||||||:||  |
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
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Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||:|||||||||||:|||||||| |||||:||||::|| |||||||||||||||||||||
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Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
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Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              |||||||||||||||||||||||||:|||||||||| ||||:|:|||||||||:|
Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              |::|:|||||||||||:|||||||||||||:|||||||:|||||||||||||||||:||
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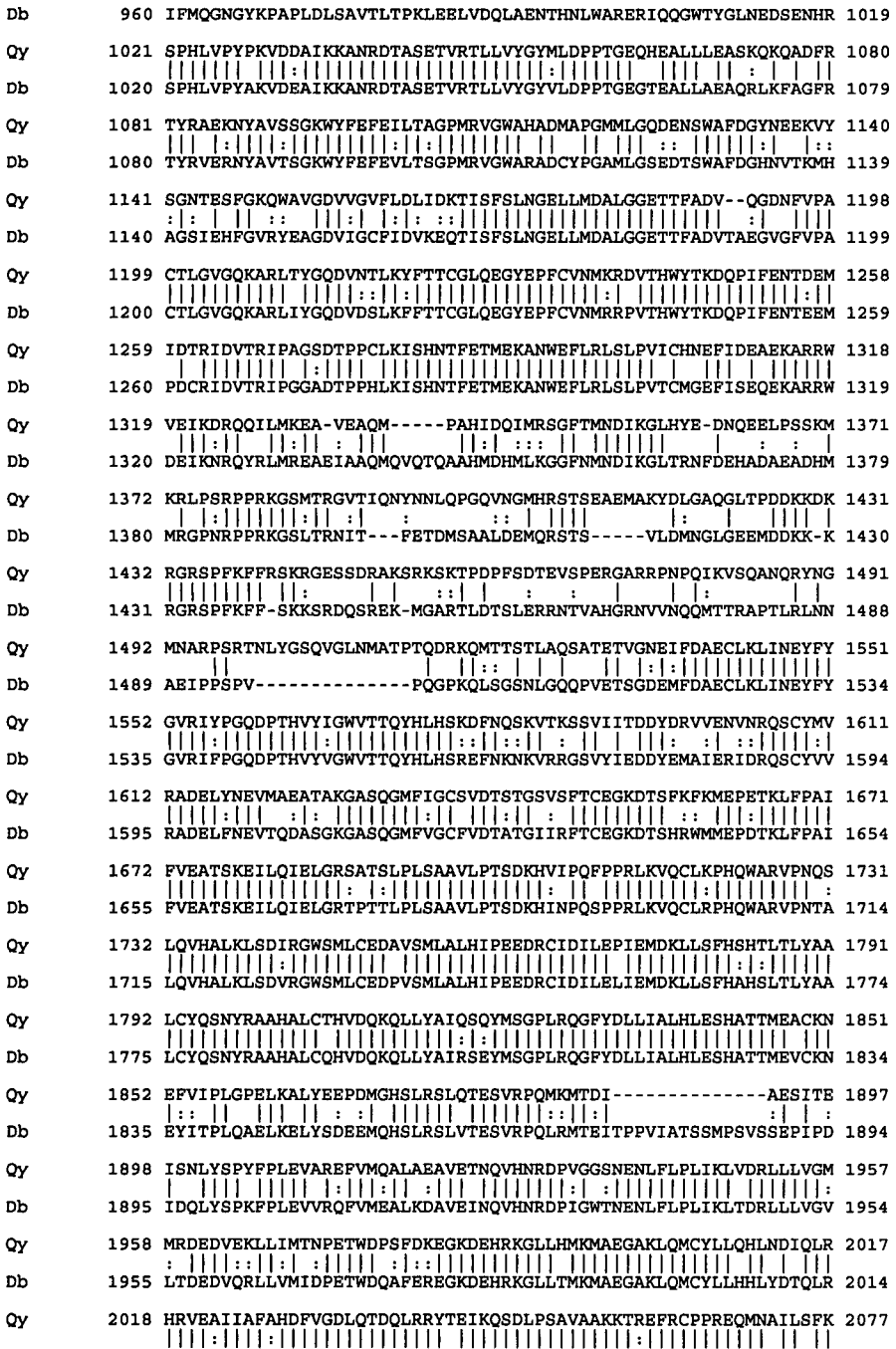
Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              |||:||:||||| |     |||:|||||||| |:||:|||| | ||||:| ||| :|||:
Db        720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779

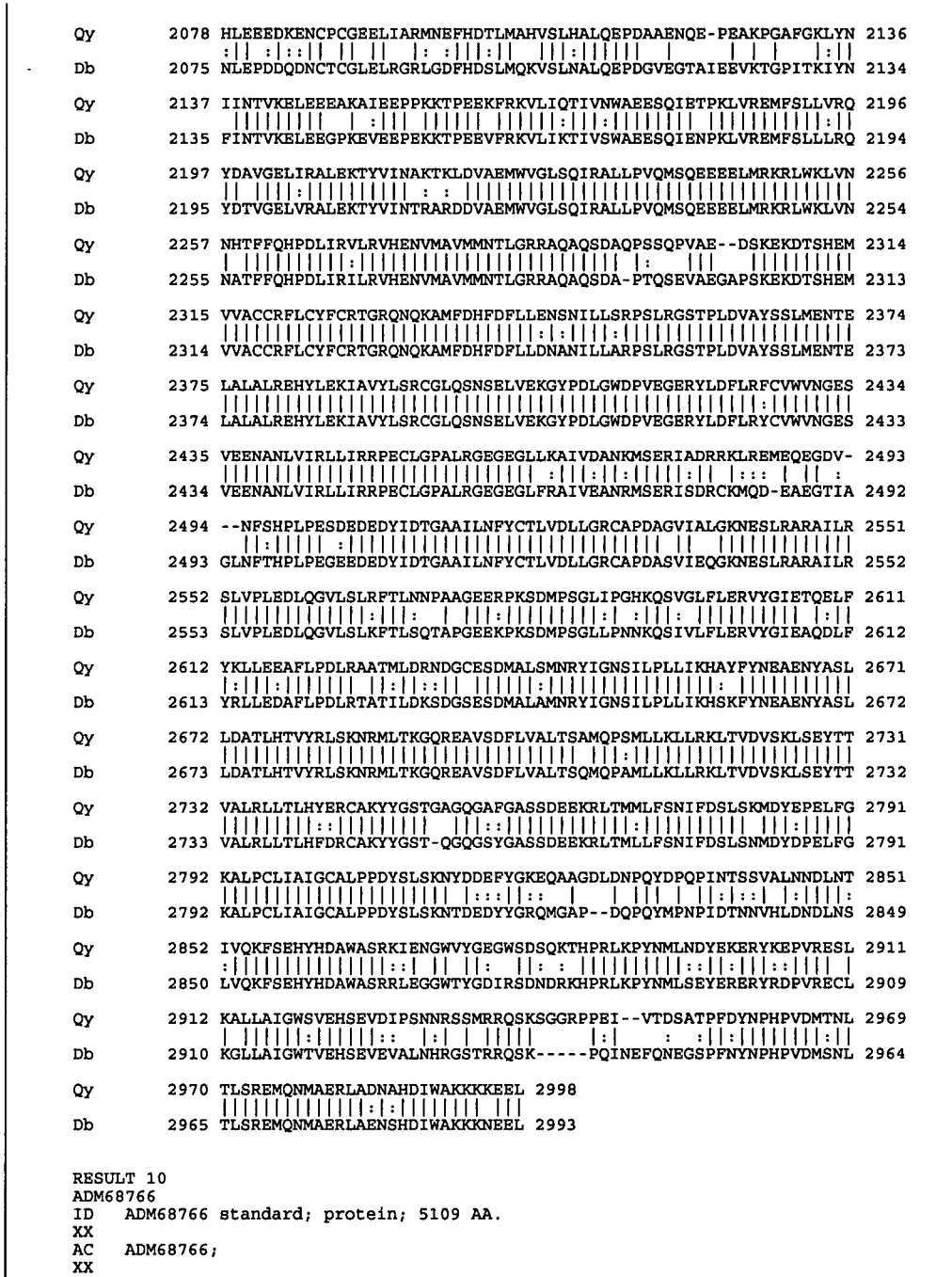
Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||:|||||||||| ||:||||::| | |:| ||: |:|||||||:||||||:|
Db        780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              |||| |::|||||||| ||||  :|||: |:||::||||||||||:|||||| :|:
Db        840 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 899

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              |:| |:|||||  ||:|| |||||| ||||||||::|||||::|||||||| ||||||
Db        900 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 959

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
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RESULT 10
ADM68766
ID ADM68766 standard; protein; 5109 AA.
XX
AC ADM68766;
XX
DT 17-JUN-2004 (first entry)

XX
DE Drosophila melanogaster ryanodine receptor protein SEQ ID NO:10.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism.
XX
OS Drosophila melanogaster.
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR N-PSDB; ADM68765.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 15; SEQ ID NO 10; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 5109 AA;

Query Match 79.1%; Score 12460.5; DB 8; Length 5109;
Best Local Similarity 78.7%; Pred. No. 0;
Matches 2371; Conservative 273; Mismatches 316; Indels 53; Gaps 20;

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Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:|||||:||||||||||:||||||||||||||| || ||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDGLIPVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||||||||||||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |||||||||:|:||||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFCLRQEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 359

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||||||||||||| ||||||||||:|||||||||||:||   |
Db        360 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 419

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| |||||:|| ||| |||||||||||:||::|||||||||:||||||||||||
Db        420 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 479

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||:|||||||||:|:|||||||| |||||:||||::|| |||||||||||||||||||
Db        480 EGVLNLILEAIDKVNIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 539

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
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Db        540 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVVISLLEKHGR 599

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
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Db        600 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 659

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              |::|:|||||||||||:|||||||||||:|||||||:|:|||||||||||||||||:||
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Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              |||:||:||||| |     |||:|||||||:||:|||| | ||||:| ||| :|||:
Db        720 DGAFLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 779

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
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Db        780 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 839

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              |||| |::||||||| |||| :|||: |:||::|||||||||:|||||| :|:
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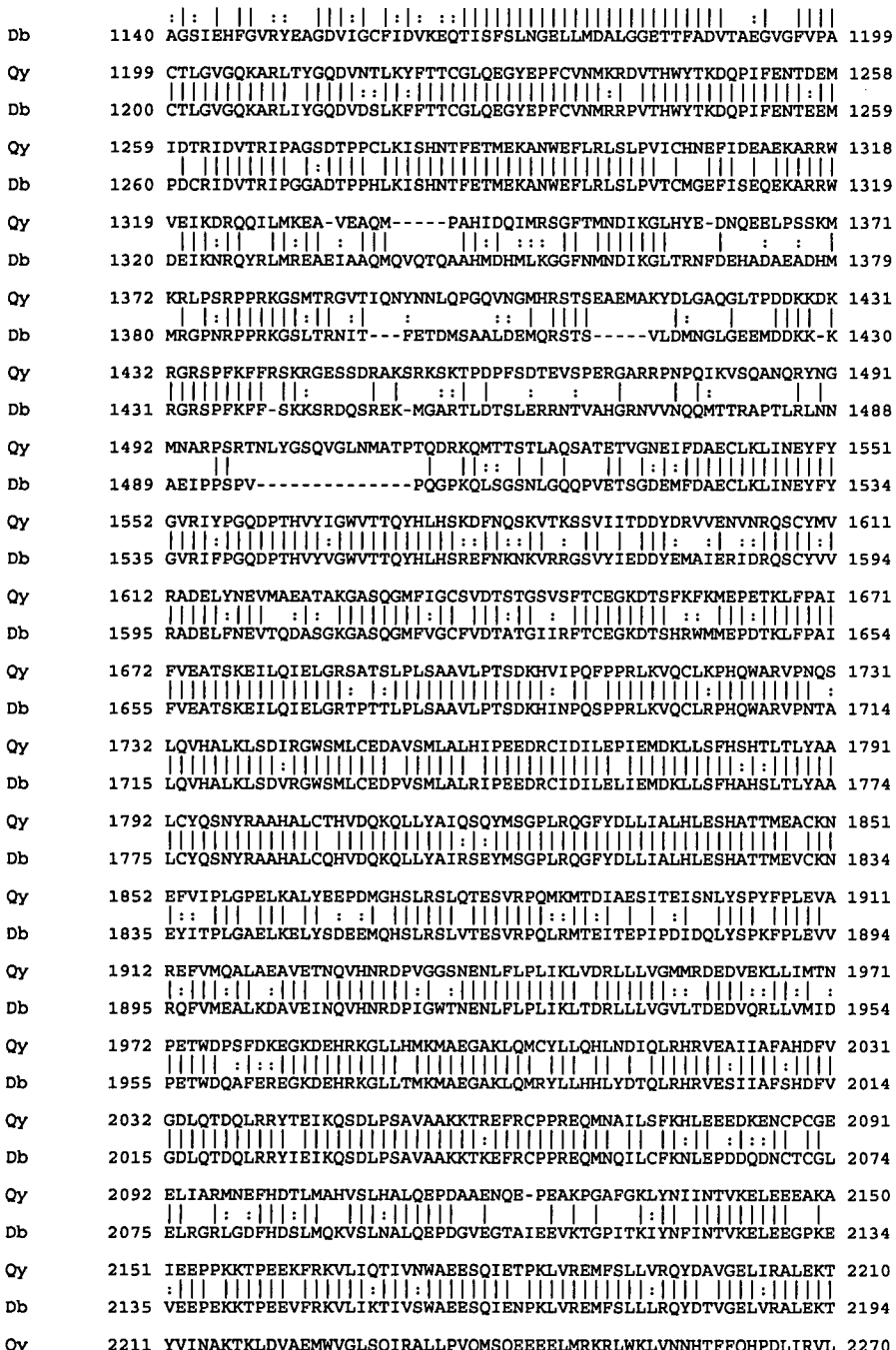
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Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              ||| |||||||||||||::|||||||||||||||||||||||||||||||: ||
Db        960 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1019

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||| |||:|||||||||||||||||||:||||||| |||| || : | | ||
Db       1020 SPHLVPYAKVDEAIKKANRDTASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFR 1079

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
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Db       1080 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMH 1139

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
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RESULT 11
ADM68762
ID ADM68762 standard; protein; 5104 AA.
XX
AC ADM68762;
XX
DT 17-JUN-2004 (first entry)
XX
DE Periplaneta americana ryanodine receptor protein SEQ ID NO:6.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism.
XX
OS Periplaneta americana.
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.

XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR N-PSDB; ADM68761.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 15; SEQ ID NO 6; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 5104 AA;

Query Match 79.0%; Score 12445; DB 8; Length 5104;
Best Local Similarity 78.3%; Pred. No. 0;
Matches 2383; Conservative 266; Mismatches 294; Indels 100; Gaps 32;

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              ||::| |:||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db          1 MADSE-GSSEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCYLENIADKNIPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGK-GTGSGHRTLLYGNAILLRHLNSDMYLACLS 119
              |||||||||||||||||||||  |: || ||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTATSSQEGKGGTGSGHRTLLYGNAILLRHQNSDMYLACLS 119

Qy        120 TSSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTT 179
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Db        120 TSSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTA 179

Qy        180 KENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKD 239
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Db        180 KENELSVVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWSNV 239

Qy        240 GGQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNEL 299
              |||||:||||||||||||||||||||||||||||||||||||:|||||||||: |||
Db        240 SGQNIVIYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHLTTGRYLGVNENNEL 299

Qy        300 YLVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLS 359
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Db        300 HLVCREEATTASSTFFLRQEKDDQKIILEDKDLEVIGAPIIKYGDSTVLVQHSDTGLWLT 359

Qy        360 YKSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFING 419
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||:||:|
Db        360 YKSYETKKKGVGKVEEKQAVLHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTQFISG 419

Qy        420 LETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQ 479
              || || ||| |:| : ||| |||||||||||||||:||||||||||:||||||||||||
Db        420 LENLQSNRRSSLFCSFVNLNEMVMCLEDLINYFAQPEEDMEHEEKQNRFRALRNRQDLFQ 479

Qy        480 EEGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCA 539
              |||||||||||||:|:|||||||:   ||||||||||:|||||||||||||||||||||
Db        480 EEGILNLILEAIDKVNIITSQGFMVS-LAGDESGQSWDVISGYLYQLLAAIIKGNHTNCA 538

Qy        540 QFANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHG 599
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Qy        600 RDPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVE 659
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Db        599 RDPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASVRPNIFVGHVS 658

Qy        660 GSAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYG 719
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Qy        780 EGMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLS 839
              :|||||||||||: |||||||:||||::  |: :||| |||||||||:::|||||||||
Db        778 DGMFFPVISCSSKVGCRFLLGGDHGRLKFTPPDEFSPLFESLLPQQILTIDPCFYFGNLS 837

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Qy        900 QREDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPN 959
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Db        898 KRNDTRKYHPCLIQFDKLPPAEKRYDSQLAVQTLKTVIALGYHISIDNPPSRIKTVRLPN 957

Qy        960 EPFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMH 1019
              |||||||||||||||: |: ||:||:|||||||||||:|||||||||||||:  |
Db        958 EPFMQSNGYKPAPLDLSAINLSGKMEELIDQLAENTHNLWAKERIQQGWTYGLNEELQML 1017

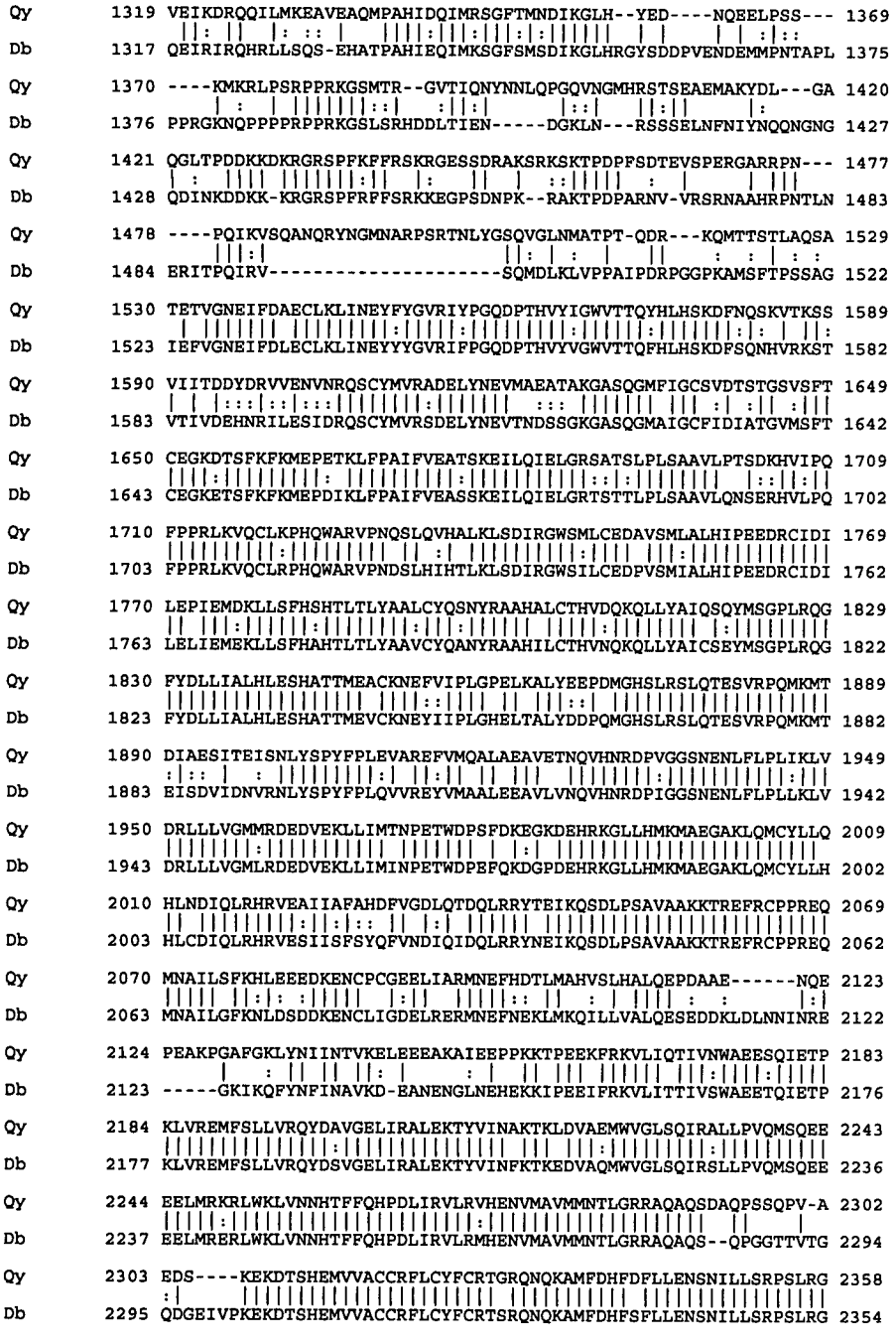
Qy       1020 RSPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEA-LLLEASKQKQAD 1078
              |||||||| |||||||||||||||||||||||||||| ||||||| :|| || : :  :
Db       1018 RSPHLVPYSKVDDAIKKANRDTASETVRTLLVYGYNLDPPTGETNEATLLTDENTNRYLT 1077

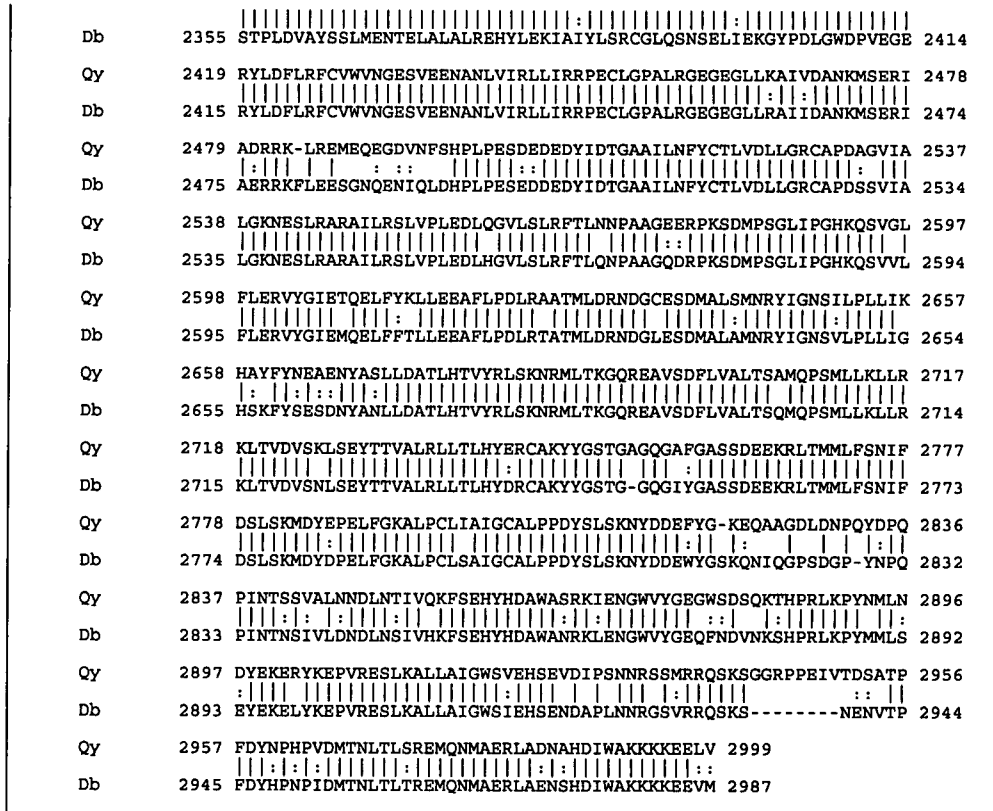
Qy       1079 FRTYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEK 1138
              |||||||| |||:|||||||||||| ||||||||     :||  :| ||||||||||||||
Db       1078 FRTYRAEKTYAVASGKWYFEFEILTNGPMRVGWARFTCSPGYQIGSDENSWAFDGYNEEK 1137

Qy       1139 VYSGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADVQGDNFVPA 1198
              :| |  ||||:|| |||||||||||:| |||||||||||||| ||||||::|||: ||||
Db       1138 IYMGTAESFGRQWQVGDVVGVFLDLMDHTISFSLNGELLMDTLGGETTFSEVQGEGFVPA 1197

Qy       1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
              |||:||||:||:|||||:|||||||||||||||||||| ||:||||||||||||:
Db       1198 FTLGLGQKAKLTFGQDVNSLKYFTTCGLQEGYEPFCVNMKRPVTYWYTKDQPIFENTDD- 1256

Qy       1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
                : |||||||||||||||||||||||||:|||||||||||||   |||| || |||
Db       1257 FSSVIDVTRIPAGSDTPPCLKISHNTFETMERANWEFLRLSLPVICLPNFIDEQEKQRRW 1316
```





RESULT 12
ABB65257
ID ABB65257 standard; protein; 5107 AA.
XX
AC ABB65257;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 22563.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.

DR N-PSDB; ABL09360.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 22563; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 5107 AA;

Query Match 78.6%; Score 12384; DB 4; Length 5107;
Best Local Similarity 78.3%; Pred. No. 0;
Matches 2356; Conservative 272; Mismatches 314; Indels 66; Gaps 20;

```
Qy         22 MVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDLSQCVFVIEQALSVRALQELVT 81
              ||                                  :                        
Db          1 MVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDLSQCVFVIEQALSVRALQELVT 60

Qy         82 AAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLSTSSSQDKLAFDVGLQQHSQGEA 141
                                  |||||||||||||| |||:||||||:||||||        
Db         61 AAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLSTSSSNDKLSFDVGLQEHSQGEA 120

Qy        142 CWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTKENEVSIVNASFHVTHWSVQPY 201
              ||||:|||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 CWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTKENEQSIVNASFHVTHWSVQPY 180

Qy        202 GTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDGGQNIVVYEGGSVMSQARSLWR 261
              |||||||||||||||||||||||||||||||||||||| :: |||||:|||| ||:|||||||
Db        181 GTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREAGQNIVIYEGGVVMAQARSLWR 240

Qy        262 LELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELYLVSREEATTASCAFCLRQEKD 321
              |||||||| |||||||||||||||||||||| ||| || :|||: |:  ||||||||
Db        241 LELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELILVKKEEASIATTTFCLRQEKD 300

Qy        322 DQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSYKSYETKKKGVGKVEEKQAILH 381
              |:|:|||||||||||:|||||||:|||||| || ||||||||||||||||||||||||||||
Db        301 DEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSYKSYETKKKGVGKVEEKQAILH 360

Qy        382 EEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGLETLQENRRHSMFFASVNLGEM 441
              ||||||| |||||||||:|||||||||||||:||  ||||| |||||:||  ||| ||
Db        361 EEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITALETLQSNRRHSIFFQKVNLNEM 420

Qy        442 VMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQEEGILNLILEAIDKINVITSQG 501
              ||||||||||:||::|||||||||:|||||||||||||||:||||||||||:|||||
Db        421 VMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQEEGVLNLILEAIDKINIITSQG 480

Qy        502 FLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASGE 561
              ||| ||||||:||||::|| ||||||||||||||||||||||||||||||||||||| |
Db        481 FLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQFANSNRLNWLFSRLGSQASSE 540

Qy        562 GTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRS 621
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGRDPKVLDVLCSLCVGNGVAVRS 600

Qy        622 SQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEGSAVYRKWYFEVTMDHIEKTTH 681
              |||||||:|||||||||| |||||:|:|||||||||:||::|:|||||||||||:|||
Db        601 SQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDGSSMYQKWYFEVTMDHIEQTTH 660

Qy        682 MMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGFDGAYLWSGGRKTPVNRTHAEE 741
              ||||||||||:|||||||:|||||||||||||||:|||||:|:|||||  |      ||
Db        661 MMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGFDGAFLWTGGRKTLVVDALPEE 720

Qy        742 PYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLEGMFFPVISCSSKLSCRFLLGG 801
              |:|||||||| |:||:|||| | ||||:| ||| :|||:||||||:|||||||||| ||
Db        721 PFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLDGMFFPVMSCSSKLSCRFLFGG 780

Qy        802 EHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSKRALAGPPLVQDDTAFVPTPVD 861
              :||||::| | |:| ||: |:|||||||:||||||||:|  |||| |::|||||| |||
Db        781 DHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAKNVLAGPWLIEDDTAFVPKPVD 840

Qy        862 TLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQREDLHKIHPCLVPFERLPPAE 921
              |  :|||: |:||::|||||||||||:|||||| :|: |:| |:|||||  ||:|| ||
Db        841 TTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEHRDDYHRIHPCLTHFEKLPAAE 900

Qy        922 KRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNEPFMQSNGYKPAPLDLSAVTLT 981
              |||| ||||||||||::|||||::|||||||| |||||| ||| ||||||||||||||||
Db        901 KRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNEIFMQGNGYKPAPLDLSAVTLT 960

Qy        982 PKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHRSPHLVPYPKVDDAIKKANRDT 1041
              ||::|||||||||||||||||||||||||||||||||||||: |||||||| |||:|||||||
Db        961 PKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHRSPHLVPYAKVDEAIKKANRDT 1020

Qy       1042 ASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFRTYRAEKNYAVSSGKWYFEFEI 1101
              ||||||||||||:|||||||  |||| || : | | |||||  |:||||:|||||||||:
Db       1021 ASETVRTLLVYGYVLDPPTGEGTEALLAEAQRLKFAGFRTYRVERNYAVTSGKWYFEFEV 1080

Qy       1102 LTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVYSGNTESFGKQWAVGDVVGVFL 1161
              ||:|||||||  ||  || ||| :: ||||||:|  |:::|: | || ::  |||:| |:
Db       1081 LTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNVTKMHAGSIEHFGVRYEAGDVIGCFI 1140

Qy       1162 DLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPACTLGVGQKARLTYGQDVNTLK 1219
              |: ::|||||||||||||||||||||||| :|  |||||||||||||| |||||::||
Db       1141 DVKEQTISFSLNGELLMDALGGETTFADVTAEGVGFVPACTLGVGQKARLIYGQDVDSLK 1200

Qy       1220 YFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEMIDTRIDVTRIPAGSDTPPCLK 1279
              :|||||||||||||||:| ||||||||||||||:|| | |||||||| |:|||| ||
Db       1201 FFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEMPDCRIDVTRIPGGADTPPHLK 1260

Qy       1280 ISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRWVEIKDRQQILMKEA-VEAQM- 1337
              |||||||||||||||||||||| |  ||| | |||||| |||:||  ||:|| : |||
Db       1261 ISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRWDEIKNRQYRLMREAEIAAQMQ 1320

Qy       1338 ----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKMKRLPSRPPRKGSMTRGVTIQN 1392
                  ||:| ::: || |||||||     |   :  :  | | |:||||||:|| :|
Db       1321 VQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHMMRGPNRPPRKGSLTRNIT--- 1377

Qy       1393 YNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDKRGRSPFKFFRSKRGESSDRAK 1452
              :      :: | ||||       |:   |   |||| |||||||||| ||:     | |
Db       1378 FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-KRGRSPFKFF-SKKSRDQSREK 1430

Qy       1453 SRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNGMNARPSRTNLYGSQVGLNMAT 1512
                ::| |   :   :   |    | |:        | |     ||
Db       1431 -MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNNAEIPPSPV------------- 1476

Qy       1513 PTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFYGVRIYPGQDPTHVYIGWVTTQ 1572
              |  ||:: | | |   || |:|:|||||||||||||||||:|||||||:||||||
Db       1477 -PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFYGVRIFPGQDPTHVYVGWVTTQ 1535

Qy       1573 YHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMVRADELYNEVMAEATAKGASQG 1632
              |||||::||::|| : || | |||:  :| ::|||||:||||||:|||  :|: ||||||
Db       1536 YHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVVRADELFNEVTQDASGKGASQG 1595

Qy       1633 MFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAIFVEATSKEILQIELGRSATSL 1692
              ||:|| |||:|| : |||||||| :: |||:|||||||||||||||||||||||||: |:|
Db       1596 MFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAIFVEATSKEILQIELGRTPTTL 1655

Qy       1693 PLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQSLQVHALKLSDIRGWSMLCEDA 1752
              |||||||||||: || |||||||:|||||||| :|||||||||:|||||||||
Db       1656 PLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTALQVHALKLSDVRGWSMLCEDP 1715

Qy       1753 VSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAALCYQSNYRAAHALCTHVDQKQ 1812
              |||||||||||||||||| ||||||||||:|:|||||||||||||||||||| ||||||
Db       1716 VSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAALCYQSNYRAAHALCQHVDQKQ 1775

Qy       1813 LLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKNEFVIPLGPELKALYEEPDMGH 1872
```

```
Db       1776 LLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKNEYITPLGAELKELYSDEEMQH 1835

Qy       1873 SLRSLQTESVRPQMKMTDI----------AESITEISNLYSPYFPLEVAREFVMQA 1918

Db       1836 SLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPDIDQLYSPKFPLEVVRQFVMEA 1895

Qy       1919 LAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTNPETWDPS 1978

Db       1896 LKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGVLTDEDVQRLLVMIDPETWDQA 1955

Qy       1979 FDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFVGDLQTDQ 2038

Db       1956 FEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLRHRVESIIAFSHDFVGDLQTDQ 2015

Qy       2039 LRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGEELIARMN 2098

Db       2016 LRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFKNLEPDDQDNCTCGLELRGRLG 2075

Qy       2099 EFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYNIINTVKELEEEAKAIEEPPKK 2157

Db       2076 DFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYNFINTVKELEEGPKEVEEPEKK 2135

Qy       2158 TPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKTYVINAKT 2217

Db       2136 TPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQYDTVGELVRALEKTYVINTRA 2195

Qy       2218 KLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVLRVHENVM 2277

Db       2196 RDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNATFFQHPDLIRILRVHENVM 2255

Qy       2278 AVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2335

Db       2256 AVMMNTLGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRTGRQNQKA 2314

Qy       2336 MFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2395

Db       2315 MFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIAVYLSRCG 2374

Qy       2396 LQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIRRPECLGP 2455

Db       2375 LQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGESVEENANLVIRLLIRRPECLGP 2434

Qy       2456 ALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDEDEDYIDTG 2512

Db       2435 ALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEEDEDYIDTG 2493

Qy       2513 AAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSLRFTLNNP 2572

Db       2494 AAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARAILRSLVPLEDLQGVLSLKFTLSQT 2553

Qy       2573 AAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRAATMLDRN 2632

Db       2554 APGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRTATILDKS 2613

Qy       2633 DGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKNRMLTKGQ 2692

Db       2614 DGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASLLDATLHTVYRLSKNRMLTKGQ 2673

Qy       2693 REAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCAKYYGSTG 2752

Db       2674 REAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHFDRCAKYYGST- 2732

Qy       2753 AGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALPPDYSLSK 2812

Db       2733 QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALPPDYSLSK 2792

Qy       2813 NYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWASRKIENG 2872

Db       2793 NTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWASRRLEGG 2850

Qy       2873 WVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSEVDIPSNN 2932

Db       2851 WTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSEVEVALNH 2910

Qy       2933 RSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNLTLSREMQNMAERLADNAHDIW 2990

Db       2911 RGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNLTLSREMQNMAERLAENSHDIW 2965

Qy       2991 AKKKKEEL 2998

Db       2966 AKKKNEEL 2973
```

RESULT 13
ADM68881
ID ADM68881 standard; protein; 5112 AA.
XX
AC ADM68881;
XX
DT 17-JUN-2004 (first entry)
XX
DE Drosophila melanogaster ryanodine receptor protein SEQ ID NO:125.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism.
XX
OS Drosophila melanogaster.
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Disclosure; SEQ ID NO 125; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid

CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 5112 AA;

Query Match 78.4%; Score 12354; DB 8; Length 5112;
Best Local Similarity 78.2%; Pred. No. 0;
Matches 2359; Conservative 265; Mismatches 337; Indels 54; Gaps 21;

```
Qy          1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
              ||||||| ||||||||||||||| |||||||||||||||||||||||||||||:||||
Db          1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59

Qy         61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119

Qy        121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
              ||| |||:|||||:||||||||||:||||||||||||||||||||||||||||||||||
Db        120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179

Qy        181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db        180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239

Qy        241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
              |||||:|||| ||:|||||||||||||| |||||||||||||||||||||||| |||
Db        240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299

Qy        301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
              || :|||: |:  |   |||||:|:||||||||||:|||||||:|||||| || |||||
Db        300 LVKKEEASIATTTFSW-QEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358

Qy        361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
              |||||||||||||||||||||||||||| ||||||||||:|||||||||||:||  |
Db        359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 418

Qy        421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
              |||| |||||:|| |||  |||||||||||||:||::|||||||||:||||||||||||
Db        419 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 478

Qy        481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
              ||:|||||||||||:|||||||| ||||||:||||::|| ||||||||||||||||||||
Db        479 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 538

Qy        541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
              |||||||||||||||||| ||:||||||||||||||||||||||||||||||||||||||
Db        539 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598

Qy        601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
              |||||||||||||||||||||||||:|||||||||| |||||:|:|||||||||:|
Db        599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 658

Qy        661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
              |::|:|||||||||||:|||||||||||||:|||||||:|||||||||||||||:||
Db        659 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 718

Qy        721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
              |||:||:||||| |     |||:|||||||| |:||:|||| | ||||:| ||| :|||:
Db        719 DGAFLWTGGRKTLVVDALPEEPPIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 778

Qy        781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
              ||||||:|||||||||| ||:||||::| | |:| ||: |:|||||||:||||||:|
Db        779 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 838

Qy        841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
              |||| |::|||||||| ||||  :|||: |:||::|||||||||:||||||| :|:
Db        839 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 898

Qy        901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
              |:| |:|||||  ||:|| |||||| ||||||||||::|||||::|||||||| ||||||
Db        899 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 958

Qy        961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
              ||| |||||||||||||||||::|||||||||||||||||||||||||||||||: ||
Db        959 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1018

Qy       1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
              ||||||| |||:||||||||||||||        |    | ::      : :
Db       1019 SPHLVPYAKVDEAIKKANRDTASETSANAPGLRICLGSSSDGRRNGGTSGRGTTPQVRRIP 1078

Qy       1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
              ||| |:|||:|||||||||:||:|||||||| ||  || ||| :: |||||:||||||
Db       1079 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNEEKVY 1138

Qy       1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
              | :|||||    ||:|||||||| | |||||||||||||||||||||||  :|  ||||
Db       1139 GGVSESFGKQCGPGDIVGVFLDLADHTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1198

Qy       1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
              |||||||||| |||||::||:||||||||||||||:| ||||||||||||||:||
Db       1199 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1258

Qy       1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
              | ||||||||| |:|||| |||||||||||||||||||||||| | ||| | ||||||
Db       1259 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1318

Qy       1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
              |||:||  ||:|| : |||       ||:| ::: || |||||||     |  :  :  |
Db       1319 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1378

Qy       1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
              | |:|||||:|| :|   :      :: | ||||          |:   |  |||| |
Db       1379 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1429

Qy       1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
              |||||||| ||:      | |  ::| |   :   :   |     | |:       | |
Db       1430 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1487

Qy       1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
                 ||                |  ||:: | | |   || |:|:|||||||||||||
Db       1488 AEIPPSPV--------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1533

Qy       1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
              ||||:|||||||||:|||||||||::||::|| : || | |||:  :| ::||||||:|
Db       1534 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1593

Qy       1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
              |||||:|||  :|: |||||||||:|| |||:|| : |||||||| :: |||:|||||||
Db       1594 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1653

Qy       1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
              |||||||||||||||: |:|||||||||||||: || |||||||||:||||||||  :
Db       1654 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1713

Qy       1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
              ||||||||||:|||||||| ||||||||||||||||||| ||||||||||:|:||||||
Db       1714 LQVHALKLSDVRGWSMLCEDPVSMLALHIPEEDRCIDILELIEMDKLLSFHAHSLTLYAA 1773

Qy       1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
              ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||| |||
Db       1774 LCYQSNYRAAHALCQHVDQKQLLYAIRSEYMSGPLRQGFYDLLIALHLESHATTMEVCKN 1833

Qy       1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDIAESITEISNLYSPYFPLEVA 1911
              |:: ||| ||| || : :| |||||| |||||||::||:| | | :|  |||| |||||
Db       1834 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITEPIPDIDQLYSPKFPLEVV 1893

Qy       1912 REFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGMMRDEDVEKLLIMTN 1971
              |:|||:|| :||| |||||||:| :|||||||||| |||||||:: ||||::||:| :
Db       1894 RQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGVLTDEDVQRLLVMID 1953

Qy       1972 PETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLRHRVEAIIAFAHDFV 2031
```

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          ||||| :|::|||||||||||| |||||||||||||| || | |||||||:||||:||||
Db       1954 PETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLRHRVESIIAFSHDFV 2013

Qy       2032 GDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFKHLEEEDKENCPCGE 2091
          |||||||||| |||||||||||||||:|||||||||| || ||:|| :|::|| ||
Db       2014 GDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFKNLEPDDQDNCTCGL 2073

Qy       2092 ELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYNIINTVKELEEEAKA 2150
          ||  |: :|||:||  |||:|||||  |     | | |   |:|| |||||||||  |
Db       2074 ELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYNFINTVKELEEGPKE 2133

Qy       2151 IEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQYDAVGELIRALEKT 2210
          :||| |||||| ||||||:|||:|||||||| |||||||||||:|||| ||||:||||||
Db       2134 VEEPEKKTPEEVFRKVLIKTIVSWAEESQIENPKLVREMFSLLLRQYDTVGELVRALEKT 2193

Qy       2211 YVINAKTKLDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNHTFFQHPDLIRVL 2270
          |||| : : |||||||||||||||||||||||||||||||||||||| ||||||||||:|
Db       2194 YVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVNNATFFQHPDLIRIL 2253

Qy       2271 RVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEMVVACCRFLCYFCRT 2328
          |||||||||||||:|||||||||| |:   |||   |||||||||||||||||||||||
Db       2254 RVHENVMAVMMNTIGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEMVVACCRFLCYFCRT 2312

Qy       2329 GRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2388
          |||||||||||||||:|:||||:||||||||||||||||||||||||||||||||||||||
Db       2313 GRQNQKAMFDHFDFLLDNANILLARPSLRGSTPLDVAYSSLMENTELALALREHYLEKIA 2372

Qy       2389 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGESVEENANLVIRLLIR 2448
          ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db       2373 VYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGESVEENANLVIRLLIR 2432

Qy       2449 RPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV---NFSHPLPESDED 2505
          |||||||||||||||| :|||:||:|||||:|| |::: | || :   ||:||||| :||
Db       2433 RPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIAGLNFTHPLPEGEED 2491

Qy       2506 EDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILRSLVPLEDLQGVLSL 2565
          |||||||||||||||||||||||||||||||| ||  |||||||||| ||||||||||||||||
Db       2492 EDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARASLRSLVPLEDLQGVLSL 2551

Qy       2566 RFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELFYKLLEEAFLPDLRA 2625
          :|||:  | |||:|||||||||:| :|||: |||||||||| |:|||:|||:|||||||
Db       2552 KFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLFYRLLEDAFLPDLRT 2611

Qy       2626 ATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASLLDATLHTVYRLSKN 2685
          ||:||::|| ||||||:||||||||||||||||: ||||||||||||||||||||||||
Db       2612 ATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASLLDATLHTVYRLSKN 2671

Qy       2686 RMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTTVALRLLTLHYERCA 2745
          |||||||||||||||||| |||:||||||||||||||||||||||||||||||||::|||
Db       2672 RMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTTVALRLLTLHFDRCA 2731

Qy       2746 KYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFGKALPCLIAIGCALP 2805
          ||||||  |||::||||||||||||:|||||||||| |||:||||||||||||||||||
Db       2732 KYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFGKALPCLIAIGCALP 2790

Qy       2806 PDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNTIVQKFSEHYHDAWA 2865
          |||||||| |:::||::  |   | ||| | ||:|::| |:||||::|||||||||||||
Db       2791 PDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNSLVQKFSEHYHDAWA 2848

Qy       2866 SRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESLKALLAIGWSVEHSE 2925
          ||::| || ||:  ||: : ||||||||||::||:|||::|||| || ||||||:|||||
Db       2849 SRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECLKGLLAIGWTVEHSE 2908

Qy       2926 VDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNLTLSREMQNMAERLA 2983
          |::| |:| | |||||     |:|    :  :||:||||||||:||||||||||||||||
Db       2909 VEVPLNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNLTLSREMQNMAERLA 2963

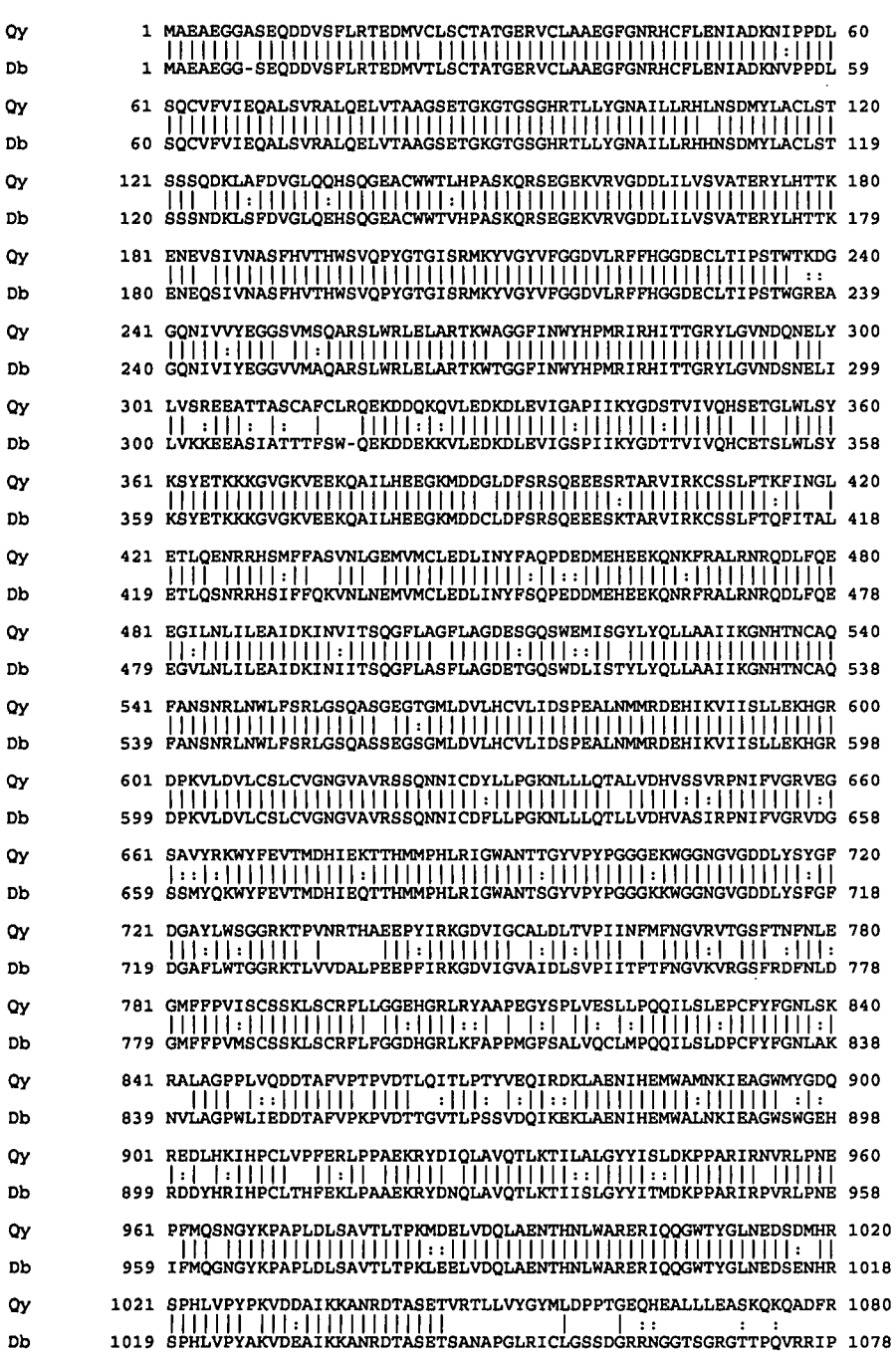
Qy       2984 DNAHDIWAKKKKEEL 2998
          :|:|||||||| |||
Db       2964 ENSHDIWAKKKNEEL 2978
```

RESULT 14

ADM68880

```
ID   ADM68880 standard; protein; 5126 AA.
XX
AC   ADM68880;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Drosophila melanogaster ryanodine receptor protein SEQ ID NO:124.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism.
XX
OS   Drosophila melanogaster.
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Disclosure; SEQ ID NO 124; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 5126 AA;
```

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  Query Match           78.3%;  Score 12338;  DB 8;  Length 5126;
  Best Local Similarity  77.9%;  Pred. No. 0;
  Matches 2359;  Conservative  266;  Mismatches  336;  Indels   68;  Gaps   22;
```


Qy 1 MAEAEGGASEQDDVSFLRTEDMVCLSCTATGERVCLAAEGFGNRHCFLENIADKNIPPDL 60
Db 1 MAEAEGG-SEQDDVSFLRTEDMVTLSCTATGERVCLAAEGFGNRHCFLENIADKNVPPDL 59
Qy 61 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHLNSDMYLACLST 120
Db 60 SQCVFVIEQALSVRALQELVTAAGSETGKGTGSGHRTLLYGNAILLRHHNSDMYLACLST 119
Qy 121 SSSQDKLAFDVGLQQHSQGEACWWTLHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 180
Db 120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179
Qy 181 ENEVSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWTKDG 240
Db 180 ENEQSIVNASFHVTHWSVQPYGTGISRMKYVGYVFGGDVLRFFHGGDECLTIPSTWGREA 239
Qy 241 GQNIVVYEGGSVMSQARSLWRLELARTKWAGGFINWYHPMRIRHITTGRYLGVNDQNELY 300
Db 240 GQNIVIYEGGVVMAQARSLWRLELARTKWTGGFINWYHPMRIRHITTGRYLGVNDSNELI 299
Qy 301 LVSREEATTASCAFCLRQEKDDQKQVLEDKDLEVIGAPIIKYGDSTVIVQHSETGLWLSY 360
Db 300 LVKKEEASIATTTFSW-QEKDDEKKVLEDKDLEVIGSPIIKYGDTTVIVQHCETSLWLSY 358
Qy 361 KSYETKKKGVGKVEEKQAILHEEGKMDDGLDFSRSQEEESRTARVIRKCSSLFTKFINGL 420
Db 359 KSYETKKKGVGKVEEKQAILHEEGKMDDCLDFSRSQEEESKTARVIRKCSSLFTQFITAL 418
Qy 421 ETLQENRRHSMFFASVNLGEMVMCLEDLINYFAQPDEDMEHEEKQNKFRALRNRQDLFQE 480
Db 419 ETLQSNRRHSIFFQKVNLNEMVMCLEDLINYFSQPEDDMEHEEKQNRFRALRNRQDLFQE 478
Qy 481 EGILNLILEAIDKINVITSQGFLAGFLAGDESGQSWEMISGYLYQLLAAIIKGNHTNCAQ 540
Db 479 EGVLNLILEAIDKINIITSQGFLASFLAGDETGQSWDLISTYLYQLLAAIIKGNHTNCAQ 538
Qy 541 FANSNRLNWLFSRLGSQASGEGTGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 600
Db 539 FANSNRLNWLFSRLGSQASSEGSGMLDVLHCVLIDSPEALNMMRDEHIKVIISLLEKHGR 598
Qy 601 DPKVLDVLCSLCVGNGVAVRSSQNNICDYLLPGKNLLLQTALVDHVSSVRPNIFVGRVEG 660
Db 599 DPKVLDVLCSLCVGNGVAVRSSQNNICDFLLPGKNLLLQTLLVDHVASIRPNIFVGRVDG 658
Qy 661 SAVYRKWYFEVTMDHIEKTTHMMPHLRIGWANTTGYVPYPGGGEKWGGNGVGDDLYSYGF 720
Db 659 SSMYQKWYFEVTMDHIEQTTHMMPHLRIGWANTSGYVPYPGGGKKWGGNGVGDDLYSFGF 718
Qy 721 DGAYLWSGGRKTPVNRTHAEEPYIRKGDVIGCALDLTVPIINFMFNGVRVTGSFTNFNLE 780
Db 719 DGAPLWTGGRKTLVVDALPEEPFIRKGDVIGVAIDLSVPIITFTFNGVKVRGSFRDFNLD 778
Qy 781 GMFFPVISCSSKLSCRFLLGGEHGRLRYAAPEGYSPLVESLLPQQILSLEPCFYFGNLSK 840
Db 779 GMFFPVMSCSSKLSCRFLFGGDHGRLKFAPPMGFSALVQCLMPQQILSLDPCFYFGNLAK 838
Qy 841 RALAGPPLVQDDTAFVPTPVDTLQITLPTYVEQIRDKLAENIHEMWAMNKIEAGWMYGDQ 900
Db 839 NVLAGPWLIEDDTAFVPKPVDTTGVTLPSSVDQIKEKLAENIHEMWALNKIEAGWSWGEH 898
Qy 901 REDLHKIHPCLVPFERLPPAEKRYDIQLAVQTLKTILALGYYISLDKPPARIRNVRLPNE 960
Db 899 RDDYHRIHPCLTHFEKLPAAEKRYDNQLAVQTLKTIISLGYYITMDKPPARIRPVRLPNE 958
Qy 961 PFMQSNGYKPAPLDLSAVTLTPKMDELVDQLAENTHNLWARERIQQGWTYGLNEDSDMHR 1020
Db 959 IFMQGNGYKPAPLDLSAVTLTPKLEELVDQLAENTHNLWARERIQQGWTYGLNEDSENHR 1018
Qy 1021 SPHLVPYPKVDDAIKKANRDTASETVRTLLVYGYMLDPPTGEQHEALLLEASKQKQADFR 1080
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Qy 1081 TYRAEKNYAVSSGKWYFEFEILTAGPMRVGWAHADMAPGMMLGQDENSWAFDGYNEEKVY 1140
Db 1079 TYRVERNYAVTSGKWYFEFEVLTSGPMRVGWARADCYPGAMLGSEDTSWAFDGHNEEKVY 1138
Qy 1141 SGNTESFGKQWAVGDVVGVFLDLIDKTISFSLNGELLMDALGGETTFADV--QGDNFVPA 1198
Db 1139 GGVSESFGKQCGPGDIVGVFLDLADHTISFSLNGELLMDALGGETTFADVTAEGVGFVPA 1198
Qy 1199 CTLGVGQKARLTYGQDVNTLKYFTTCGLQEGYEPFCVNMKRDVTHWYTKDQPIFENTDEM 1258
Db 1199 CTLGVGQKARLIYGQDVDSLKFFTTCGLQEGYEPFCVNMRRPVTHWYTKDQPIFENTEEM 1258
Qy 1259 IDTRIDVTRIPAGSDTPPCLKISHNTFETMEKANWEFLRLSLPVICHNEFIDEAEKARRW 1318
Db 1259 PDCRIDVTRIPGGADTPPHLKISHNTFETMEKANWEFLRLSLPVTCMGEFISEQEKARRW 1318
Qy 1319 VEIKDRQQILMKEA-VEAQM-----PAHIDQIMRSGFTMNDIKGLHYE-DNQEELPSSKM 1371
Db 1319 DEIKNRQYRLMREAEIAAQMQVQTQAAHMDHMLKGGFNMNDIKGLTRNFDEHADAEADHM 1378
Qy 1372 KRLPSRPPRKGSMTRGVTIQNYNNLQPGQVNGMHRSTSEAEMAKYDLGAQGLTPDDKKDK 1431
Db 1379 MRGPNRPPRKGSLTRNIT---FETDMSAALDEMQRSTS-----VLDMNGLGEEMDDKK-K 1429
Qy 1432 RGRSPFKFFRSKRGESSDRAKSRKSKTPDPFSDTEVSPERGARRPNPQIKVSQANQRYNG 1491
Db 1430 RGRSPFKFF-SKKSRDQSREK-MGARTLDTSLERRNTVAHGRNVVNQQMTTRAPTLRLNN 1487
Qy 1492 MNARPSRTNLYGSQVGLNMATPTQDRKQMTTSTLAQSATETVGNEIFDAECLKLINEYFY 1551
Db 1488 AEIPPSPV--------------PQGPKQLSGSNLGQQPVETSGDEMFDAECLKLINEYFY 1533
Qy 1552 GVRIYPGQDPTHVYIGWVTTQYHLHSKDFNQSKVTKSSVIITDDYDRVVENVNRQSCYMV 1611
Db 1534 GVRIFPGQDPTHVYVGWVTTQYHLHSREFNKNKVRRGSVYIEDDYEMAIERIDRQSCYVV 1593
Qy 1612 RADELYNEVMAEATAKGASQGMFIGCSVDTSTGSVSFTCEGKDTSFKFKMEPETKLFPAI 1671
Db 1594 RADELFNEVTQDASGKGASQGMFVGCFVDTATGIIRFTCEGKDTSHRWMMEPDTKLFPAI 1653
Qy 1672 FVEATSKEILQIELGRSATSLPLSAAVLPTSDKHVIPQFPPRLKVQCLKPHQWARVPNQS 1731
Db 1654 FVEATSKEILQIELGRTPTTLPLSAAVLPTSDKHINPQSPPRLKVQCLRPHQWARVPNTA 1713
Qy 1732 LQVHALKLSDIRGWSMLCEDAVSMLALHIPEEDRCIDILEPIEMDKLLSFHSHTLTLYAA 1791
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Qy 1792 LCYQSNYRAAHALCTHVDQKQLLYAIQSQYMSGPLRQGFYDLLIALHLESHATTMEACKN 1851
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Qy 1852 EFVIPLGPELKALYEEPDMGHSLRSLQTESVRPQMKMTDI----------AESITE 1897
Db 1834 EYITPLGAELKELYSDEEMQHSLRSLVTESVRPQLRMTEITPPVIATSSMPSVSSEPIPD 1893
Qy 1898 ISNLYSPYFPLEVAREFVMQALAEAVETNQVHNRDPVGGSNENLFLPLIKLVDRLLLVGM 1957
Db 1894 IDQLYSPKFPLEVVRQFVMEALKDAVEINQVHNRDPIGWTNENLFLPLIKLTDRLLLVGV 1953
Qy 1958 MRDEDVEKLLIMTNPETWDPSFDKEGKDEHRKGLLHMKMAEGAKLQMCYLLQHLNDIQLR 2017
Db 1954 LTDEDVQRLLVMIDPETWDQAFEREGKDEHRKGLLTMKMAEGAKLQMCYLLHHLYDTQLR 2013
Qy 2018 HRVEAIIAFAHDFVGDLQTDQLRRYTEIKQSDLPSAVAAKKTREFRCPPREQMNAILSFK 2077
Db 2014 HRVESIIAFSHDFVGDLQTDQLRRYIEIKQSDLPSAVAAKKTKEFRCPPREQMNQILCFK 2073
Qy 2078 HLEEEDKENCPCGEELIARMNEFHDTLMAHVSLHALQEPDAAENQE-PEAKPGAFGKLYN 2136
Db 2074 NLEPDDQDNCTCGLELRGRLGDFHDSLMQKVSLNALQEPDGVEGTAIEEVKTGPITKIYN 2133
Qy 2137 IINTVKELEEEAKAIEEPPKKTPEEKFRKVLIQTIVNWAEESQIETPKLVREMFSLLVRQ 2196

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Db       2194 YDTVGELVRALEKTYVINTRARDDVAEMWVGLSQIRALLPVQMSQEEEELMRKRLWKLVN 2253

Qy       2257 NHTFFQHPDLIRVLRVHENVMAVMMNTLGRRAQAQSDAQPSSQPVAE--DSKEKDTSHEM 2314

Db       2254 NATFFQHPDLIRILRVHENVMAVMMNTIGRRAQAQSDA-PTQSEVAEGAPSKEKDTSHEM 2312

Qy       2315 VVACCRFLCYFCRTGRQNQKAMFDHFDFLLENSNILLSRPSLRGSTPLDVAYSSLMENTE 2374

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Db       2373 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2432

Qy       2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493

Db       2433 VEENANLVIRLLIRRPECLGPALRGEGEGLFRAIVEANRMSERISDRCKMQD-EAEGTIA 2491

Qy       2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551

Db       2492 GLNFTHPLPEGEEDEDYIDTGAAILNFYCTLVDLLGRCAPDASVIEQGKNESLRARASLR 2551

Qy       2552 SLVPLEDLQGVLSLRFTLNNPAAGEERPKSDMPSGLIPGHKQSVGLFLERVYGIETQELF 2611

Db       2552 SLVPLEDLQGVLSLKFTLSQTAPGEEKPKSDMPSGLLPNNKQSIVLFLERVYGIEAQDLF 2611

Qy       2612 YKLLEEAFLPDLRAATMLDRNDGCESDMALSMNRYIGNSILPLLIKHAYFYNEAENYASL 2671

Db       2612 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2671

Qy       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731

Db       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2731

Qy       2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791

Db       2732 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2790

Qy       2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851

Db       2791 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2848

Qy       2852 IVQKFSEHYHDAWASRKIENGWVYGEGWSDSQKTHPRLKPYNMLNDYEKERYKEPVRESL 2911

Db       2849 LVQKFSEHYHDAWASRRLEGGWTYGDIRSDNDRKHPRLKPYNMLSEYERERYRDPVRECL 2908

Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969

Db       2909 KGLLAIGWTVEHSEVEVPLNHRGSTRRQSK-----PQINEFQNEGSPFNYNPHPVDMSNL 2963

Qy       2970 TLSREMQNMAERLADNAHDIWAKKKKEEL 2998

Db       2964 TLSREMQNMAERLAENSHDIWAKKKNEEL 2992


RESULT 15
ADM68812
ID   ADM68812 standard; protein; 5126 AA.
XX
AC   ADM68812;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Drosophila melanogaster ryanodine receptor related protein SEQ ID NO:56.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism.
XX
OS   Drosophila melanogaster.
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Example 4; SEQ ID NO 56; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 5126 AA;

  Query Match             78.3%;  Score 12338;  DB 8;  Length 5126;
  Best Local Similarity   77.9%;  Pred. No. 0;
  Matches 2359;  Conservative  266;  Mismatches  336;  Indels   68;  Gaps   22;

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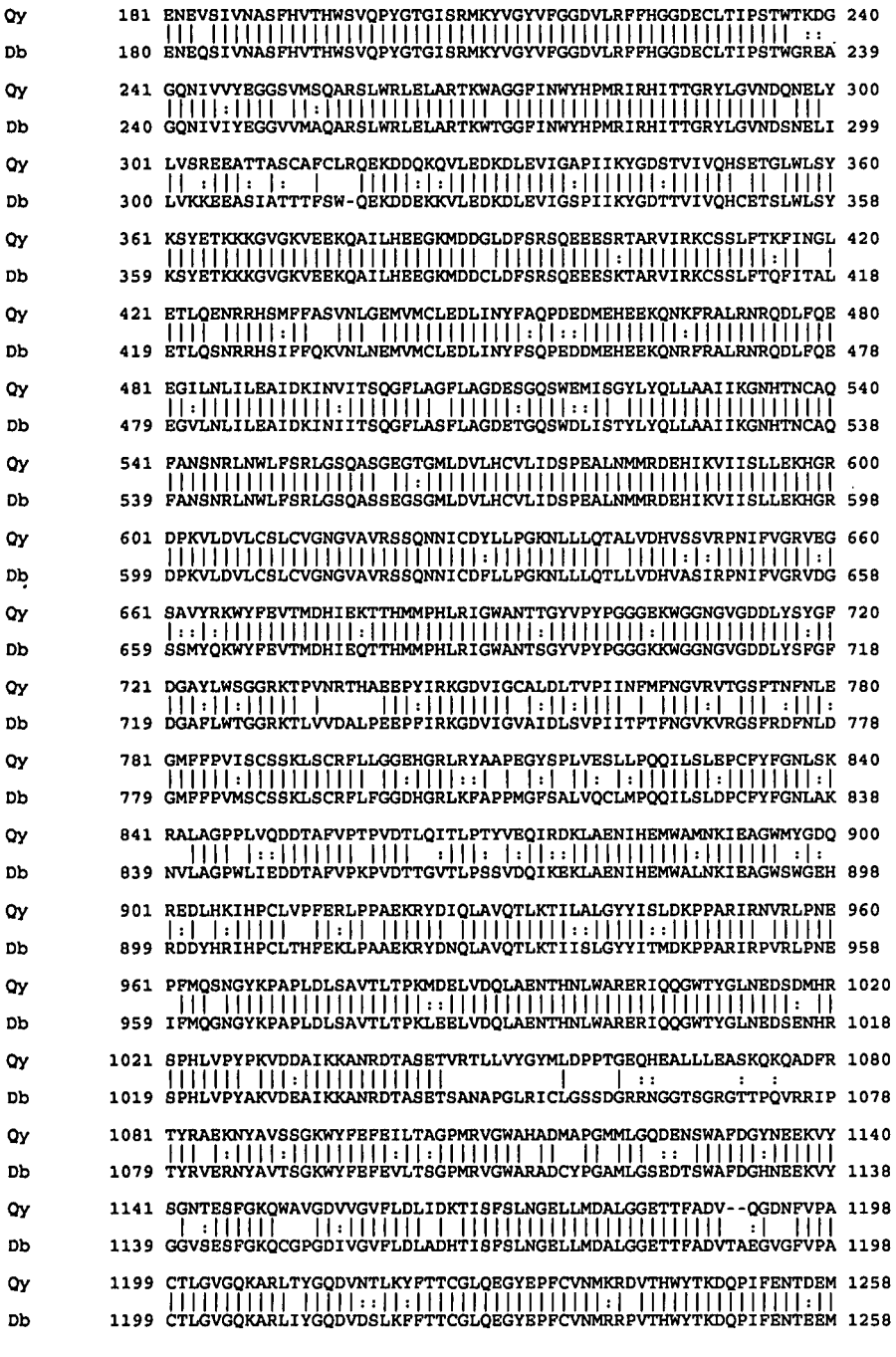
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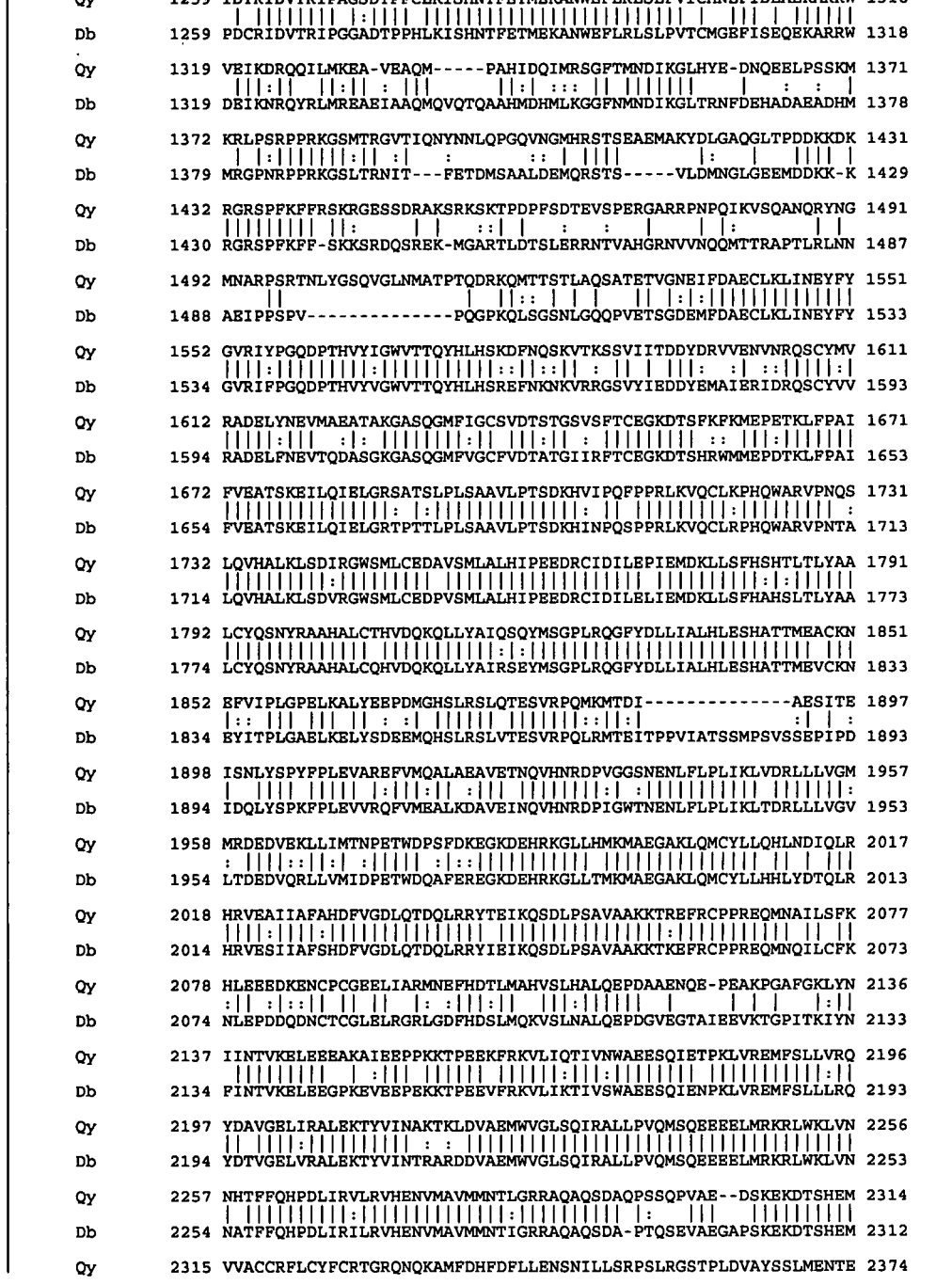
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Db       120 SSSNDKLSFDVGLQEHSQGEACWWTVHPASKQRSEGEKVRVGDDLILVSVATERYLHTTK 179
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Qy       2375 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRFCVWVNGES 2434

Db       2373 LALALREHYLEKIAVYLSRCGLQSNSELVEKGYPDLGWDPVEGERYLDFLRYCVWVNGES 2432

Qy       2435 VEENANLVIRLLIRRPECLGPALRGEGEGLLKAIVDANKMSERIADRRKLREMEQEGDV- 2493

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Qy       2494 --NFSHPLPESDEDEDYIDTGAAILNFYCTLVDLLGRCAPDAGVIALGKNESLRARAILR 2551

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Db       2612 YRLLEDAFLPDLRTATILDKSDGSESDMALAMNRYIGNSILPLLIKHSKFYNEAENYASL 2671

Qy       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSAMQPSMLLKLLRKLTVDVSKLSEYTT 2731

Db       2672 LDATLHTVYRLSKNRMLTKGQREAVSDFLVALTSQMQPAMLLKLLRKLTVDVSKLSEYTT 2731

Qy       2732 VALRLLTLHYERCAKYYGSTGAGQGAFGASSDEEKRLTMMLFSNIFDSLSKMDYEPELFG 2791

Db       2732 VALRLLTLHFDRCAKYYGST-QGQGSYGASSDEEKRLTMLLFSNIFDSLSNMDYDPELFG 2790

Qy       2792 KALPCLIAIGCALPPDYSLSKNYDDEFYGKEQAAGDLDNPQYDPQPINTSSVALNNDLNT 2851

Db       2791 KALPCLIAIGCALPPDYSLSKNTDEDYYGRQMGAP--DQPQYMPNPIDTNNVHLDNDLNS 2848

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Qy       2912 KALLAIGWSVEHSEVDIPSNNRSSMRRQSKSGGRPPEI--VTDSATPFDYNPHPVDMTNL 2969

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Db       2964 TLSREMQNMAERLAENSHDIWAKKKNEEL 2992


Search completed: April 14, 2006, 01:34:06
Job time : 329 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 14:38:23 ; Search time 2288 Seconds
(without alignments)
10846.330 Million cell updates/sec

Title: US-10-668-767-127_COPY_1000_4000
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Sequence: 1 gtcataggcgcgcccatcat.....cctaatgaaagaggcagttg 3001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3001	100.0	15387	7	US-10-668-767-127	Sequence 127, App
	2	2857	95.2	15303	7	US-10-668-767-145	Sequence 145, App
	3	2847.4	94.9	15679	7	US-10-668-767-1	Sequence 1, Appli
	4	2841	94.7	15405	7	US-10-668-767-129	Sequence 129, App
	5	2839.4	94.6	15429	7	US-10-668-767-143	Sequence 143, App
	6	1620.4	54.0	15606	10	US-11-097-143-22562	Sequence 22562, A
	7	1617.2	53.9	16363	7	US-10-668-767-9	Sequence 9, Appli
	8	1542.2	51.4	15413	7	US-10-668-767-7	Sequence 7, Appli
	9	1335.4	44.5	15315	7	US-10-668-767-5	Sequence 5, Appli
	10	1319	44.0	15845	7	US-10-668-767-3	Sequence 3, Appli
c	11	1150	38.3	24236	10	US-11-097-143-22561	Sequence 22561, A
	12	668	22.3	4078	6	US-10-305-720-1154	Sequence 1154, Ap
	13	668	22.3	14302	7	US-10-276-774-552	Sequence 552, App
	14	668	22.3	15731	9	US-10-887-553A-490	Sequence 490, App
	15	646.6	21.5	15359	7	US-10-276-774-500	Sequence 500, App
	16	646.6	21.5	15359	9	US-10-887-553A-489	Sequence 489, App
	17	646.6	21.5	15359	9	US-10-450-763-4960	Sequence 4960, Ap
	18	622.8	20.8	15453	8	US-10-723-860-5796	Sequence 5796, Ap
	19	618.4	20.6	15563	7	US-10-764-425-48	Sequence 48, Appl
	20	618.4	20.6	15563	9	US-10-887-553A-491	Sequence 491, App
	21	597	19.9	15583	9	US-10-450-763-12305	Sequence 12305, A
	22	597	19.9	15820	9	US-10-450-763-23337	Sequence 23337, A
	23	104.8	3.5	321	6	US-10-029-386-16105	Sequence 16105, A
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c	27	81.6	2.7	643	5	US-10-027-632-51124	Sequence 51124, A
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c	30	70	2.3	608	4	US-09-925-065A-169264	Sequence 169264,
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	32	61.2	2.0	587	3	US-09-864-761-8415	Sequence 8415, Ap
	33	60.8	2.0	196	3	US-09-864-761-25143	Sequence 25143, A
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	35	54.8	1.8	169	3	US-09-864-761-28441	Sequence 28441, A
	36	54.8	1.8	486	9	US-10-450-763-23333	Sequence 23333, A
	37	54.6	1.8	640	4	US-09-925-065A-356190	Sequence 356190,
	38	53.6	1.8	600	9	US-10-972-079-73805	Sequence 73805, A
	39	52.6	1.8	537	3	US-09-864-761-12147	Sequence 12147, A
	40	50.2	1.7	153	3	US-09-864-761-28727	Sequence 28727, A
	41	50.2	1.7	639	9	US-10-450-763-12306	Sequence 12306, A
	42	50.2	1.7	639	9	US-10-450-763-23332	Sequence 23332, A
c	43	44	1.5	499	9	US-10-779-543-21524	Sequence 21524, A
c	44	42.4	1.4	496	5	US-10-027-632-77061	Sequence 77061, A
c	45	42.4	1.4	496	5	US-10-027-632-77062	Sequence 77062, A

ALIGNMENTS

RESULT 1
US-10-668-767-127
; Sequence 127, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 15387
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15384)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-Hv7
US-10-668-767-127

Query Match 100.0%; Score 3001; DB 7; Length 15387;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1120 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 1179

Qy       181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
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Qy       241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
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Qy       301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
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Qy       361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
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Qy       421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
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Qy       481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
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Db      1480 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 1539

Qy       541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
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Db      1540 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 1599

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Qy       661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1660 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 1719

Qy       721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1720 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 1779

Qy       781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
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Qy       901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
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Qy       961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
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Qy      1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
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Qy      1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
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Db      2080 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 2139

Qy      1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGGAGGAAGACTCCC 1200
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Db      2140 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGGAGGAAGACTCCC 2199

Qy      1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
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Qy      1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
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Qy      1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
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Qy      1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
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Qy      1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
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Qy      1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
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Db      2680 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 2739

Qy      1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
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Qy      1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
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Db      2800 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 2859

Qy      1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
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Db      2860 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 2919

Qy      1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
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Db      2920 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 2979

Qy      1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
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Qy      2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3100 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 3159

Qy      2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 2220
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Db       3460 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 3519

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Qy       2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700
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Qy       2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTT 3000
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RESULT 2
US-10-668-767-145
; Sequence 145, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 145
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;   TYPE: DNA
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(15300)
;   OTHER INFORMATION:
;   FEATURE:
;   OTHER INFORMATION: pXL-Hv6
US-10-668-767-145

  Query Match             95.2%;  Score 2857;  DB 7;  Length 15303;
  Best Local Similarity   97.0%;  Pred. No. 0;
  Matches 2911;  Conservative    0;  Mismatches   90;  Indels    0;  Gaps    0;

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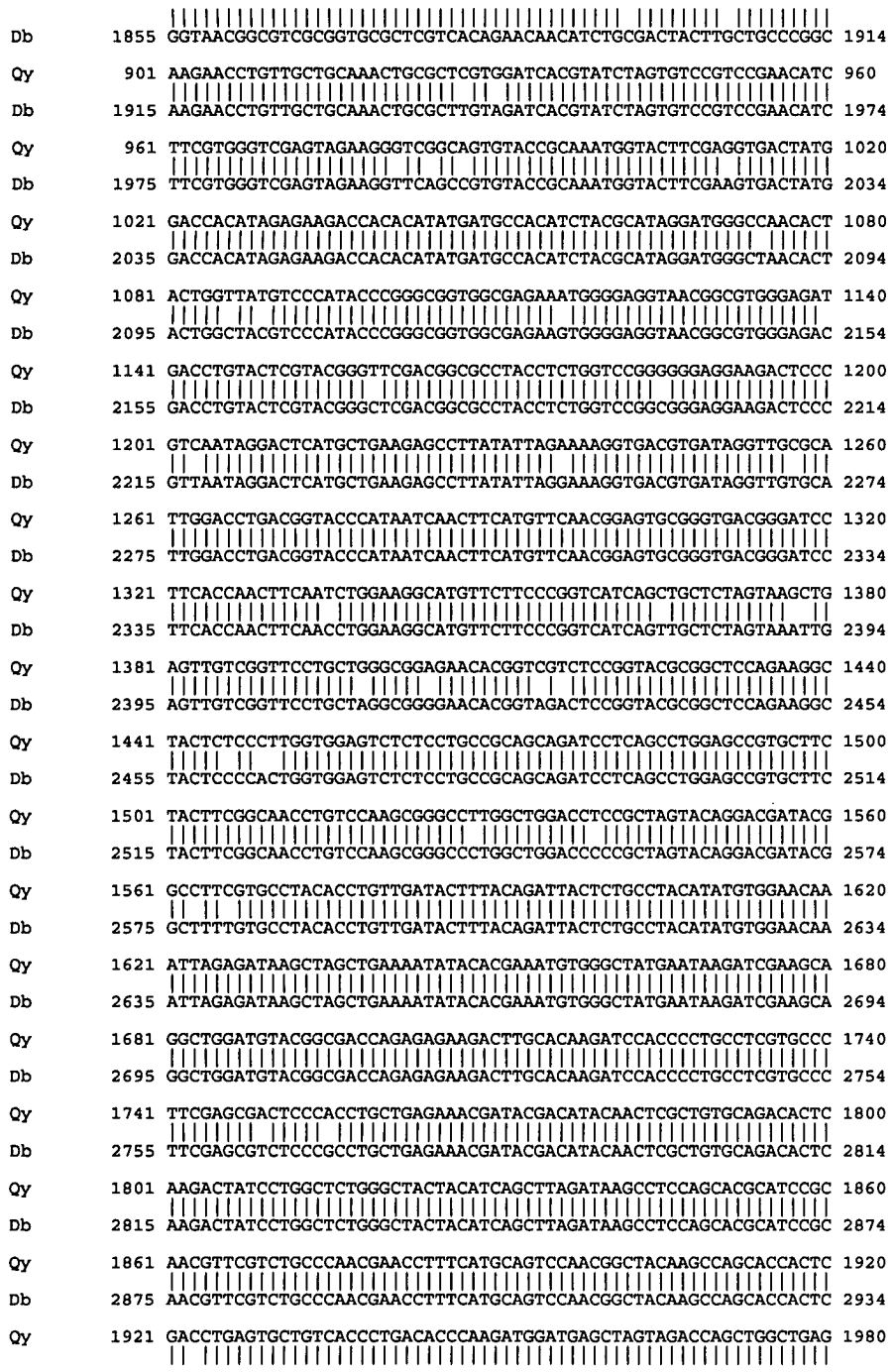
Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
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Db       1615 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGCTCAACTGGCTGTTCTCGCGC 1674

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
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Db       1735 ATAGACTCGCCTGAAGCGCTCAATATGATGCGGGACGAACACATAAAAGTGATAATTTCT 1794

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
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Db 1855 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTACTTGCTGCCCGGC 1914
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Qy 1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
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Qy 1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
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Qy 1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
Db 2755 TTCGAGCGTCTCCCGCCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 2814
Qy 1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
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Qy 1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
Db 2875 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 2934
Qy 1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
Db 2935 GATCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 2994
Qy 1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
Db 2995 AACACACACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAAT 3054
Qy 2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
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Qy 2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 2220
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Qy 2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280
Db 3235 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAAAAGAACTATGCCGTCAGCTCTGGG 3294
Qy 2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340
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Qy 2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400
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Qy 2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520
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Qy 2581 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 2640
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Qy 2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700
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Qy 2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940
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Db 4015 G 4015

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US-10-668-767-1
; Sequence 1, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 15679
;   TYPE: DNA
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (251)..(15676)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5515)
;   OTHER INFORMATION: n = c or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (13000)
;   OTHER INFORMATION: n = a or t
US-10-668-767-1

  Query Match             94.9%;  Score 2847.4;  DB 7;  Length 15679;
  Best Local Similarity   96.8%;  Pred. No. 0;
  Matches 2905;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

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Db       1265 GTCATAGGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAG 1324

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              |||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
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Db       1385 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCC 1444

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
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Db       1445 AGGTCACAGGAGGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 1504

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
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Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
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Db       1565 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCA 1624

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
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Db       1625 CAGCCCGATGAGGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAAC 1684

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
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Db       1685 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 1744

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
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Db       1745 ATCAACGTCGTCACGTCCCAGGGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGA 1804

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Db       1805 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGC 1864

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Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
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Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
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Db       1985 ATCGACTCGCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 2044

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Db       2045 CTATTAGAAAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTC 2104

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
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Db       2105 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGC 2164

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Db       2165 AAGAACCTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATC 2224

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Db       2225 TTCGTGGGCCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 2284

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Db       2345 ACTGGTTATGTCCCATACCCGGGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGGAGAC 2404

Qy       1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
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Db       2405 GACCTGTACTCGTACGGGTTTGATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGACCCCG 2464

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Db       2465 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCA 2524

Qy       1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
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Qy       1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
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Qy       1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
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Qy       1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
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Db       3905 GACGTGAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTC 3964

Qy       2701 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 2760
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Db       4025 AATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGAT 4084

Qy       2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880
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Qy       2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940
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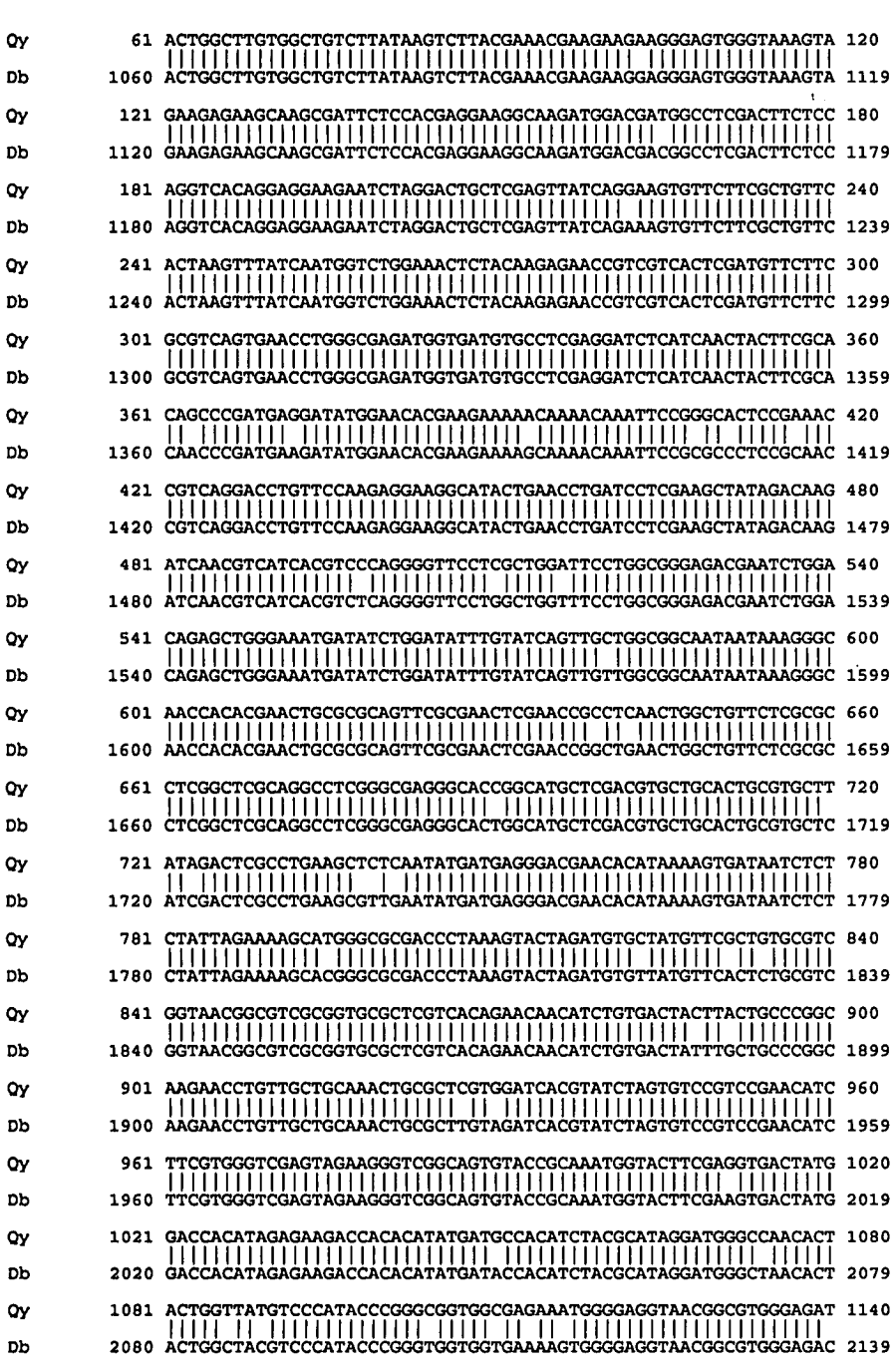
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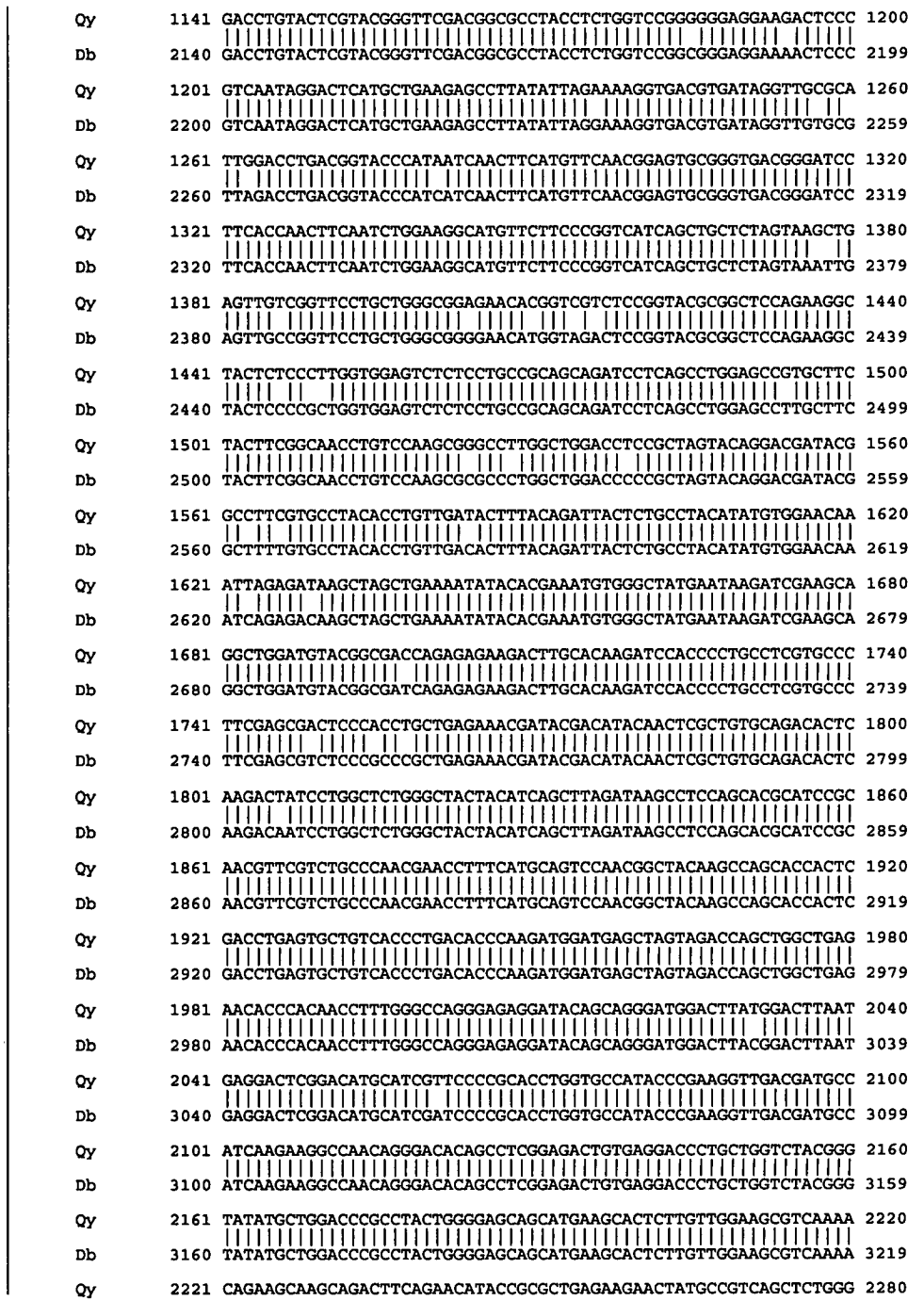
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Db       4265 G 4265
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RESULT 4
US-10-668-767-129
; Sequence 129, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 15405
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15402)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-Hv2
US-10-668-767-129

Query Match 94.7%; Score 2841; DB 7; Length 15405;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 2901; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Db       3220 CAGAAGCAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 3279

Qy       2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3280 AAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 3339

Qy       2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       3340 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCATTTGATGGT 3399

Qy       2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3400 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 3459

Qy       2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3460 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAC 3519

Qy       2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 2580
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3520 GGTGAGTTATTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 3579

Qy       2581 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 2640
             |||||||||| |||||||| |||||||||||||||||||||||||||| || ||
Db       3580 AACTTTGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAG 3639

Qy       2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700
             || || || || |||||||||||||||||||||||| ||||||||||||||||||||
Db       3640 GACGTAAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTC 3699

Qy       2701 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 2760
             || |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3700 TGTGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAG 3759

Qy       2761 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 2820
             ||||| |||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db       3760 AATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGAT 3819

Qy       2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       3820 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGG 3879

Qy       2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       3880 GAGTTCTTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAA 3939

Qy       2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTT 3000
             |||||||| |||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       3940 AAAGCCAGGCGTTGGGTAGAAATCAAGGACCGCCAACAGATCCTAATGAAAGAGGCAGTT 3999

Qy       3001 G 3001
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Db       4000 G 4000
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RESULT 5
US-10-668-767-143
; Sequence 143, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
;   LENGTH: 15429
;   TYPE: DNA
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(15429)
;   OTHER INFORMATION:
;   FEATURE:
;   OTHER INFORMATION: pXL-Hv3
US-10-668-767-143

  Query Match             94.6%;  Score 2839.4;  DB 7;  Length 15429;
  Best Local Similarity   96.6%;  Pred. No. 0;
  Matches 2900;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              |||||||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db       1015 GTCATAGGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 1074

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 1134

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1135 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGACGGCCTCGACTTCTCC 1194

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1195 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGAAAGTGTTCTTCGCTGTTC 1254

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1255 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 1314

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1315 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 1374

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              || |||||||| |||||||||||||||||| |||||||||||||| || ||||| |||
Db       1375 CAACCCGATGAAGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAAC 1434

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1435 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGTCAAG 1494

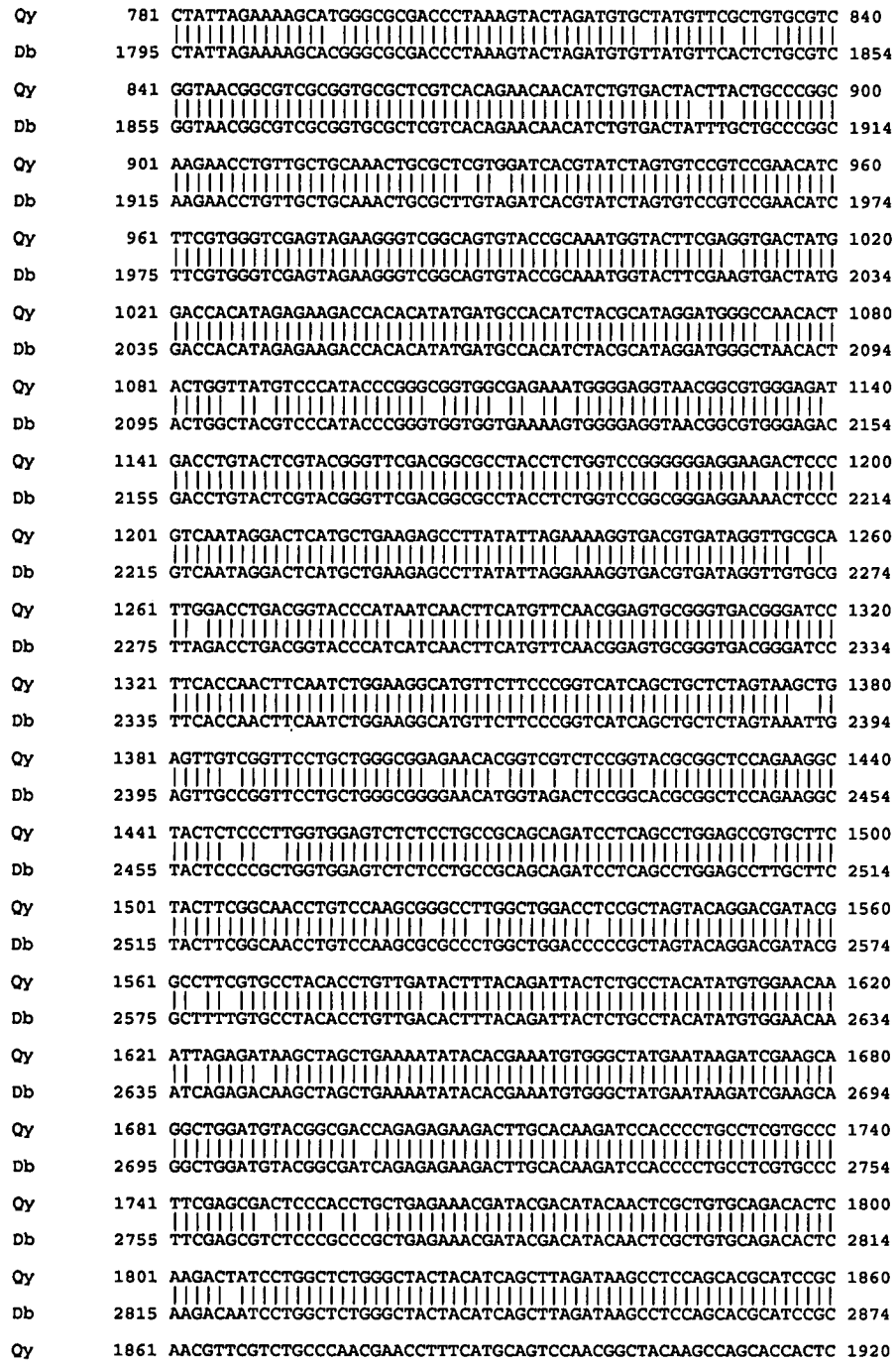
Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              |||||||||||||||| |||||||||| ||||| ||||||||||||||||||||||||||
Db       1495 ATCAACGTCATCACGTCTCAGGGGTTCCTGGCTGGTTTCCTGGCGGGAGACGAATCTGGA 1554

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1555 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGTTGGCGGCAATAATAAAGGGC 1614

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              |||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db       1615 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGCTGAACTGGCTGTTCTCGCGC 1674

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1675 CTCGGCTCGCAGGCCTCGGGCGAGGGCACTGGCATGCTCGACGTGCTGCACTGCGTGCTC 1734

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
              || ||||||||||||||  | ||||||||||||||||||||||||||||||||||||||
Db       1735 ATCGACTCGCCTGAAGCGTTGAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 1794
```


Qy 781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
Db 1795 CTATTAGAAAAGCACGGGCGCGACCCTAAAGTACTAGATGTGTTATGTTCACTCTGCGTC 1854
Qy 841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
Db 1855 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTATTTGCTGCCCGGC 1914
Qy 901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
Db 1915 AAGAACCTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATC 1974
Qy 961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
Db 1975 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAAGTGACTATG 2034
Qy 1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
Db 2035 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAACACT 2094
Qy 1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
Db 2095 ACTGGCTACGTCCCATACCCGGGTGGTGGTGAAAAGTGGGGAGGTAACGGCGTGGGAGAC 2154
Qy 1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
Db 2155 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGCGGGAGGAAAACTCCC 2214
Qy 1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
Db 2215 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCG 2274
Qy 1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
Db 2275 TTAGACCTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 2334
Qy 1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
Db 2335 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAATTG 2394
Qy 1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
Db 2395 AGTTGCCGGTTCCTGCTGGGCGGGGAACATGGTAGACTCCGGCACGCGGCTCCAGAAGGC 2454
Qy 1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
Db 2455 TACTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCTTGCTTC 2514
Qy 1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
Db 2515 TACTTCGGCAACCTGTCCAAGCGCGCCCTGGCTGGACCCCCGCTAGTACAGGACGATACG 2574
Qy 1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
Db 2575 GCTTTTGTGCCTACACCTGTTGACACTTTACAGATTACTCTGCCTACATATGTGGAACAA 2634
Qy 1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
Db 2635 ATCAGAGACAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 2694
Qy 1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
Db 2695 GGCTGGATGTACGGCGATCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 2754
Qy 1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
Db 2755 TTCGAGCGTCTCCCGCCCGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 2814
Qy 1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
Db 2815 AAGACAATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 2874
Qy 1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
Db 2875 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 2934
Qy 1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
Db 2935 GACCTGGGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 2994
Qy 1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
Db 2995 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAAT 3054
Qy 2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
Db 3055 GAGGACTCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 3114
Qy 2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160
Db 3115 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 3174
Qy 2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 2220
Db 3175 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 3234
Qy 2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280
Db 3235 CAGAAGCAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 3294
Qy 2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340
Db 3295 AAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 3354
Qy 2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400
Db 3355 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCATTTGATGGT 3414
Qy 2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460
Db 3415 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 3474
Qy 2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520
Db 3475 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAC 3534
Qy 2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 2580
Db 3535 GGTGAGTTATTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 3594
Qy 2581 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 2640
Db 3595 AACTTTGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAG 3654
Qy 2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700
Db 3655 GACGTGAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTC 3714
Qy 2701 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 2760
Db 3715 TGTGTCAATATGGAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAG 3774
Qy 2761 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 2820
Db 3775 AATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGAT 3834
Qy 2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880
Db 3835 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGG 3894
Qy 2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940
Db 3895 GAGTTCTTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAA 3954
Qy 2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTT 3000

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Db       3955 AAAGCCAGGCGTTGGGTAGAAATCAAGGACCGCCAACAGATCCTAATGAAAGAGGCAGTT 4014

Qy       3001 G 3001
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Db       4015 G 4015
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RESULT 6
US-11-097-143-22562
; Sequence 22562, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22562
; LENGTH: 15606
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-22562

Query Match 54.0%; Score 1620.4; DB 10; Length 15606;
Best Local Similarity 71.5%; Pred. No. 0;
Matches 2147; Conservative 0; Mismatches 851; Indels 6; Gaps 1;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
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Db        937 GTGATCGGCTCGCCGATCATCAAGTACGGCGACACTACCGTCATCGTTCAGCACTGCGAG 996

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              ||| ||||||||||     || |||  ||| || ||||| |||||||| || || || ||
Db        997 ACTAGCTTGTGGCTCAGCTACAAGAGTTATGAGACGAAAAAGAAGGGCGTAGGAAAGGTG 1056

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              || |||||||||||||| || |||||||| |||||||||||||| | ||||||||||
Db       1057 GAGGAGAAGCAAGCGATCCTGCACGAGGAGGGCAAGATGGACGATTGTCTCGACTTCTCG 1116

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              | || |||||||| || || | ||| ||||| || ||| | |||||       || |||
Db       1117 CGCTCCCAGGAGGAGGAGTCCAAGACAGCTCGTGTCATCCGCAAGTGCAGCAGCCTCTTC 1176

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              ||  ||||||| | |   ||||||| || ||    || || || ||||| || |||||||
Db       1177 ACCCAGTTTATTACAGCCTTGGAAACACTGCAGTCAAATCGCCGACACTCCATTTTCTTC 1236

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
                 || |||||   |||||||| |||||||| |||||  | || ||||||||  |
Db       1237 CAAAAGGTCAACCTCAACGAGATGGTCATGTGCCTTGAGGACTTGATTAACTACTTTTCG 1296

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
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                || ||||| || |||||||| ||||| || ||||| ||| |||||| || || || |||
Db       1297 CAACCCGAAGACGATATGGAGCACGAGGAGAAACAGAACCGATTCCGTGCCCTGCGCAAC 1356

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              || ||||| |||||||| ||||| ||| | || || |||||||| || || || ||||||
Db       1357 CGACAGGATCTGTTCCAGGAGGAGGGCGTGCTCAATCTGATCCTGGAGGCCATTGACAAG 1416

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              |||||| | ||||| || ||||| ||||| ||  | |||||||| || |||||  | ||
Db       1417 ATCAACATAATCACCTCGCAGGGCTTCCTAGCCAGCTTCCTGGCCGGCGACGAGACCGGC 1476

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              |||||||||||  | || ||    |||||||| ||  |  |||| || || || ||||||
Db       1477 CAGAGCTGGGATCTCATCTCCACCTATTTGTACCAACTCTTGGCCGCCATCATCAAGGGC 1536

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              |||||||||||||||| ||||||||||||    ||||| |||||||||| ||||| |||
Db       1537 AACCACACGAACTGCGCCCAGTTCGCGAACAGTAACCGACTCAACTGGCTATTCTCCCGC 1596

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
              ||||| || |||||||  |||||||  ||||||||  | ||||| || ||||||||||||
Db       1597 CTCGGTTCCCAGGCCTCCAGCGAGGGTTCCGGCATGTTGGACGTACTTCACTGCGTGCTG 1656

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
              || || ||||| || || || || |||||| |||| || ||||| || ||||| |||||
Db       1657 ATCGATTCGCCAGAGGCACTAAACATGATGCGGGATGAGCACATCAAGGTGATCATCTCC 1716

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
              ||  | || ||||| ||  | ||||| ||||| ||||| || || |||||  |||||||
Db       1717 CTGCTGGAGAAGCACGGCAGGGACCCGAAAGTCCTAGACGTTCTGTGTTCCTTGTGCGTG 1776

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
              ||||| || || |||||||| || || |||||||||||| || ||||  || || || |||
Db       1777 GGTAATGGAGTGGCGGTGCGATCCTCCCAGAACAACATTTGCGACTTTTTGCTACCGGGC 1836

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
              ||||| |||||||| || ||    || ||||| || ||  | ||  |||| |||||||||
Db       1837 AAGAATCTGTTGCTACAGACGCTCCTGGTGGACCATGTGGCCAGCATCCGACCGAACATC 1896

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
              |||||||||| || || || ||  |  ||||||  || ||||||||||||||||| |||
Db       1897 TTCGTGGGTCGCGTGGACGGTTCTTCCATGTACCAGAAGTGGTACTTCGAGGTGACCATG 1956

Qy       1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
              || ||||| ||  ||||||| || |||||||| || || ||||| || ||||| || |||
Db       1957 GATCACATCGAACAGACCACGCACATGATGCCCCACCTGCGCATTGGCTGGGCTAATACT 2016

Qy       1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
              | || ||||| || || || || || ||| |||| ||||| || || || || || |||
Db       2017 TCCGGGTATGTACCGTATCCCGGAGGCGGCAAGAAGTGGGGTGGCAATGGAGTAGGCGAT 2076

Qy       1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
              |||||||||| |  || || || || ||||  || ||| | || ||  | || || |
Db       2077 GACCTGTACTCCTTTGGATTTGATGGTGCCTTTCTTTGGACGGGAGGTCGCAAAACACTA 2136

Qy       1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
              ||         | |   | || ||||| | |||  | ||||| || || || ||    ||
Db       2137 GTGGTGGACGCGCTGCCCGAGGAGCCCTTTATCCGTAAAGGCGATGTTATTGGCGTTGCC 2196

Qy       1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
              | |||||  | || |||||  ||||  || | || ||||||||     |||   ||    |
Db       2197 ATTGACCTTTCTGTGCCCATCATCACGTTTACTTTTAACGGAGTAAAAGTGCGCGGTAGC 2256

Qy       1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
              || |   |||| || ||||| || |||||||| || || || || |||||     || ||
Db       2257 TTTAGGGACTTTAACCTGGACGGAATGTTCTTTCCCGTGATGAGTTGCTCATCAAAACTA 2316

Qy       1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
              || ||||| |||||  | || || || || |||||| |    ||  ||  | ||    ||
Db       2317 AGCTGTCGCTTCCTTTTCGGAGGTGATCATGGTCGTTTAAAGTTTGCCCCGCCCATGGGA 2376

Qy       1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
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Db       2377 TTCTCTGCCCTCGTGCAGTGTCTCATGCCGCAGCAGATCCTCAGTCTGGATCCTTGCTTC 2436

Qy       1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560

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Qy       1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620

Db       2497 GCTTTTGTTCCGAAGCCCGTTGATACCACGGGTGTGACATTGCCAAGTTCTGTGGACCAA 2556

Qy       1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680

Db       2557 ATCAAGGAGAAGCTGGCGGAGAATATCCACGAGATGTGGGCTCTAAACAAAATCGAGGCG 2616

Qy       1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740

Db       2617 GGCTGGTCGTGGGGCGAGCACCGAGATGACTACCACCGCATCCATCCTTGCCTCACCCAT 2676

Qy       1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800

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Qy       2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100

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Db       3097 TATGTCTTGGATCCTCCGACTGGCGAAGGAACGGAGGCACTTCTGGCCGAGGCACAACGC 3156

Qy       2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280

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Qy       2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340

Db       3217 AAGTGGTACTTCGAATTCGAGGTCCTCACGTCCGGACCAATGCGAGTGGGTTGGGCACGG 3276

Qy       2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400

Db       3277 GCCGATTGCTATCCGGGAGCGATGCTGGGCAGCGAGGACACCAGTTGGGCCTTCGATGGA 3336

Qy       2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460

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Qy       2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520

Db       3397 GGCGATGTCATTGGTTGTTTCATCGATGTCAAGGAGCAAACGATCAGCTTCTCGTTGAAC 3456

Qy       2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGT------CCAG 2574

Db       3457 GGAGAACTCCTGATGGACGCGCTGGGCGGCGAGACGACCTTTGCCGACGTAACCGCCGAG 3516

Qy       2575 GGTGACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATAT 2634

Db       3517 GGGGTGGGCTTCGTGCCCGCCTGCACCCTGGGAGTGGGCCAGAAGGCGCGCCTCATCTAC 3576

Qy       2635 GGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAA 2694

Db       3577 GGCCAGGACGTGGACTCACTCAAGTTCTTCACCACTTGTGGCCTGCAAGAGGGATACGAG 3636

Qy       2695 CCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATC 2754

Db       3637 CCGTTCTGCGTGAACATGCGCCGCCCGGTTACCCACTGGTACACCAAGGACCAGCCCATT 3696

Qy       2755 TTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGT 2814

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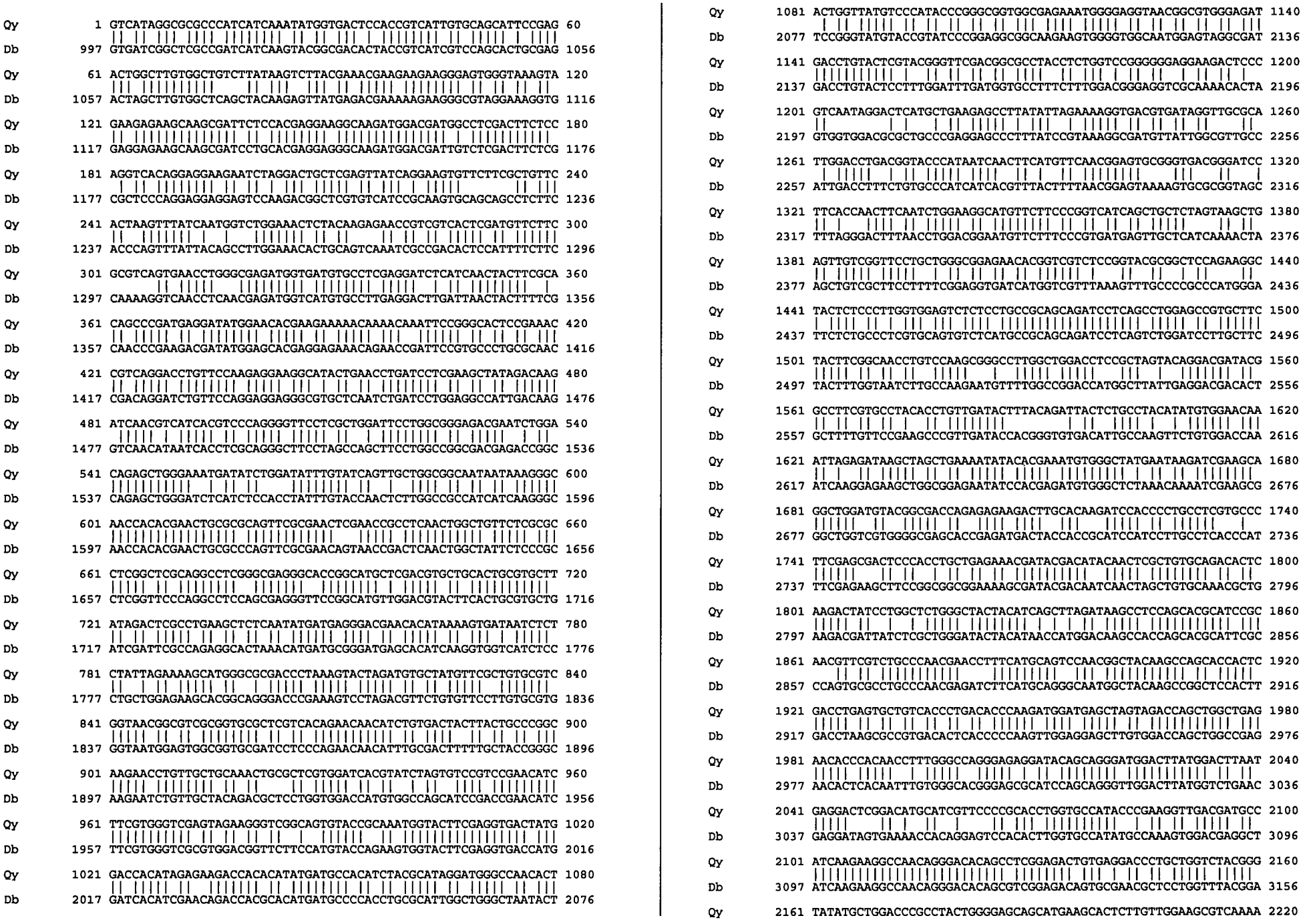
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Db       3937 GCGG 3940
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RESULT 7
US-10-668-767-9
; Sequence 9, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16363
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15890)..(15890)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15327)
; OTHER INFORMATION:
US-10-668-767-9

Query Match 53.9%; Score 1617.2; DB 7; Length 16363;
Best Local Similarity 71.4%; Pred. No. 0;
Matches 2145; Conservative 0; Mismatches 853; Indels 6; Gaps 1;



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Db       3157 TATGTCTTGGATCCTCCGACGGGCGAAGGAACGGAGGCACTTCTGGCCGAGGCACAACGC 3216

Qy       2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280

Db       3217 CTCAAGTTCGCCGGATTCCGGACTTACAGGGTGGAGCGCAACTACGCCGTGACATCGGGC 3276

Qy       2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340

Db       3277 AAGTGGTACTTCGAATTCGAGGTCCTCACGTCCGGACCAATGCGAGTGGGTTGGGCACGG 3336

Qy       2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400

Db       3337 GCCGATTGCTATCCGGGAGCGATGCTGGGCAGCGAGGACACCAGTTGGGCCTTCGATGGA 3396

Qy       2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460

Db       3397 CACAATGTGACCAAAATGCACGCCGGATCCATTGAGCACTTCGGAGTGCGGTATGAGGCT 3456

Qy       2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520

Db       3457 GGCGATGTCATTGGTTGTTTCATCGATGTCAAGGAGCAAACGATCAGCTTCTCGTTGAAC 3516

Qy       2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGT------CCAG 2574

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Qy       2575 GGTGACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATAT 2634

Db       3577 GGGGTGGGCTTCGTGCCCGCCTGCACCCTGGGAGTGGGCCAGAAGGCGCGCCTCATCTAC 3636

Qy       2635 GGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAA 2694

Db       3637 GGCCAGGACGTGGACTCACTCAAGTTCTTCACCACTTGTGGCCTGCAAGAGGGATACGAG 3696

Qy       2695 CCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATC 2754

Db       3697 CCGTTCTGCGTGAACATGCGCCGCCCGGTTACCCACTGGTACACCAAGGACCAGCCCATT 3756

Qy       2755 TTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGT 2814

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Db       3997 GCGG 4000


RESULT 8
US-10-668-767-7
; Sequence 7, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 15413
;   TYPE: DNA
;   ORGANISM: Peregrinus maidis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1264)
;   OTHER INFORMATION: n = a,c,g, or t
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (17)..(15397)
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US-10-668-767-7

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  Matches 2101;  Conservative    1;  Mismatches  890;  Indels    6;  Gaps    2;

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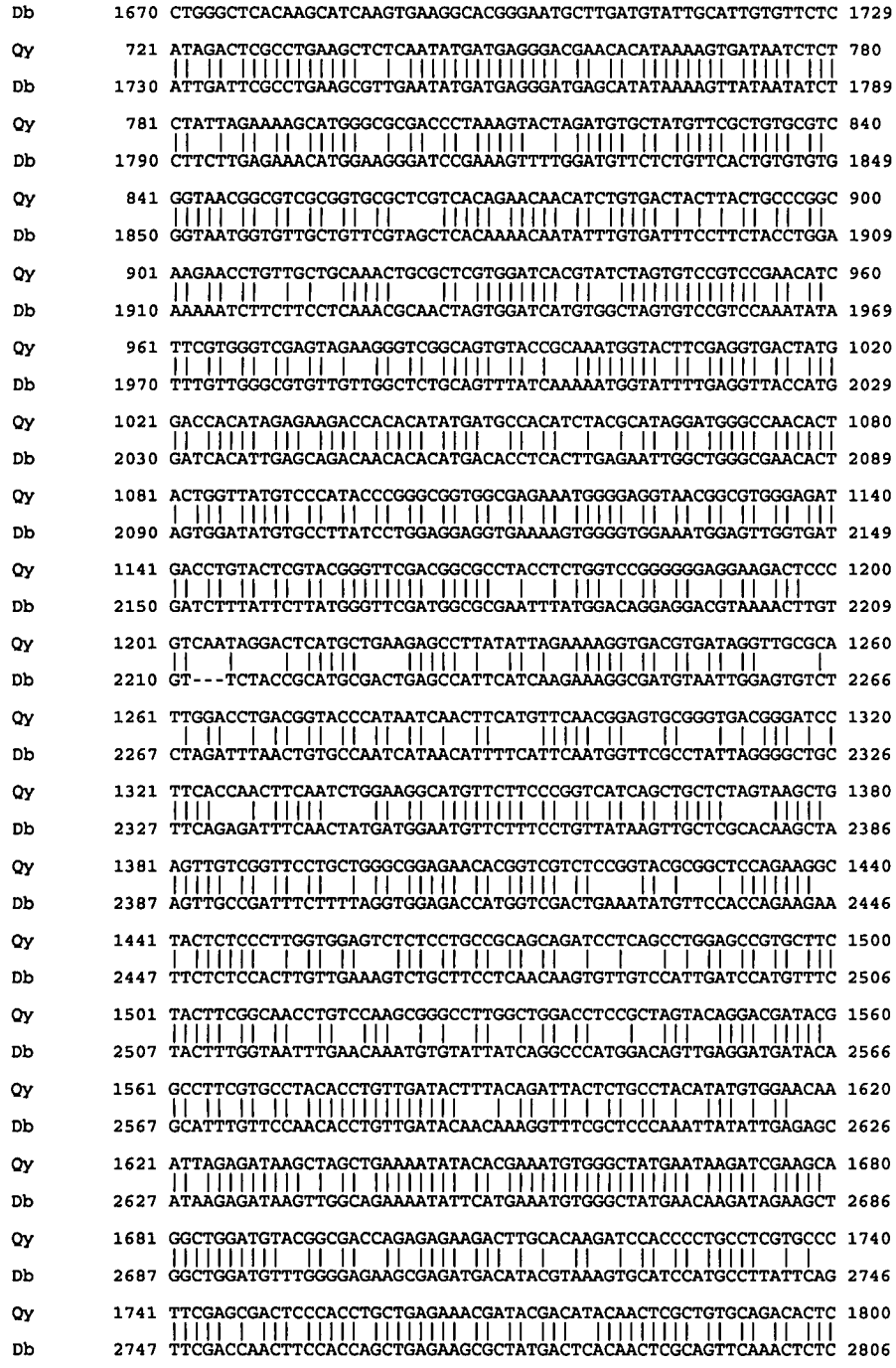
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Db 1670 CTGGGCTCACAAGCATCAAGTGAAGGCACGGGAATGCTTGATGTATTGCATTGTGTTCTC 1729
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Db 2507 TACTTTGGTAATTTGAACAAATGTGTATTATCAGGCCCATGGACAGTTGAGGATGATACA 2566
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Qy 1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
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Qy 2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
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Qy 2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340
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Qy 2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400
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Db 3407 TTCAACGAGGAAAAAGTGTACTTGGGAACAGGCGAGTCGTTTGGTCGCCAGTGGCAGGTT 3466
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Db 3467 GGAGATGTGGTTGGAGTATTTCTTGATCTATTGGACCATACCATGAGTTTCTCTTTGAAT 3526
Qy 2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 2580
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Db 3707 TGTGTCAATATGAACAGAGCGGTAACGTATTGGTACACCAAGGACCACCCAATTTTTGAG 3766
Qy 2761 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 2820
Db 3767 AATACTGAAGATTATGCCGACTCACGAATTGATGTTACAAGAATTCCAGCTGGTTCGGAT 3826
Qy 2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880
Db 3827 ACTCCACCTTGCCTCAAAATAAGTCACAACCTATTCGAGTCAATGGAAAAAGCCAATTGG 3886

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Qy       2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940
Db       3887 GAATTCCTCAGACTCTCACTCCCAGTTATTTGCCACTCATCATTTATCGAAGAGAGTGAA 3946

Qy       2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAG 2998
Db       3947 AAATTGAAACGTTGGCAGGAGATAAGAATCCGTCAGCATAGACTGTTAGTCGAGGCTG 4004
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RESULT 9
US-10-668-767-5
; Sequence 5, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15315
; TYPE: DNA
; ORGANISM: Periplaneta americana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15312)
; OTHER INFORMATION:
US-10-668-767-5

Query Match 44.5%; Score 1335.4; DB 7; Length 15315;
Best Local Similarity 66.2%; Pred. No. 0;
Matches 1988; Conservative 0; Mismatches 1001; Indels 12; Gaps 4;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
Db       1000 GTAATTGGAGCACCTATTATTAAGTATGGTGACAGTACGGTATTAGTACAACATTCTGAT 1059

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
Db       1060 ACAGGTTTATGGTTAACATACAAGTCTTATGAAACAAAAAAAAAAGGCGTCGGTAAAGTA 1119

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
Db       1120 GAAGAAAAACAAGCAGTATTACATGAAGAAGGTAAAATGGACGATGGGTTAGACTTTAGT 1179

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
Db       1180 AGGAGTCAAGAAGAAGAGTCTAGAACTGCTAGAGTGATACGTAAATGCTCCTCATTATTC 1239

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
Db       1240 ACACAGTTTATTTCCGGACTGGAAAATTTACAAAGTAACAGACGTTCGTCATTATTTTGT 1299

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
Db       1300 TCATTCGTTAATCTAAATGAAATGGTCATGTGTCTAGAAGATTTAATAAATTATTTTGCT 1359

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
Db       1360 CAACCTGAAGAAGATATGGAACACGAAGAAAAACAAAATCGATTTAGAGCATTAAGAAAT 1419

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
Db       1420 AGACAAGATTTATTTCAAGAAGAAGGCATATTAAATCTGATTCTAGAAGCTATTGATAAA 1479

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
Db       1480 GTTAATATTATTACGTCACAAGGATTTATGGTCAGTT---TAGCTGGTGATGAGTCTGGA 1536

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
Db       1537 CAAAGTTGGGATGTGATTTCTGGTTATTTATACCAGTTGCTAGCTGCAATTATAAAGGGA 1596

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
Db       1597 AATCATACTAATTGTGCTCAATTTGCTAACACTAACCGATTAAATTGGTTATTTAGTCGA 1656

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
Db       1657 TTAGGATCTCAAGCATCCAGTGAGGGAACTGGTATGTTAGATGTACTTCACTGTGTTCTC 1716

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
Db       1717 ATTGATTCTCCGGAAGCTTTAAATATGATGAAAGATGAACATATAAAAGTAATAATATCT 1776

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
Db       1777 CTTTTGGAAAAACATGGTCGTGATCCAAAAGTGTTAGACGTTTTATGTTCCCTATGCGTT 1836

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
Db       1837 GGTAACGGTGTGGCCGTAAGAAGTTCACAAAATAATATATGTGATTTCTTATTACCAGGA 1896

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
Db       1897 AAAAATTTACTTCTTCAGACCTTACTTGTTGATCATGTAGCCAGTGTACGTCCCAATATT 1956

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
Db       1957 TTTGTTGGTCATGTTAGTGGATCTGCCGTTTATCGAAAATGGTATTATGAAGTAGCAATA 2016

Qy       1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
Db       2017 GATCATGTAGAACAAACTACACATTTAAATCCACACATTCGAATTGGATGGGCAAATACT 2076

Qy       1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
Db       2077 GCAGGTTATGTTCCGTATCCTGGTGGCGGAGAAAAATGGGGTGGAAATGGCGTTGGGGAT 2136

Qy       1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
Db       2137 GATTTATATTCTTTCGGATTTGATGGGTCATATTTATGGACAGGAGGACGTAAATCAGAA 2196

Qy       1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
Db       2197 GT---GATGCCTGGTTCAGAAATTTCTAACATTAAAAAAGGTGATGTAATCGGTTGTGCA 2253

Qy       1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
Db       2254 TTAGATTTAACTATTCCAATTATAACTTTTACATTGAACGGTCAATTGGTCCAAGGAGCC 2313

Qy       1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
Db       2314 TTCAGAGACTTCAATTTAGATGGGATGTTTTTCCCAGTAATTAGTTGTTCATCAAAAGTC 2373

Qy       1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
Db       2374 GGCTGTCGTTTTTTATTGGGCGGAGATCATGGTCGATTGAAGTTTACTCCTCCAGACGAA 2433

Qy       1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
Db       2434 TTTTCTCCTCTATTTGAAAGTTTATTACCTCAACAAATTTTGACAATCGATCCGTGCTTC 2493

Qy       1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
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Db       2494 TATTTTGGAAATCTTAGTAAATGCGTACTCACGGGACCGTGGTATGTTGAAGATGATACA 2553

Qy       1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620

Db       2554 GCATTTGTTCCAAATCCAGTTGATACATCAATGGTCACTTTACCTAGTTACATAGAAAAT 2613

Qy       1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680

Db       2614 ATTAAAGATAAATTAGCAGAGAATATTCATGAAATGTGGGCAATGAATAAAATTGAAGCT 2673

Qy       1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740

Db       2674 GGTTGGCAATATGGTGATAAAAGAAATGATACTAGGAAATATCATCCATGTTTAATACAG 2733

Qy       1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800

Db       2734 TTTGACAAGTTGCCTCCAGCCGAGAAGCGTTATGATTCTCAATTAGCTGTGCAAACGCTT 2793

Qy       1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860

Db       2794 AAAACGGTTATTGCGTTGGGATATCACATATCCATCGATAATCCACCGTCCCGCATTAAA 2853

Qy       1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920

Db       2854 ACGGTACGGTTGCCCAACGAACCATTTATGCAATCCAATGGTTACAAACCAGCACCACTA 2913

Qy       1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980

Db       2914 GATTTATCTGCAATAAATTTGTCAGGGAAAATGGAAGAATTAATTGACCAGTTAGCTGAG 2973

Qy       1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040

Db       2974 AATACACATAATTTATGGGCAAAAGAAAGAATACAACAAGGATGGACGTATGGTTTAAAT 3033

Qy       2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100

Db       3034 GAAGAATTACAAATGTTACGCAGTCCTCATTTAGTACCGTACAGCAAAGTAGATGACGCT 3093

Qy       2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160

Db       3094 ATTAAAAAAGCTAATAGAGATACAGCAAGTGAAACAGTCCGCACTTTATTAGTATATGGT 3153

Qy       2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAG---CACTCTTGTTGGAAGCGTCA 2217

Db       3154 TACAACTTAGACCCACCGACTGGAGAAACAAACGAAGCGACACTCCTAACAGACGAAAAC 3213

Qy       2218 AAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCT 2277

Db       3214 ACTAATAGATACTTGACGTTCAGAACATATCGTGCTGAAAAAACATATGCTGTTGCAAGT 3273

Qy       2278 GGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCT 2337

Db       3274 GGAAAATGGTATTTCGAGTTTGAGATATTGACAAACGGGCCCATGCGAGTTGGATGGGCC 3333

Qy       2338 CACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGAT 2397

Db       3334 AGGTTTACATGTTCTCCGGGTTATCAAATCGGTAGTGACGAAAATTCTTGGGCATTTGAT 3393

Qy       2398 GGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCT 2457

Db       3394 GGTTATAACGAAGAAAAAATTTATATGGGCACAGCCGAATCATTTGGGAGGCAGTGGCAA 3453

Qy       2458 GTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTC 2517

Db       3454 GTTGGAGATGTCGTGGGAGTGTTTTTAGACCTAATGGATCATACAATAAGTTTTTCGTTG 3513

Qy       2518 AATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGT 2577

Db       3514 AATGGAGAATTACTAATGGATACATTGGGAGGAGAAACTACGTTTTCTGAAGTTCAAGGA 3573

Qy       2578 GACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGC 2637

Db       3574 GAAGGATTTGTACCTGCATTTACTCTGGGACTAGGACAAAAAGCAAAATTAACTTTTGGT 3633

Qy       2638 CAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCA 2697

Db       3634 CAAGACGTAAACTCATTGAAATACTTCACGACTTGTGGTCTTCAAGAAGGATATGAACCA 3693

Qy       2698 TTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTC 2757

Db       3694 TTTTGCGTAAACATGAAGAGACCAGTAACATATTGGTATACTAAGGATCAACCAATATTT 3753

Qy       2758 GAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCA 2817

Db       3754 GAAAATACTGATGA---CTTTTCGTCTGTAATTGATGTTACAAGAATTCCAGCTGGTTCA 3810

Qy       2818 GATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAAC 2877

Db       3811 GATACACCACCGTGTCTAAAAATAAGTCATAATACATTTGAAACCATGGAAAGAGCTAAT 3870

Qy       2878 TGGGAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCA 2937

Db       3871 TGGGAATTTTTACGGCTATCTTTGCCTGTCATATGTCTACCAAATTTTATTGATGAACAA 3930

Qy       2938 GAAAAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCA 2997

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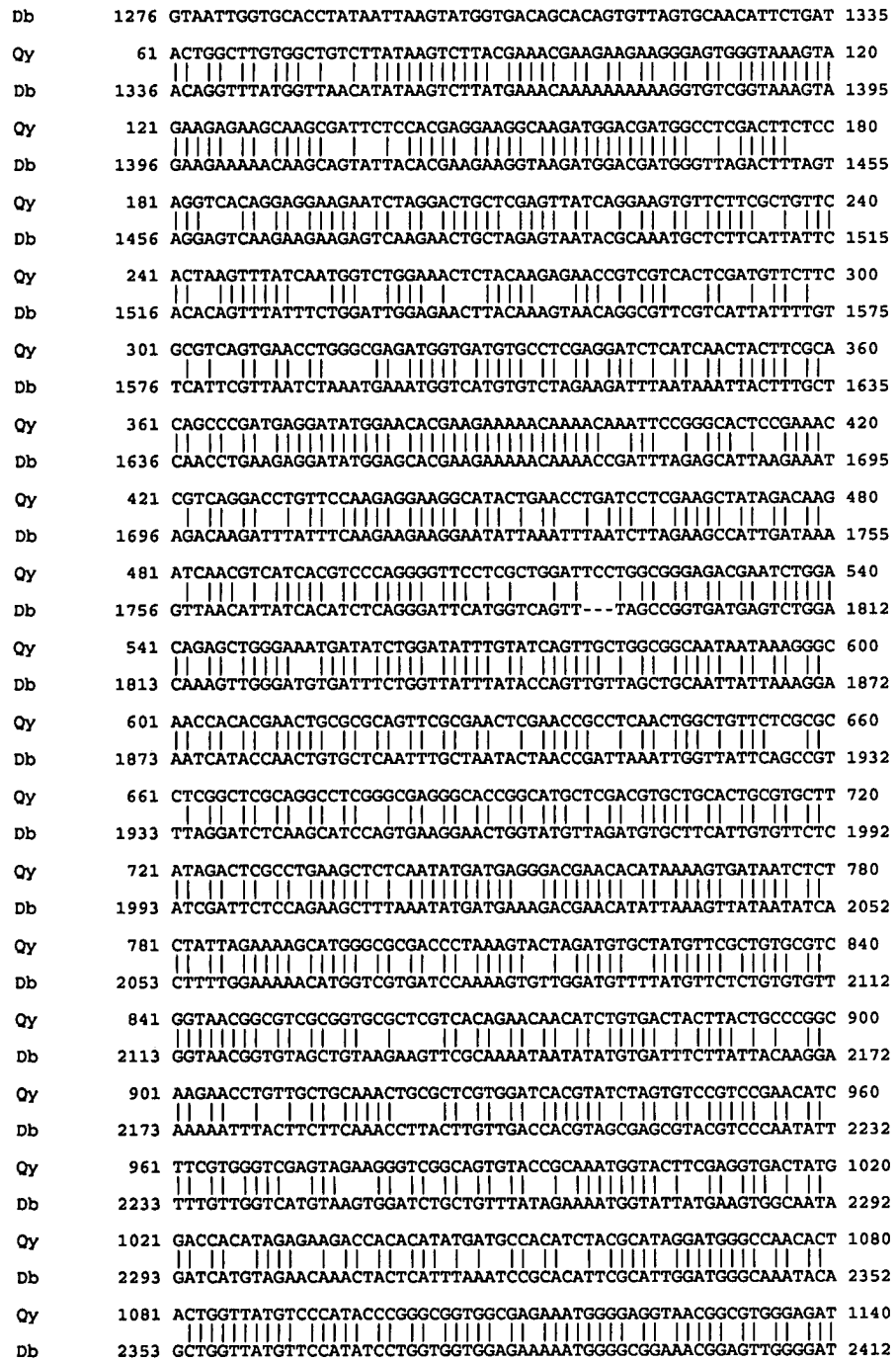
Qy       2998 G 2998

Db       3991 G 3991
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RESULT 10
US-10-668-767-3
; Sequence 3, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 15845
; TYPE: DNA
; ORGANISM: Myzus persicae
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (36)..(37)
; OTHER INFORMATION: n = A, C, G, or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5807)
; OTHER INFORMATION: n = a or t
US-10-668-767-3

Query Match 44.0%; Score 1319; DB 7; Length 15845;
Best Local Similarity 66.0%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 1005; Indels 12; Gaps 4;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
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Db 1276 GTAATTGGTGCACCTATAATTAAGTATGGTGACAGCACAGTGTTAGTGCAACATTCTGAT 1335
Qy 61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
Db 1336 ACAGGTTTATGGTTAACATATAAGTCTTATGAAACAAAAAAAAAAGGTGTCGGTAAAGTA 1395
Qy 121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
Db 1396 GAAGAAAAACAAGCAGTATTACACGAAGAAGGTAAGATGGACGATGGGTTAGACTTTAGT 1455
Qy 181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
Db 1456 AGGAGTCAAGAAGAAGAGTCAAGAACTGCTAGAGTAATACGCAAATGCTCTTCATTATTC 1515
Qy 241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
Db 1516 ACACAGTTTATTTCTGGATTGGAGAACTTACAAAGTAACAGGCGTTCGTCATTATTTTGT 1575
Qy 301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
Db 1576 TCATTCGTTAATCTAAATGAAATGGTCATGTGTCTAGAAGATTTAATAAATTACTTTGCT 1635
Qy 361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
Db 1636 CAACCTGAAGAGGATATGGAGCACGAAGAAAAACAAAACCGATTTAGAGCATTAAGAAAT 1695
Qy 421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
Db 1696 AGACAAGATTTATTTCAAGAAGAAGGAATATTAAATTTAATCTTAGAAGCCATTGATAAA 1755
Qy 481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
Db 1756 GTTAACATTATCACATCTCAGGGATTCATGGTCAGTT---TAGCCGGTGATGAGTCTGGA 1812
Qy 541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
Db 1813 CAAAGTTGGGATGTGATTTCTGGTTATTTATACCAGTTGTTAGCTGCAATTATTAAAGGA 1872
Qy 601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
Db 1873 AATCATACCAACTGTGCTCAATTTGCTAATACTAACCGATTAAATTGGTTATTCAGCCGT 1932
Qy 661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
Db 1933 TTAGGATCTCAAGCATCCAGTGAAGGAACTGGTATGTTAGATGTGCTTCATTGTGTTCTC 1992
Qy 721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
Db 1993 ATCGATTCTCCAGAAGCTTTAAATATGATGAAAGACGAACATATTAAAGTTATAATATCA 2052
Qy 781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
Db 2053 CTTTTGGAAAAACATGGTCGTGATCCAAAAGTGTTGGATGTTTTATGTTCTCTGTGTGTT 2112
Qy 841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
Db 2113 GGTAACGGTGTAGCTGTAAGAAGTTCGCAAAATAATATATGTGATTTCTTATTACAAGGA 2172
Qy 901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
Db 2173 AAAAATTTACTTCTTCAAACCTTACTTGTTGACCACGTAGCGAGCGTACGTCCCAATATT 2232
Qy 961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
Db 2233 TTTGTTGGTCATGTAAGTGGATCTGCTGTTTATAGAAAATGGTATTATGAAGTGGCAATA 2292
Qy 1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
Db 2293 GATCATGTAGAACAAACTACTCATTTAAATCCGCACATTCGCATTGGATGGGCAAATACA 2352
Qy 1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
Db 2353 GCTGGTTATGTTCCATATCCTGGTGGTGGAGAAAAATGGGGCGGAAACGGAGTTGGGGAT 2412
Qy 1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
Db 2413 AATTTATACTCTTTTGGATTTGATGGATCATATTTATGGACAGGAGGACGTAAGTCAGGA 2472
Qy 1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
Db 2473 GT---GATGCCCGGAACACAAATTTCTAACATTAAAAAAAGTGATGTGATTGGCTGTGCA 2529
Qy 1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
Db 2530 TTAGATTTAACTATTCCAATTATAACTTTTACATTGAACGGTCAACTTGTCCAAGGTGCC 2589
Qy 1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
Db 2590 TTTAGAGACTTCAATTTAGATGGGATGTTTTTCCCAGTAATTAGTTGTTCGTCAAAAGTC 2649
Qy 1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
Db 2650 AGTTGTCGTTTTTTATTGGGTGGAGATCACGGTCGATTGAAGTTTACTCCTCCAGACGAA 2709
Qy 1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
Db 2710 TTTTCTCCCCTATTTGAAACCTTATTACCTCAACAAATTTTGACAATTGATCCCTGTTTT 2769
Qy 1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
Db 2770 TATTTTGGGAACCTAAATAAATGCGTGCTCACGGGTCCATGGTATGTTGAAGACGGTACA 2829
Qy 1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
Db 2830 GCATTTGTTCCAAATCCAGTTGATACTTCGATGGTCACCTTGCCTAGTTACATAGAAAAT 2889
Qy 1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
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Db 2950 GGTTGGCAATATGGCGATAAAAGAAATGATACTAGGAAGTATCATCCATGTTTAATACAG 3009
Qy 1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
Db 3010 TTTGACAAGTTGCCTCCAGCCGAGAAGCGTTATGATTCTCAATTAGCTGTGCAAACGCTT 3069
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Db 3070 AAAACGGTTATTGCGTTAGGTTATCACATATCTATTGATAATCCACCGTCCCGCATTAAA 3129
Qy 1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
Db 3130 ACAGTCCGGCTGCCCAACGAACCATTTATGCAATCCAATGGATATAAACCAGCACCACTA 3189
Qy 1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
Db 3190 GATTTATCTGCTATCATTTTGTCAGGAAAAATGGAAGAACTAATTGATCAGTTAGCCGGG 3249
Qy 1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
Db 3250 AATACACATAATCTATGGGCAAAAGAAAGAATACAGCAAGGATGGACATATGGATTAAAT 3309
Qy 2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
Db 3310 GAAGAATTACAAATGTTGCGCAGTCCTCATTTAGTACCGTACAGCAAAGTAGACGACGCT 3369
Qy 2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160
Db 3370 ATTAAAAAAGCTAATAGAGATACAGCAAGCGAAACAGTCCGCACATTATTGGTATATGGT 3429
Qy 2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAG---CACTCTTGTTGGAAGCGTCA 2217
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Qy       2218 AAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCT 2277
Db       3490 TCTAATAGATATTTGACGTTCAGAACATATCGTGCGGAAAAAACGTATGCCGTTTCTAGT 3549

Qy       2278 GGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCT 2337
Db       3550 GGAAAATGGTACTTCGAATTTGAGATACTGACAAGTGGACCTATGCGGGTTGGATGGGCC 3609

Qy       2338 CACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGAT 2397
Db       3610 AGGTTCACATGTTCCCCGGGTTATCAAATCGGCAGTGATGAAAATTCTTGGGCATTTGAT 3669

Qy       2398 GGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCT 2457
Db       3670 GGTTATAACGAAGAAAAAATTTACATGGGGACAGCCGAATCATTTGGTAGACAGTGGCAA 3729

Qy       2458 GTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTC 2517
Db       3730 GTTGGAGATGTCGTGGGAGTGTTTTTAGATTTAATGGACCATACAATAAGCTTTTCGATG 3789

Qy       2518 AATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGT 2577
Db       3790 AACGGAGAATTACTAATGGATACGTTAGGAGGGGAAACAACATTCTCTGAAGTCCAAGGA 3849

Qy       2578 GACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGC 2637
Db       3850 GAAGGATTTGTACCTGCGTTTACGCTGGGACTAGGACAAAAAGCAAAATTGACATTTGGT 3909

Qy       2638 CAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCA 2697
Db       3910 CAAGACGTTAACTCATTGAAATACTTCACGACTTGTGGACTTCAAGAAGGATATGAACCA 3969

Qy       2698 TTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTC 2757
Db       3970 TTCTGTGTAAATATGAAGAGGCCTGTTGCTTATTGGTATACTAAGGATCAACCAATTTTT 4029

Qy       2758 GAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCA 2817
Db       4030 GAGAATACTGACGA---TTTTTCGTCTGTTATTGATGTTACAAGAATACCAGCTGGTTCA 4086

Qy       2818 GATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAAC 2877
Db       4087 GATACACCACCTTGTCTAAAGATAAGTCATAATACATTTGAAACCATGGAAAAAGCCAAT 4146

Qy       2878 TGGGAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCA 2937
Db       4147 TGGGAATTTTTACGGCTATCATTACCTGTCATATGTCTACCAAGTTTTATTGGCGATCAA 4206

Qy       2938 GAAAAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATG 2988
Db       4207 GAAAAACAAAGGGGATGGCAAGAAATAAGAATTAGGCAACACAGGTTATTG 4257
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RESULT 11
US-11-097-143-22561/c
; Sequence 22561, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22561
;   LENGTH: 24236
;   TYPE: DNA
;   ORGANISM: DROSOPHILA
US-11-097-143-22561

  Query Match             38.3%;  Score 1150;  DB 10;  Length 24236;
  Best Local Similarity   67.7%;  Pred. No. 0;
  Matches 1749;  Conservative    0;  Mismatches  660;  Indels  173;  Gaps    3;
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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
Db      21229 GTGATCGGCTCGCCGATCATCAAGTACGGCGACACTACCGTCATCGTTCAGCACTGCGAG 21170

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
Db      21169 ACTAGCTTGTGGCTCAGCTACAAGAGTTATGAGACGAAAAAGAAGGGCGTAGGAAAGGTG 21110

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
Db      21109 GAGGAGAAGCAAGCGATCCTGCACGAGGAGGGCAAGATGGACGATTGTCTCGACTTCTCG 21050

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
Db      21049 CGCTCCCAGGAGGAGGAGTCCAAGACAGCTCGTGTCATCCGCAAGTGCAGCAGCCTCTTC 20990

Qy        241 ACTAAGTTTA---------------------------------------------------- 250
Db      20989 ACCCAGTTTATTACGTAGGTGACTTGGAAGTCCTTTACGAGTGATTTTCTTATCGTATTC 20930

Qy        251 ---------TCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTCG 301
Db      20929 ACACTCATTTCAGAGCCTTGGAAACACTGCAGTCAAATCGCCGACACTCCATTTTCTTCC 20870

Qy        302 CGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCAC 361
Db      20869 AAAAGGTCAACCTCAACGAGATGGTCATGTGCCTTGAGGACTTGATTAACTACTTTTCGC 20810

Qy        362 AGCCCGATGAGGATATG---------------------------------------------- 378
Db      20809 AACCCGAAGACGATATGGGTAAGGTCATTCAAAATATGACCCTAAGATGTTCAATAAAAT 20750

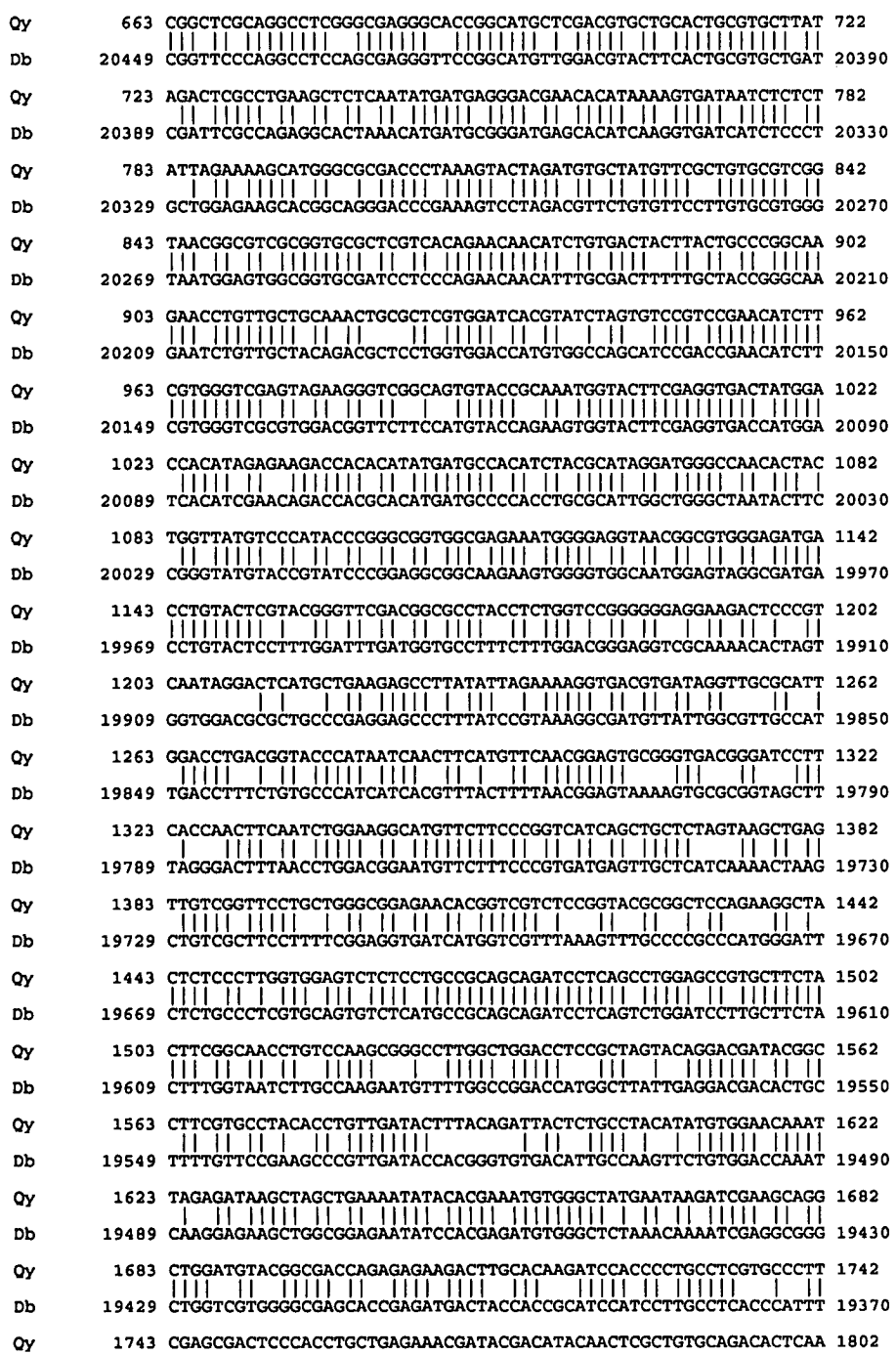
Qy        379 ---------------GAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAACCG 422
Db      20749 CTATAACTAATTTTCAGAGCACGAGGAGAAACAGAACCGATTCCGTGCCCTGCGCAACCG 20690

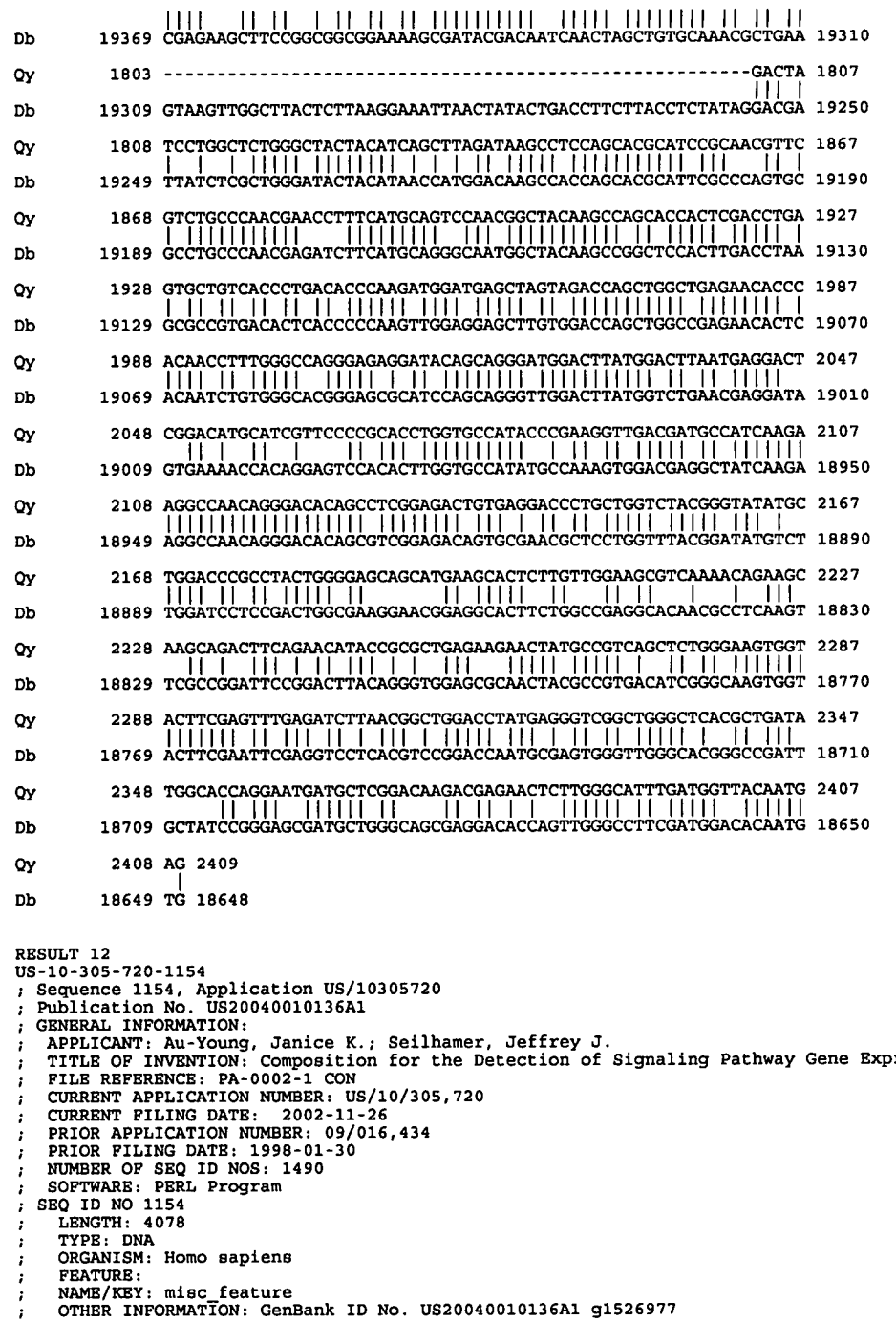
Qy        423 TCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGAT 482
Db      20689 ACAGGATCTGTTCCAGGAGGAGGGCGTGCTCAATCTGATCCTGGAGGCCATTGACAAGAT 20630

Qy        483 CAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGACA 542
Db      20629 CAACATAATCACCTCGCAGGGCTTCCTAGCCAGCTTCCTGGCCGGCGACGAGACCGGCCA 20570

Qy        543 GAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGCAA 602
Db      20569 GAGCTGGGATCTCATCTCCACCTATTTGTACCAACTCTTGGCCGCCATCATCAAGGGCAA 20510

Qy        603 CCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGCCT 662
Db      20509 CCACACGAACTGCGCCCAGTTCGCGAACAGTAACCGACTCAACTGGCTATTCTCCCGCCT 20450
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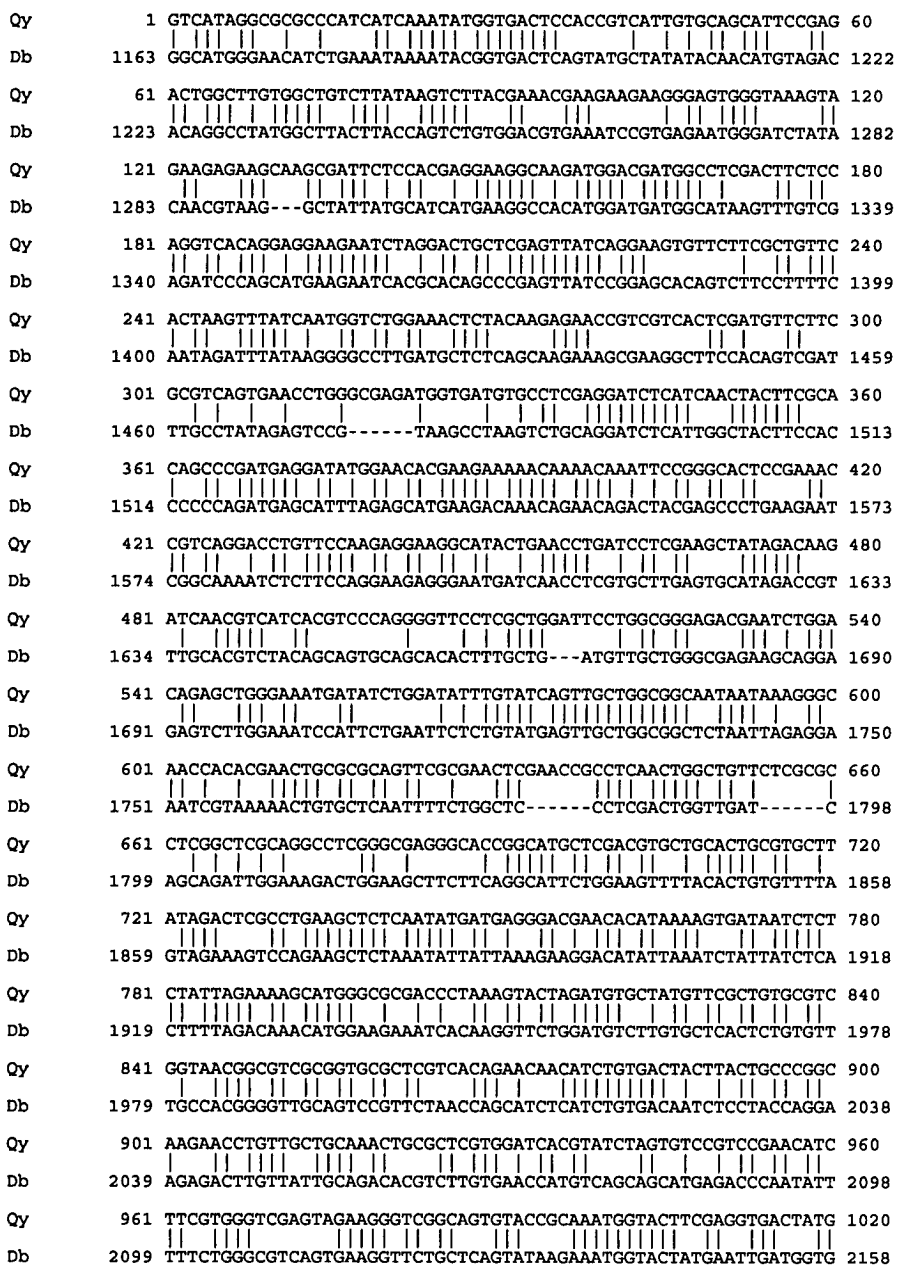


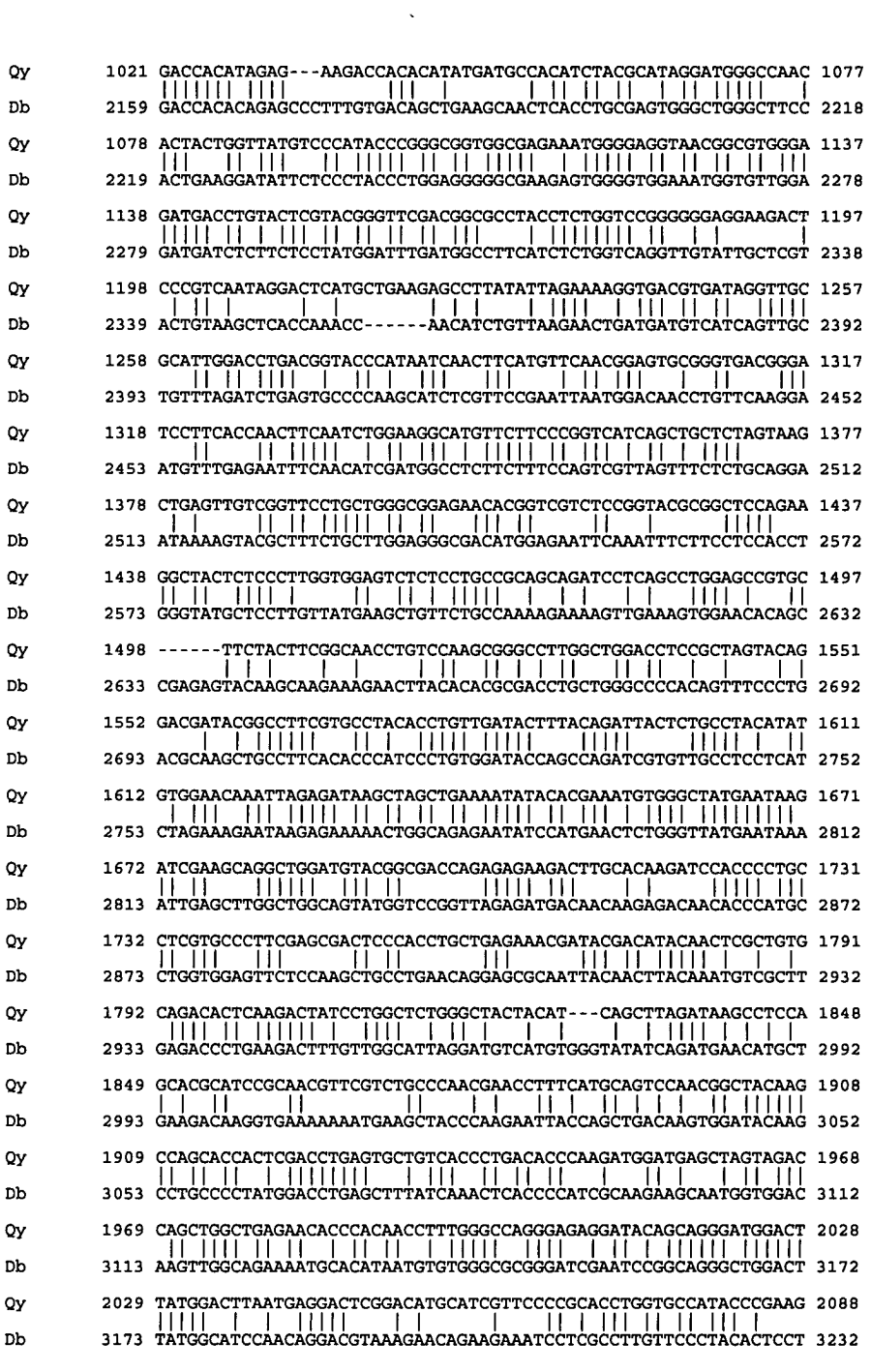


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RESULT 12
US-10-305-720-1154
; Sequence 1154, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
;  APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
;  TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Express
;  FILE REFERENCE: PA-0002-1 CON
;  CURRENT APPLICATION NUMBER: US/10/305,720
;  CURRENT FILING DATE:  2002-11-26
;  PRIOR APPLICATION NUMBER: 09/016,434
;  PRIOR FILING DATE: 1998-01-30
;  NUMBER OF SEQ ID NOS: 1490
;  SOFTWARE: PERL Program
; SEQ ID NO 1154
;   LENGTH: 4078
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GenBank ID No. US20040010136A1 g1526977
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US-10-305-720-1154

Query Match 22.3%; Score 668; DB 6; Length 4078;
Best Local Similarity 55.4%; Pred. No. 1.6e-205;
Matches 1590; Conservative 0; Mismatches 1225; Indels 57; Gaps 13;





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Qy       2089 GTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTG 2148
Db       3233 CTGGATGACCGAACCAAGAAATCCAACAAGGACAGCCTCCGCGAGGCTGTGCGCACGCTG 3292

Qy       2149 CTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTG 2208
Db       3293 CTGGGGTACGGCTACAACTTGGAAGCACC------AGATCAAGATCATGCAGCCAGAGCC 3346

Qy       2209 GAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCC 2268
Db       3347 GAAGTGTGCAGCGGCACCGGGGAAAGGTTCCGAATCTTCCGTGCCGAGAAGACCTATGCA 3406

Qy       2269 GTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTC 2328
Db       3407 GTGAAGGCCGGACGGTGGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGGTT 3466

Qy       2329 GGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGG 2388
Db       3467 GGTTGGAGTCGTCCTGGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTGCCTTT 3526

Qy       2389 GCATTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAG 2448
Db       3527 GCCTTTGATGGCTTCAAGGCCCAGCGGTGGCATCAGGG---CAATGAACACTATGGGCGC 3583

Qy       2449 CAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGT 2508
Db       3584 TCTTGGCAAGCAGGCGATGTCGTGGGGTGTATGGTTGACATGAACGAACACACCATGATG 3643

Qy       2509 TTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGAT 2568
Db       3644 TTCACACTGAATGGTGAAATCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTCAAGGAC 3703

Qy       2569 GTCCAGGGTGACAA---CTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGG 2625
Db       3704 TTTGATGTTGGCGATGGATTCATACCTGTGTGTAGCCTTGGAGTGGCTCAAGTGGGTAGG 3763

Qy       2626 TTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAG 2685
Db       3764 ATGAACTTTGGAAAGGATGTCAGCACCTTGAAATATTTCACCATCTGTGGCTTACAAGAG 3823

Qy       2686 GGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGAC 2745
Db       3824 GGCTATGAACCATTTGCCGTTAATACAAACAGGGATATTACCATGTGGCTGAGCAAGAGG 3883

Qy       2746 CAGCCGATCTTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATA 2805
Db       3884 CTTCCTCAGTT---TCTTCAAGTTCCATCAAACCATGAACATATAGAGGTGACCAGAATA 3940

Qy       2806 CCAGCTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCG 2857
Db       3941 GACGGCACCATAGACAGTTCCCCATGTTTAAAGGTCACTCAGAAGTCTTTTG 3992
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RESULT 13
US-10-276-774-552
; Sequence 552, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang, Y, Tom et al
;  TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-030
;  CURRENT APPLICATION NUMBER: US/10/276,774
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 2700
;  SOFTWARE: Custom
; SEQ ID NO 552
;   LENGTH: 14302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-276-774-552

  Query Match            22.3%;  Score 668;  DB 7;  Length 14302;
  Best Local Similarity  55.4%;  Pred. No. 3.4e-205;
  Matches 1590;  Conservative    0;  Mismatches 1225;  Indels   57;  Gaps   13;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
Db       1163 GGCATGGGAACATCTGAAATAAAATACGGTGACTCAGTATGCTATATACAACATGTAGAC 1222

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
Db       1223 ACAGGCCTATGGCTTACTTACCAGTCTGTGGACGTGAAATCCGTGAGAATGGGATCTATA 1282

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
Db       1283 CAACGTAAG---GCTATTATGCATCATGAAGGCCACATGGATGATGGCATAAGTTTGTCG 1339

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
Db       1340 AGATCCCAGCATGAAGAATCACGCACAGCCCGAGTTATCCGGAGCACAGTCTTCCTTTTC 1399

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
Db       1400 AATAGATTTATAAGGGGCCTTGATGCTCTCAGCAAGAAAGCGAAGGCTTCCACAGTCGAT 1459

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
Db       1460 TTGCCTATAGAGTCCG------TAAGCCTAAGTCTGCAGGATCTCATTGGCTACTTCCAC 1513

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
Db       1514 CCCCCAGATGAGCATTTAGAGCATGAAGACAAACAGAACAGACTACGAGCCCTGAAGAAT 1573

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
Db       1574 CGGCAAAATCTCTTCCAGGAAGAGGGAATGATCAACCTCGTGCTTGAGTGCATAGACCGT 1633

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
Db       1634 TTGCACGTCTACAGCAGTGCAGCACACTTTGCTG---ATGTTGCTGGGCGAGAAGCAGGA 1690

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
Db       1691 GAGTCTTGGAAATCCATTCTGAATTCTCTGTATGAGTTGCTGGCGGCTCTAATTAGAGGA 1750

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
Db       1751 AATCGTAAAAACTGTGCTCAATTTTCTGGCTC------CCTCGACTGGTTGAT------C 1798

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
Db       1799 AGCAGATTGGAAAGACTGGAAGCTTCTTCAGGCATTCTGGAAGTTTTACACTGTGTTTTA 1858

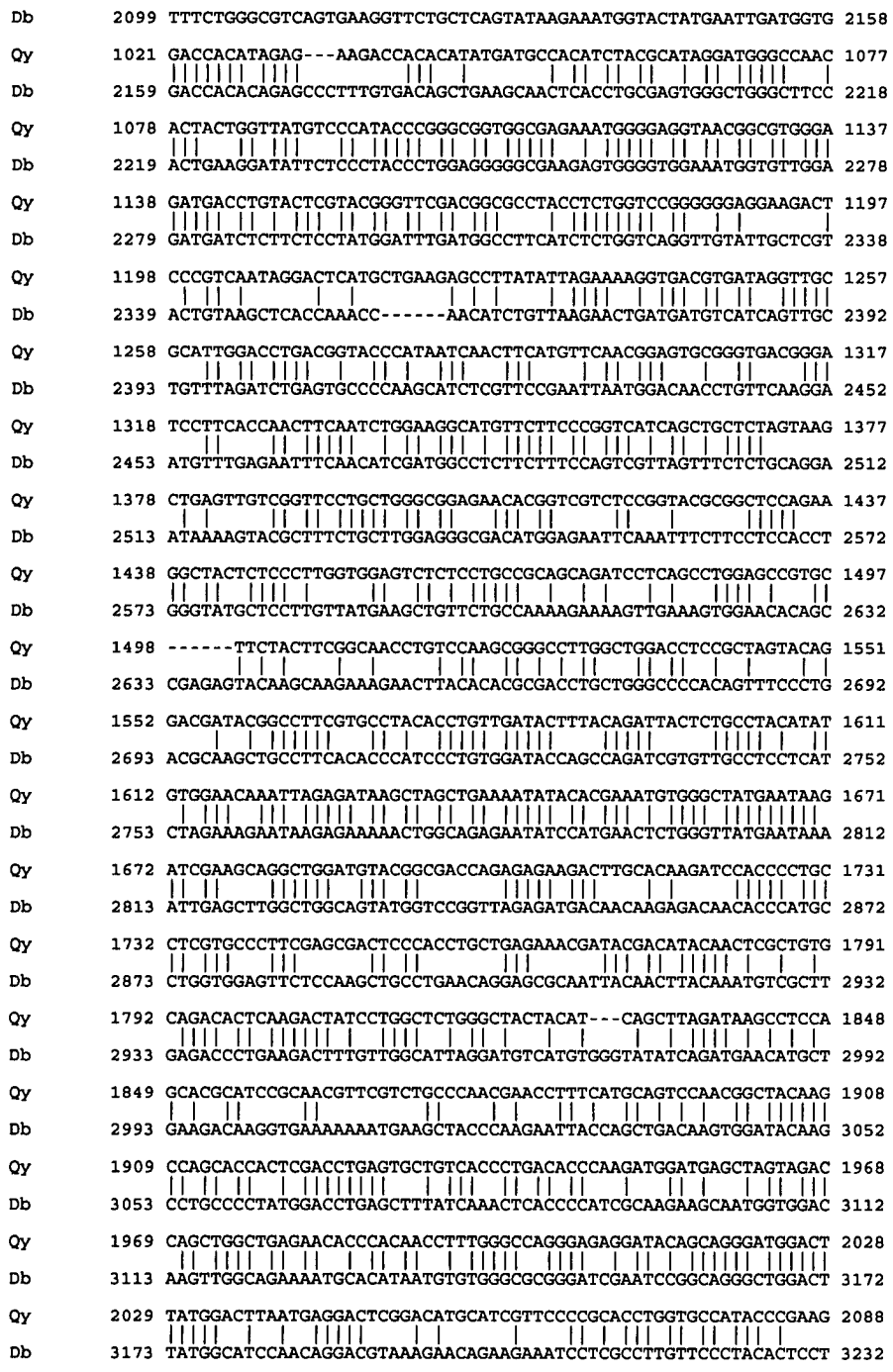
Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
Db       1859 GTAGAAAGTCCAGAAGCTCTAAATATTATTAAAGAAGGACATATTAAATCTATTATCTCA 1918

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
Db       1919 CTTTTAGACAAACATGGAAGAAATCACAAGGTTCTGGATGTCTTGTGCTCACTCTGTGTT 1978

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
Db       1979 TGCCACGGGGTTGCAGTCCGTTCTAACCAGCATCTCATCTGTGACAATCTCCTACCAGGA 2038

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
Db       2039 AGAGACTTGTTATTGCAGACACGTCTTGTGAACCATGTCAGCAGCATGAGACCCAATATT 2098

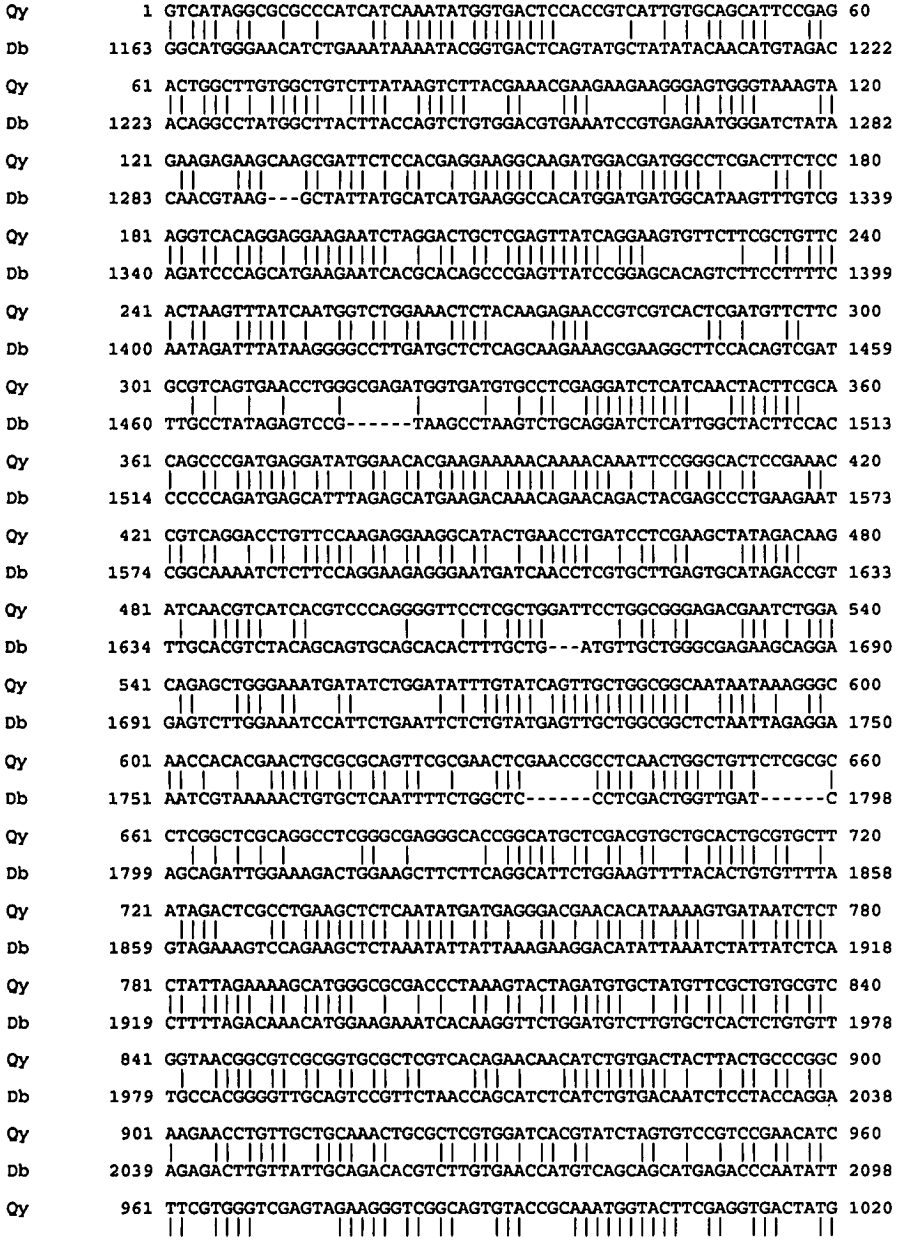
Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
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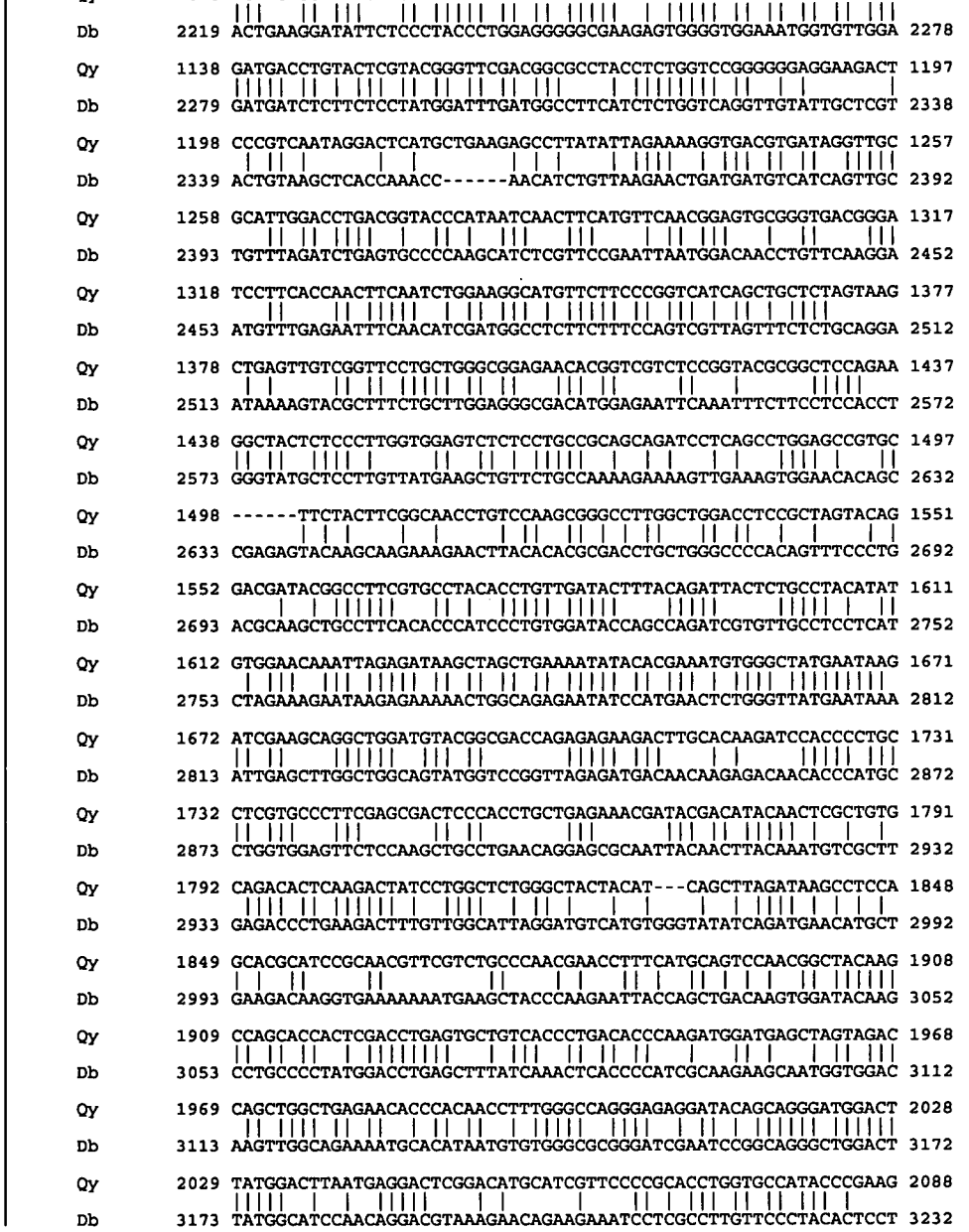



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RESULT 14
US-10-887-553A-490
; Sequence 490, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
;  APPLICANT: Garza, Dan
;  APPLICANT:  Li, Hao
;  TITLE OF INVENTION: Method to treat conditions associated
;  TITLE OF INVENTION:  with insulin signalling dysregulation
;  FILE REFERENCE: 4-33262
;  CURRENT APPLICATION NUMBER: US/10/887,553A
;  CURRENT FILING DATE:  2004-07-08
;  PRIOR APPLICATION NUMBER: 60/485,883
;  PRIOR FILING DATE: 2003-08-07
;  NUMBER OF SEQ ID NOS: 1208
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 490
;   LENGTH: 15731
;   TYPE: DNA
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; ORGANISM: human
US-10-887-553A-490

Query Match 22.3%; Score 668; DB 9; Length 15731;
Best Local Similarity 55.4%; Pred. No. 3.6e-205;
Matches 1590; Conservative 0; Mismatches 1225; Indels 57; Gaps 13;





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Qy       2089 GTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTG 2148
Db       3233 CTGGATGACCGAACCAAGAAATCCAACAAGGACAGCCTCCGCGAGGCTGTGCGCACGCTG 3292

Qy       2149 CTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTG 2208
Db       3293 CTGGGGTACGGCTACAACTTGGAAGCACC------AGATCAAGATCATGCAGCCAGAGCC 3346

Qy       2209 GAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCC 2268
Db       3347 GAAGTGTGCAGCGGCACCGGGGAAAGGTTCCGAATCTTCCGTGCCGAGAAGACCTATGCA 3406

Qy       2269 GTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTC 2328
Db       3407 GTGAAGGCCGGACGGTGGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGGTT 3466

Qy       2329 GGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGG 2388
Db       3467 GGTTGGAGTCGTCCTGGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTGCCTTT 3526

Qy       2389 GCATTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAG 2448
Db       3527 GCCTTTGATGGCTTCAAGGCCCAGCGGTGGCATCAGGG---CAATGAACACTATGGGCGC 3583

Qy       2449 CAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGT 2508
Db       3584 TCTTGGCAAGCAGGCGATGTCGTGGGGTGTATGGTTGACATGAACGAACACACCATGATG 3643

Qy       2509 TTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGAT 2568
Db       3644 TTCACACTGAATGGTGAAATCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTCAAGGAC 3703

Qy       2569 GTCCAGGGTGACAA---CTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGG 2625
Db       3704 TTTGATGTTGGCGATGGATTCATACCTGTGTGTAGCCTTGGAGTGGCTCAAGTGGGTAGG 3763

Qy       2626 TTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAG 2685
Db       3764 ATGAACTTTGGAAAGGATGTCAGCACCTTGAAATATTTCACCATCTGTGGCTTACAAGAG 3823

Qy       2686 GGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGAC 2745
Db       3824 GGCTATGAACCATTTGCCGTTAATACAAACAGGGATATTACCATGTGGCTGAGCAAGAGG 3883

Qy       2746 CAGCCGATCTTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATA 2805
Db       3884 CTTCCTCAGTT---TCTTCAAGTTCCATCAAACCATGAACATATAGAGGTGACCAGAATA 3940

Qy       2806 CCAGCTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCG 2857
Db       3941 GACGGCACCATAGACAGTTCCCCATGTTTAAAGGTCACTCAGAAGTCTTTTG 3992
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RESULT 15
US-10-276-774-500
; Sequence 500, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang, Y, Tom et al
;  TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-030
;  CURRENT APPLICATION NUMBER: US/10/276,774
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 2700
;  SOFTWARE: Custom
; SEQ ID NO 500
;   LENGTH: 15359
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-276-774-500

  Query Match             21.5%;  Score 646.6;  DB 7;  Length 15359;
  Best Local Similarity   55.3%;  Pred. No. 3.3e-198;
  Matches 1537;  Conservative    0;  Mismatches 1184;  Indels   60;  Gaps   12;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
Db       1124 GGCATGGGCCCCCCTGAGATCAAGTACGGGGAGTCACTGTGCTTCGTGCAGCATGTGGCC 1183

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
Db       1184 TCAGGACTGTGGCTCACCTATGCCGCTCCAGACCCCAAGGCCCTGCGGCTCGG---CGTG 1240

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
Db       1241 CTCAAGAAGAAGGCCATGCTGCACCAGGAGGGCCACATGGACGACGCACTGTCGCTGACC 1300

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
Db       1301 CGCTGCCAGCAGGAGGAGTCCCAGGCCGCCCGCATGATCCACAGCACCAATGGCCTATAC 1360

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
Db       1361 AACCAGTTCATCAAGAGCCTGGACAGCTTCAGCGGGAAGCCACGGGGCTCGGGGCCACCC 1420

Qy        301 G------CGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTAC 354
Db       1421 GCTGGCACGGCGCTGCCCATCGAGGGCGTTATCCTGAGCCTGCAGGACCTCATCATCTAC 1480

Qy        355 TTCGCACAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTC 414
Db       1481 TTCGAGCCTCCCTCCGAGGACTTGCAGCACGAGGAGAAGCAGAGCAAGCTGCGAAGCCTG 1540

Qy        415 CGAAACCGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATA 474
Db       1541 CGCAACCGCCAGAGCCTCTTCCAGGAGGAGGGGATGCTCTCCATGGTCCTGAATTGCATA 1600

Qy        475 GACAAGATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAA 534
Db       1601 GACCGCCTAAATGTCTACACCACTGCTGCCCACTTTGCTGAGT---TTGCAGGGGAGGAG 1657

Qy        535 TCTGGACAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATA 594
Db       1658 GCAGCCGAGTCCTGGAAAGAGATTGTGAATCTTCTCTATGAACTCCTAGCTTCTCTAATC 1717

Qy        595 AAGGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTC 654
Db       1718 CGTGGCAATCGTAGCAACTGTGCCCTCTT------CTCCACAAACTTGGACTGGCTGGTC 1771

Qy        655 TCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGC 714
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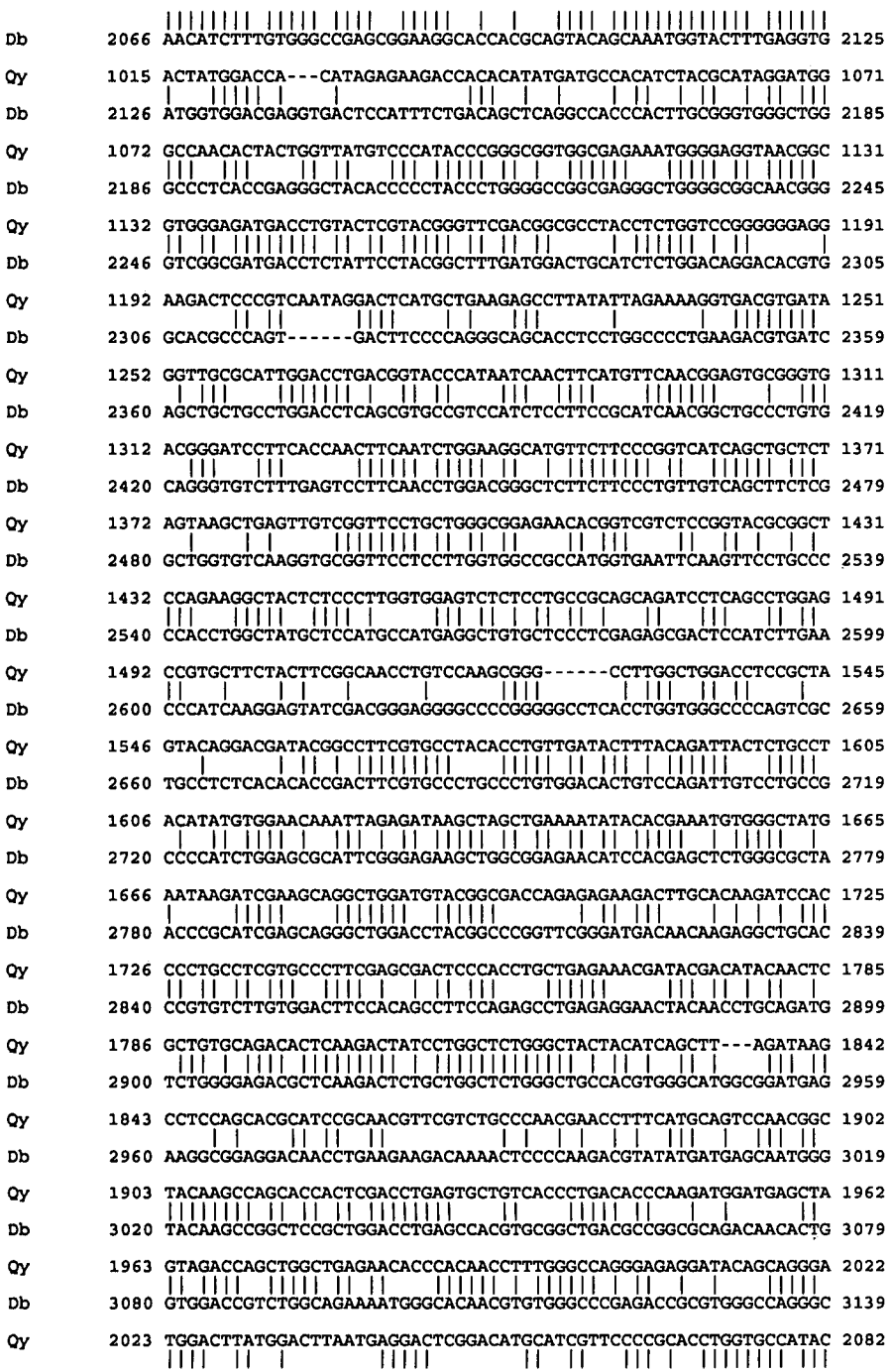
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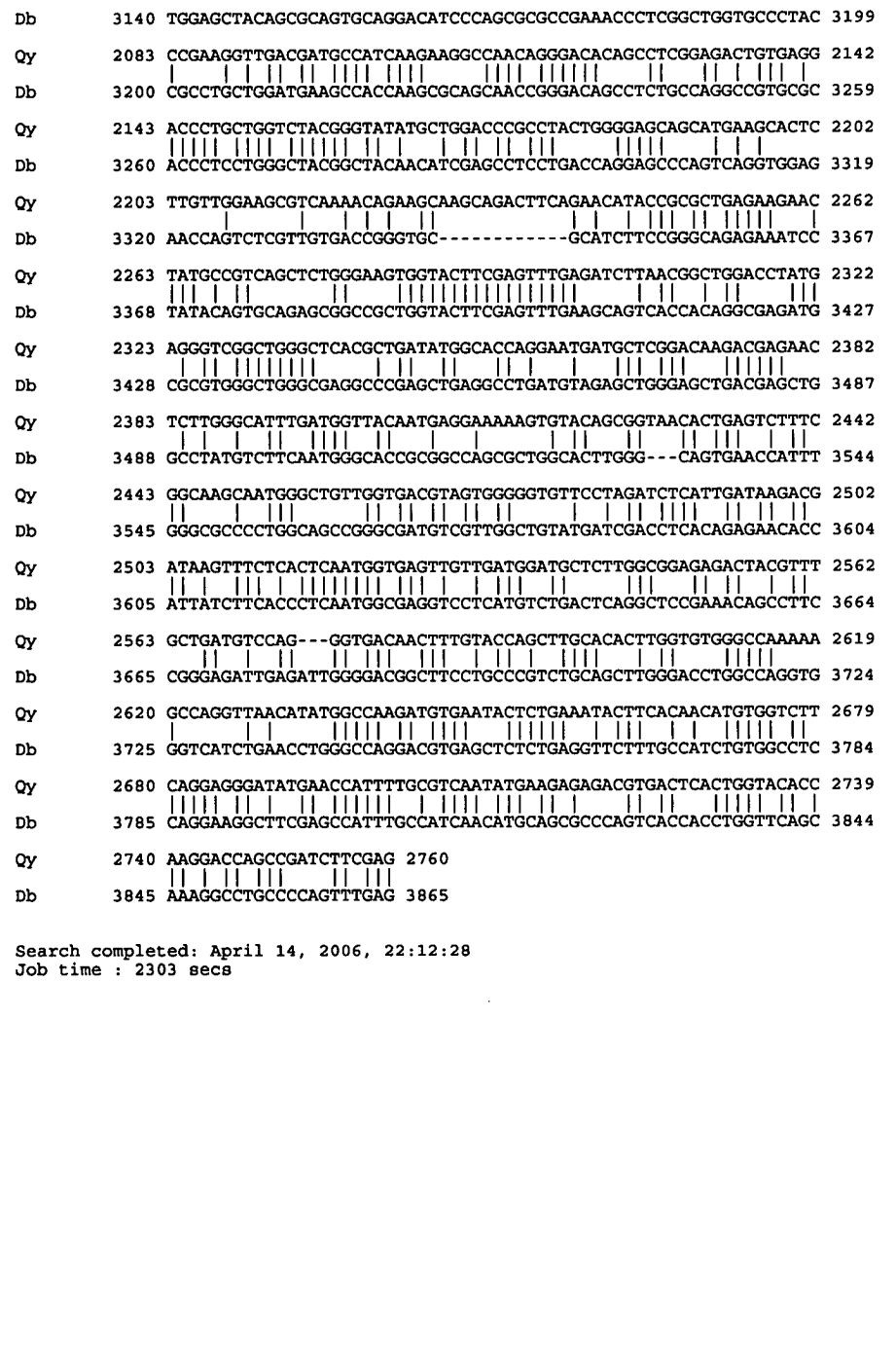
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Search completed: April 14, 2006, 22:12:28
Job time : 2303 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 13:55:27 ; Search time 14479.5 Seconds
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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	1150	38.3	24236	6	CQ594803	CQ594803 Sequence
3	1150	38.3	168601	2	AC007471	AC007471 Drosophil
4	1150	38.3	271696	2	AE003835	AE003835 Drosophil
5	1138	37.9	100002	14	AC020372	AC020372 Drosophil
6	1127	37.6	25680	2	DRORYRH	D17389 Drosophila
7	819.4	27.3	16879	2	AB051576	AB051576 Hemicentr
8	674.2	22.5	15253	4	SSCRCRNA	X62880 S.scrofa mR
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21	653	21.8	15361	4	OCRRR	X15750 Rabbit skel
22	653	21.8	15823	4	OCRYAN	X15209 O.cuniculus
23	651.6	21.7	16313	5	MNU97329	U97329 Makaira nig
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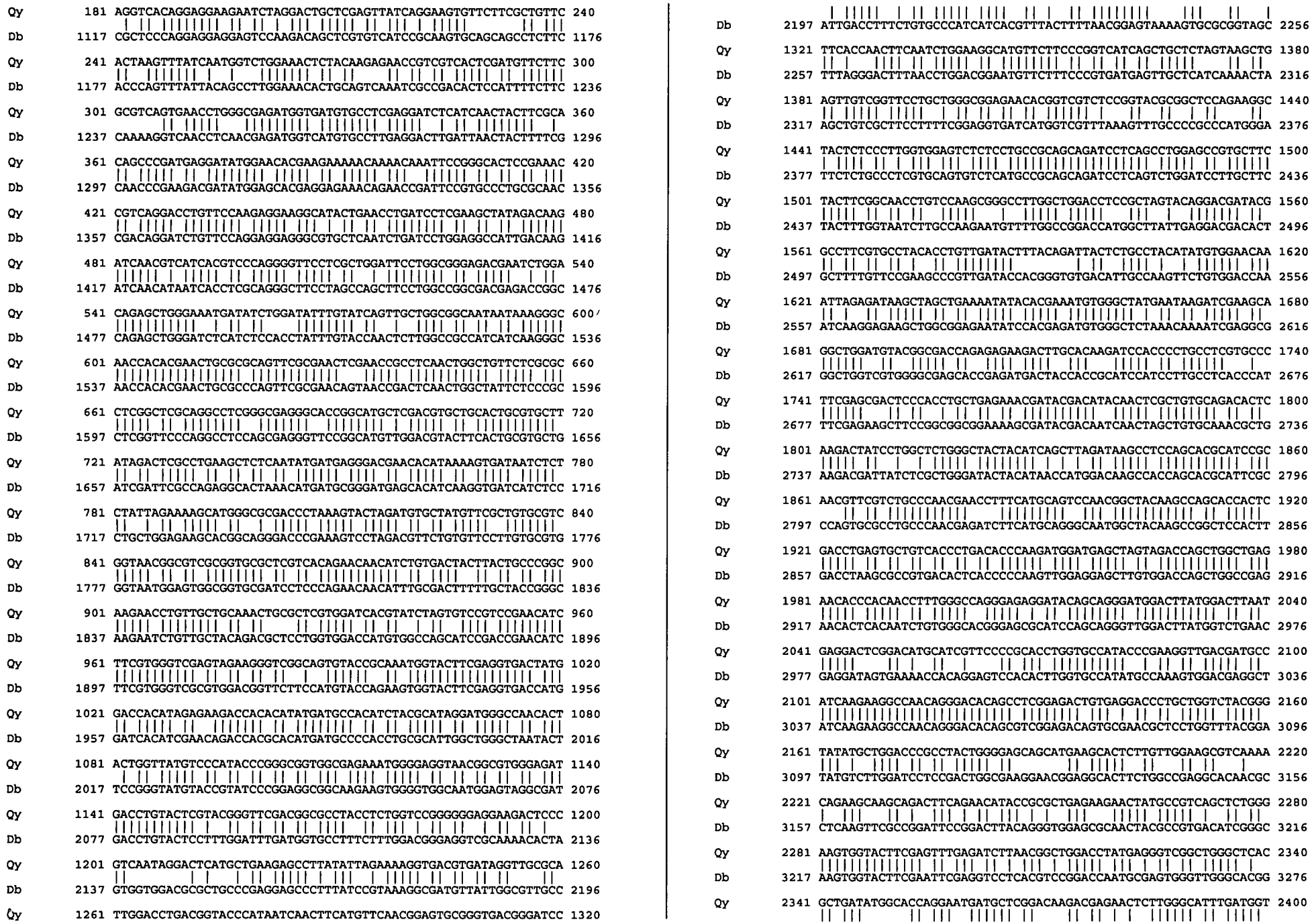
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DEFINITION Sequence 22562 from Patent WO0171042.
ACCESSION CQ594804
VERSION CQ594804.1 GI:41651849
KEYWORDS .
SOURCE Drosophila sp.
ORGANISM Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1
AUTHORS Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
TITLE Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof
JOURNAL Patent: WO 0171042-A 22562 27-SEP-2001;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
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ORIGIN

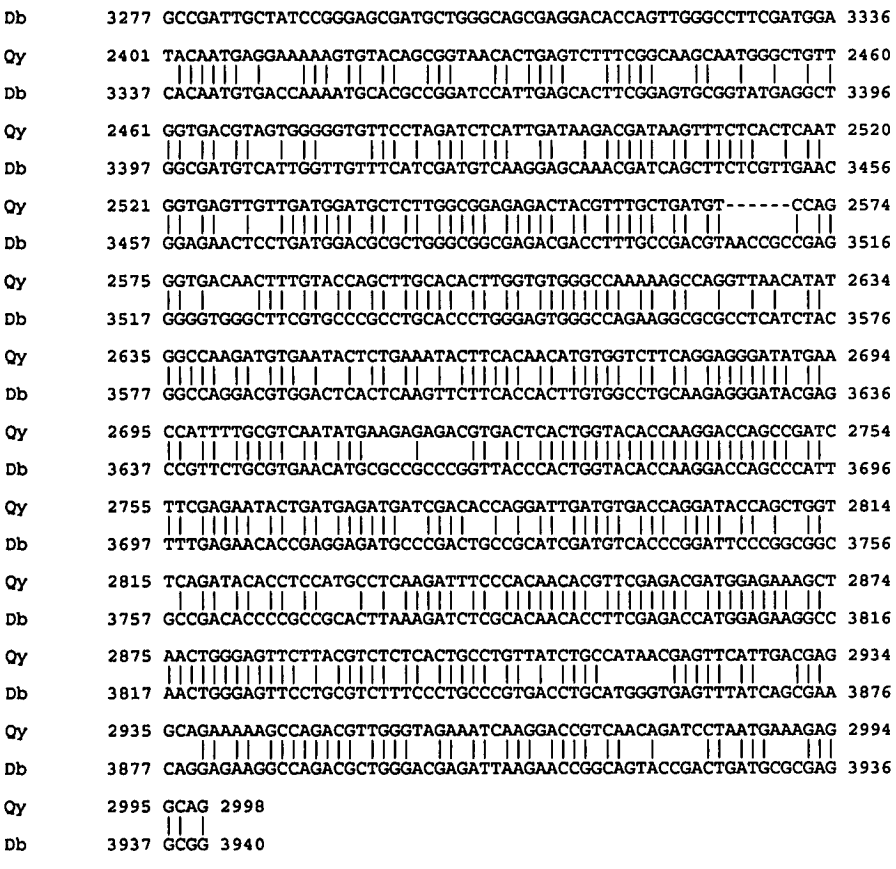
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Best Local Similarity 71.5%; Pred. No. 0;
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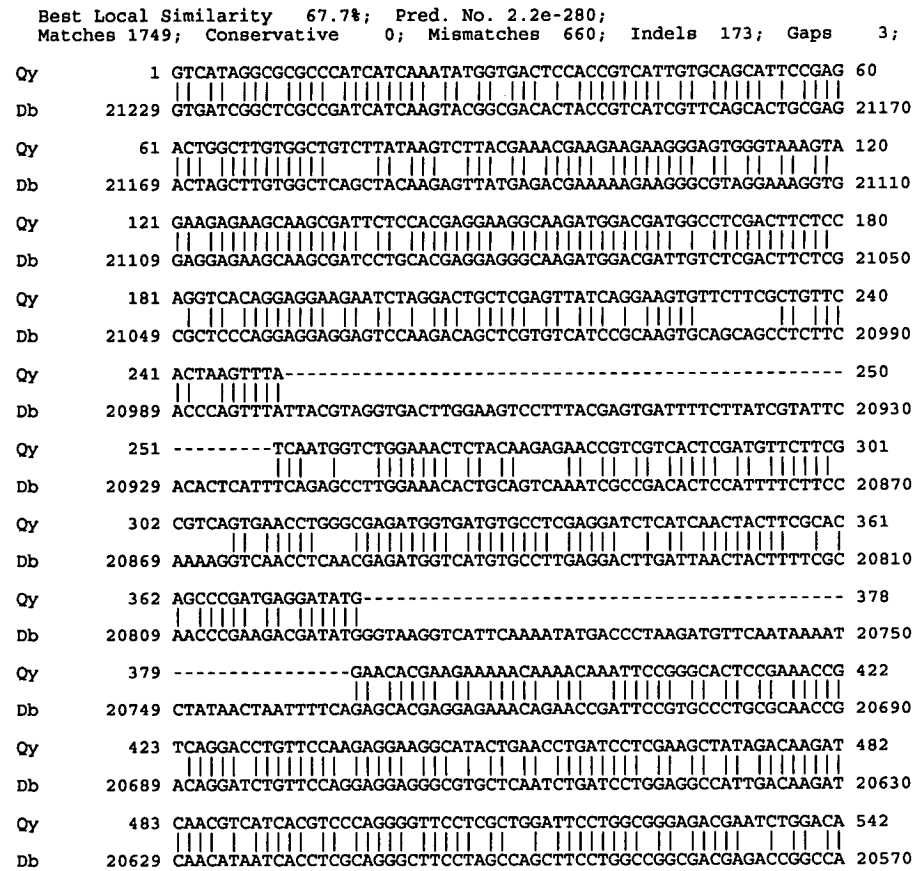
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LOCUS       CQ594803               24236 bp    DNA     linear   PAT 02-FEB-2004
DEFINITION  Sequence 22561 from Patent WO0171042.
ACCESSION   CQ594803
VERSION     CQ594803.1  GI:41651848
KEYWORDS    .
SOURCE      Drosophila sp.
  ORGANISM  Drosophila sp.
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1
  AUTHORS   Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
  TITLE     Detection kits, such as nucleic acid arrays, for detecting the
            expression of 10,000 or more Drosophila genes and uses thereof
  JOURNAL   Patent: WO 0171042-A 22561 27-SEP-2001;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
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Db      18829 TCGCCGGATTCCGGACTTACAGGGTGGAGCGCAACTACGCCGTGACATCGGGCAAGTGGT 18770

Qy       2288 ACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATA 2347

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Qy       2348 TGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGTTACAATG 2407

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Qy       2408 AG 2409

Db      18649 TG 18648
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RESULT 3
AC007471

LOCUS	AC007471 168601 bp DNA linear INV 27-FEB-2001
DEFINITION	Drosophila melanogaster, chromosome 2R, region 44F-45A, BAC clone BACR02C23, complete sequence.
ACCESSION	AC007471
VERSION	AC007471.4 GI:13129409
KEYWORDS	HTG.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 168601)
AUTHORS	Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
TITLE	Sequencing of Drosophila chromosome 2R, region 44F-45A
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 168601)
AUTHORS	Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.

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  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-1999) Drosophila Genome Center, Lawrence Berkeley
            Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT     On Feb 27, 2001 this sequence version replaced gi:5670626.
            Sequence submitted by:
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory, MS 64-121
            Berkeley, CA 94720
            This sequence was assembled using end sequences from a whole genome
            shotgun and from subclones of this BAC and its neighboring clones.
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site (http://www.fruitfly.org/sequence/) or send email
            to bdgp@fruitfly.berkeley.edu.
FEATURES             Location/Qualifiers
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RESULT 4
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DEFINITION  Drosophila melanogaster chromosome 2R, section 15 of 74 of the
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ACCESSION   AE003835 AE002787 AE013599
VERSION     AE003835.4  GI:23240369
KEYWORDS    .
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 271696)
  AUTHORS   Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
            Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
            George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N.,
            Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,
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            Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
  TITLE     The genome sequence of Drosophila melanogaster
  JOURNAL   Science 287 (5461), 2185-2195 (2000)
   PUBMED   10731132
REFERENCE   2  (bases 1 to 271696)
  AUTHORS   Celniker,S.E., Wheeler,D.A., Kronmiller,B., Carlson,J.W.,
            Halpern,A., Patel,S., Adams,M., Champe,M., Dugan,S.P., Frise,E.,
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            Sutton,G.G., Venter,C., Weinstock,G., Scherer,S.E., Myers,E.W.,
            Gibbs,R.A. and Rubin,G.M.
  TITLE     Finishing a whole-genome shotgun: release 3 of the Drosophila
            melanogaster euchromatic genome sequence
  JOURNAL   Genome Biol. 3 (12), RESEARCH0079 (2002)
   PUBMED   12537568
REFERENCE   3  (bases 1 to 271696)
  AUTHORS   Misra,S., Crosby,M.A., Mungall,C.J., Matthews,B.B., Campbell,K.S.,
            Hradecky,P., Huang,Y., Kaminker,J.S., Millburn,G.H., Prochnik,S.E.,
            Smith,C.D., Tupy,J.L., Whitfied,E.J., Bayraktaroglu,L.,
            Berman,B.P., Bettencourt,B.R., Celniker,S.E., de Grey,A.D.,
            Drysdale,R.A., Harris,N.L., Richter,J., Russo,S., Schroeder,A.J.,
            Shu,S.Q., Stapleton,M., Yamada,C., Ashburner,M., Gelbart,W.M.,
            Rubin,G.M. and Lewis,S.E.
  TITLE     Annotation of the Drosophila melanogaster euchromatic genome: a
            systematic review
  JOURNAL   Genome Biol. 3 (12), RESEARCH0083 (2002)
   PUBMED   12537572
REFERENCE   4  (bases 1 to 271696)
  AUTHORS   Kaminker,J.S., Bergman,C.M., Kronmiller,B., Carlson,J.,
            Svirskas,R., Patel,S., Frise,E., Wheeler,D.A., Lewis,S.E.,
            Rubin,G.M., Ashburner,M. and Celniker,S.E.
  TITLE     The transposable elements of the Drosophila melanogaster
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          euchromatin: a genomics perspective
  JOURNAL   Genome Biol. 3 (12), RESEARCH0084 (2002)
   PUBMED   12537573
REFERENCE   5  (bases 1 to 271696)
  AUTHORS   Celniker,S., Carlson,J., Wan,K., Pfeiffer,B., Frise,E., George,R.,
            Hoskins,R., Stapleton,M., Pacleb,J., Park,S., Svirskas,R.,
            Smith,E., Yu,C. and Rubin,G.
  CONSRTM   Berkeley Drosophila Genome Project
  TITLE     Drosophila melanogaster release 4 sequence
  JOURNAL   Unpublished
REFERENCE   6  (bases 1 to 271696)
  AUTHORS   Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
REFERENCE   7  (bases 1 to 271696)
  AUTHORS   .
  CONSRTM   FlyBase
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUL-2005) FlyBase, Harvard University, Biological
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COMMENT     On Sep 20, 2002 this sequence version replaced gi:21645554.
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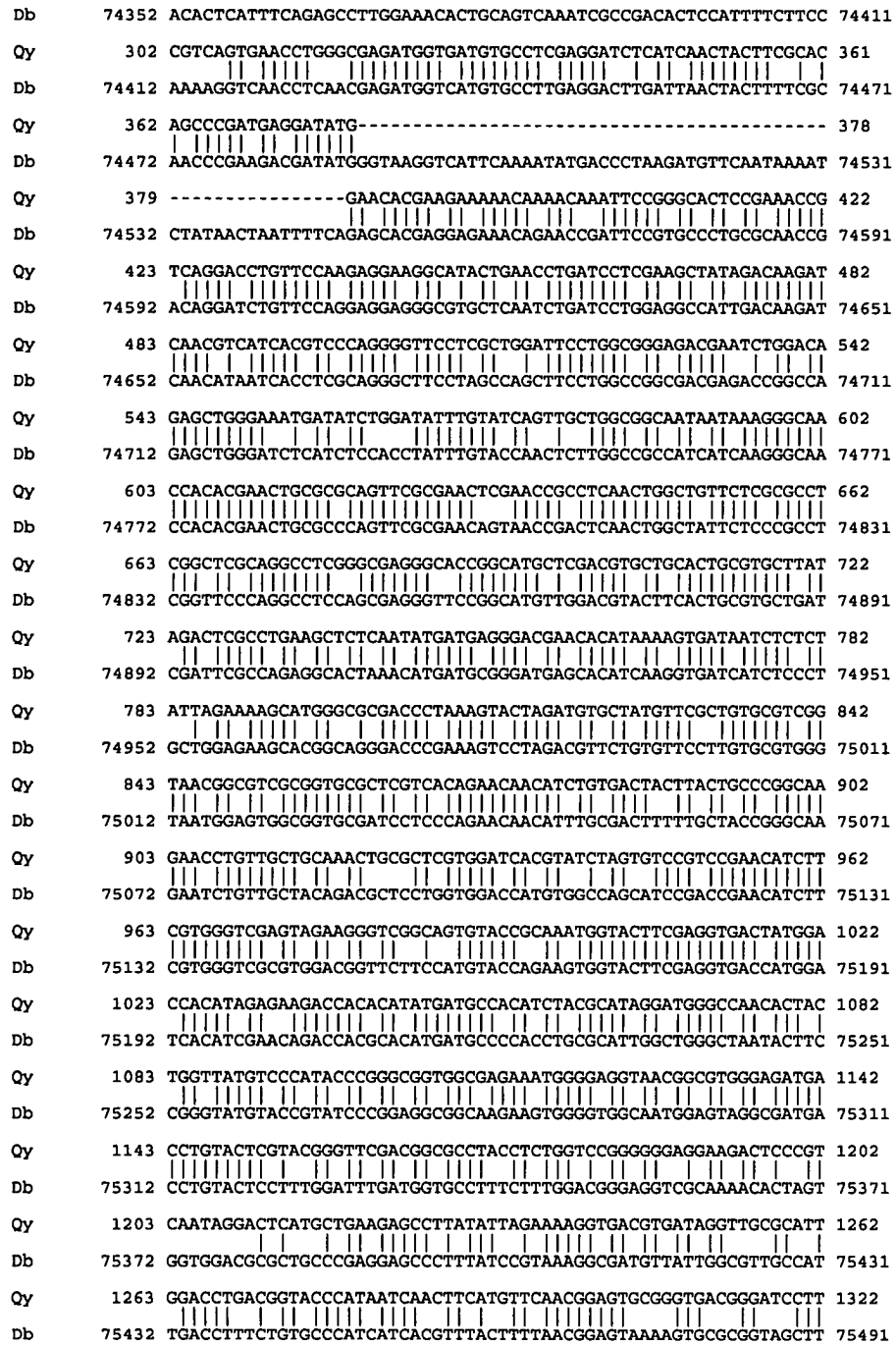
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Db      74232 CGCTCCCAGGAGGAGGAGTCCAAGACAGCTCGTGTCATCCGCAAGTGCAGCAGCCTCTTC 74291

Qy        241 ACTAAGTTTA---------------------------------------------------- 250
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Qy        251 ---------TCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTCG 301
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Db 74412 AAAAGGTCAACCTCAACGAGATGGTCATGTGCCTTGAGGACTTGATTAACTACTTTTCGC 74471
Qy 362 AGCCCGATGAGGATATG---------- 378
Db 74472 AACCCGAAGACGATATGGGTAAGGTCATTCAAAATATGACCCTAAGATGTTCAATAAAAT 74531
Qy 379 ----------GAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAACCG 422
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Qy 423 TCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGAT 482
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RESULT 5
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DEFINITION  Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
ACCESSION   AC020372
VERSION     AC020372.1  GI:6664525
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
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            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 100002)
  AUTHORS   Adams,M. and Venter,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
            Rockville, MD, USA
COMMENT     This sequence was identified as CDM:10212949 by the submitter.
            For more information on this record e-mail to fly@celera.com.
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
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ORIGIN

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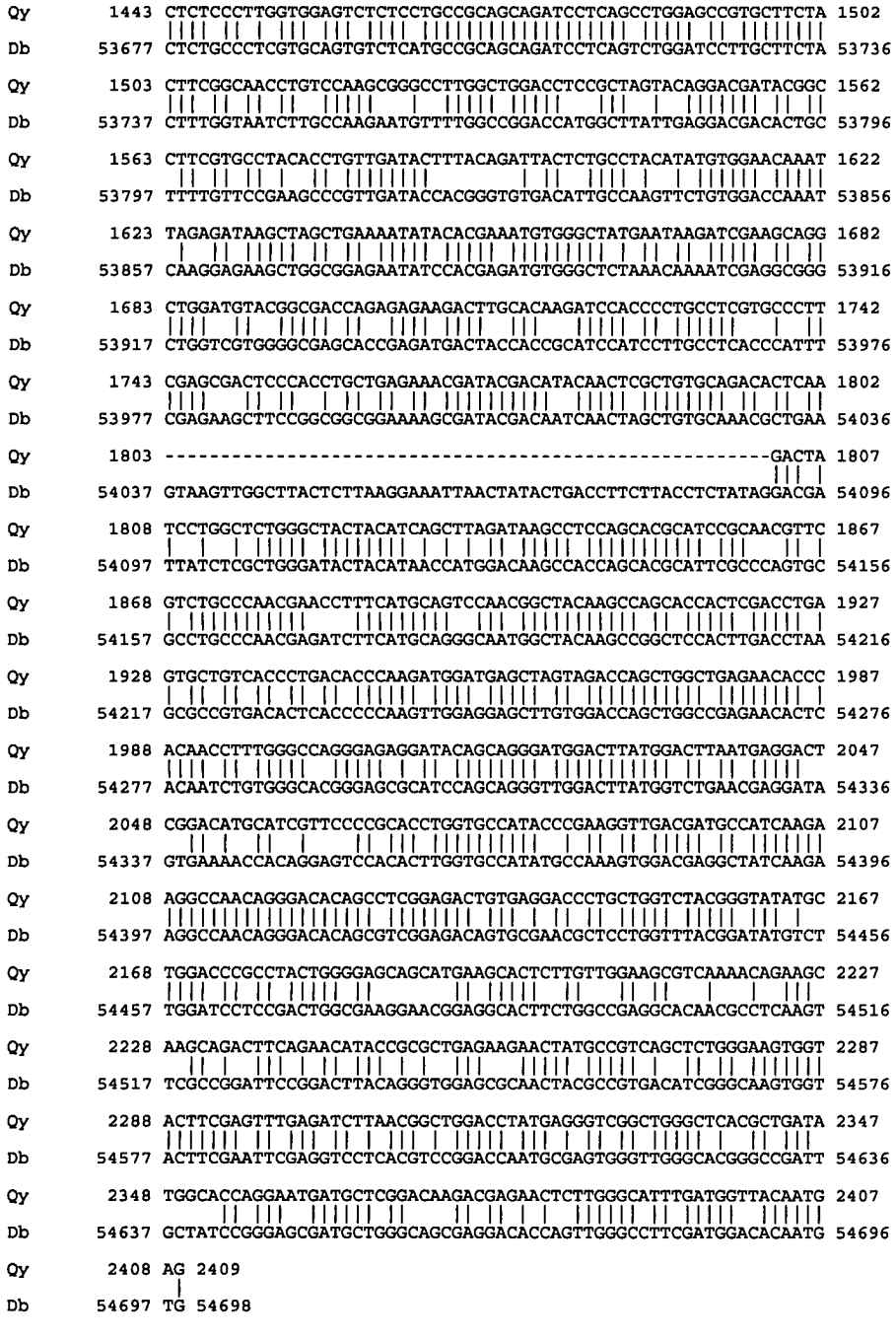
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RESULT 6
DRORYRH
LOCUS       DRORYRH                25680 bp    DNA     linear   INV 25-MAR-1999
DEFINITION  Drosophila melanogaster DNA for ryanodine receptor homologue,
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ACCESSION   D17389
VERSION     D17389.1  GI:456161
KEYWORDS    Ca2+ binding; alternative splicing; ER-transmembrane protein;
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SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
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REFERENCE   1  (sites)
  AUTHORS   Takeshima,H., Nishi,M., Iwabe,N., Miyata,T., Hosoya,T., Masai,I.
            and Hotta,Y.
  TITLE     Isolation and characterization of a gene for a ryanodine
            receptor/calcium release channel in Drosophila melanogaster
  JOURNAL   FEBS Lett. 337 (1), 81-87 (1994)
   PUBMED   8276118
REFERENCE   2  (bases 1 to 25680)
  AUTHORS   Takeshima,H.
  JOURNAL   Unpublished
COMMENT     Submitted (09-Aug-1993) to DDBJ by:
            Hiroshi Takeshima
            International Institute for
            Advanced Studies
            c/o Shimadzu Corporation N-80
            1 Nishinokyo-Kuwahara-cho
            Kyoto 604
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            Phone: 075-823-1208
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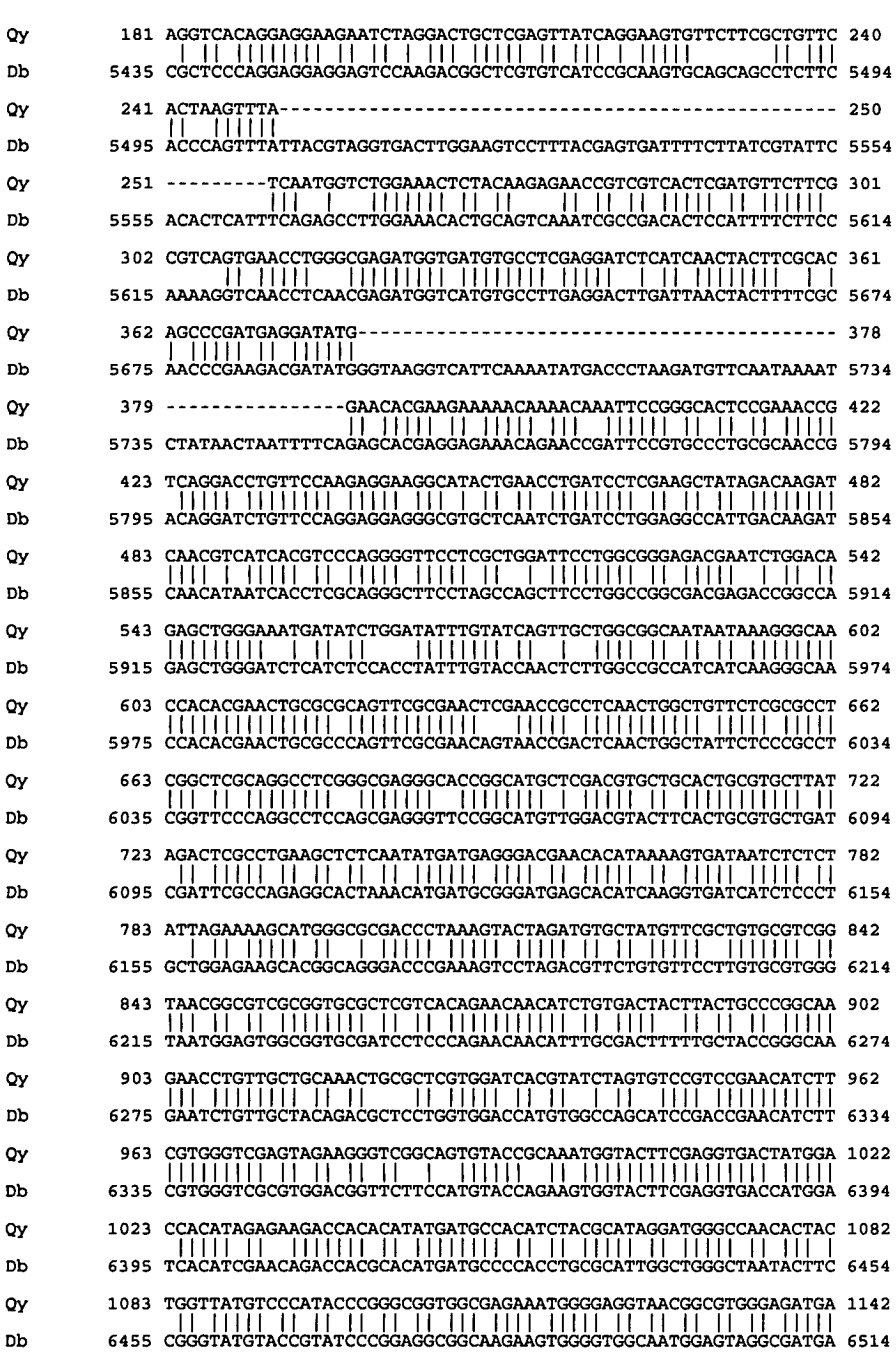
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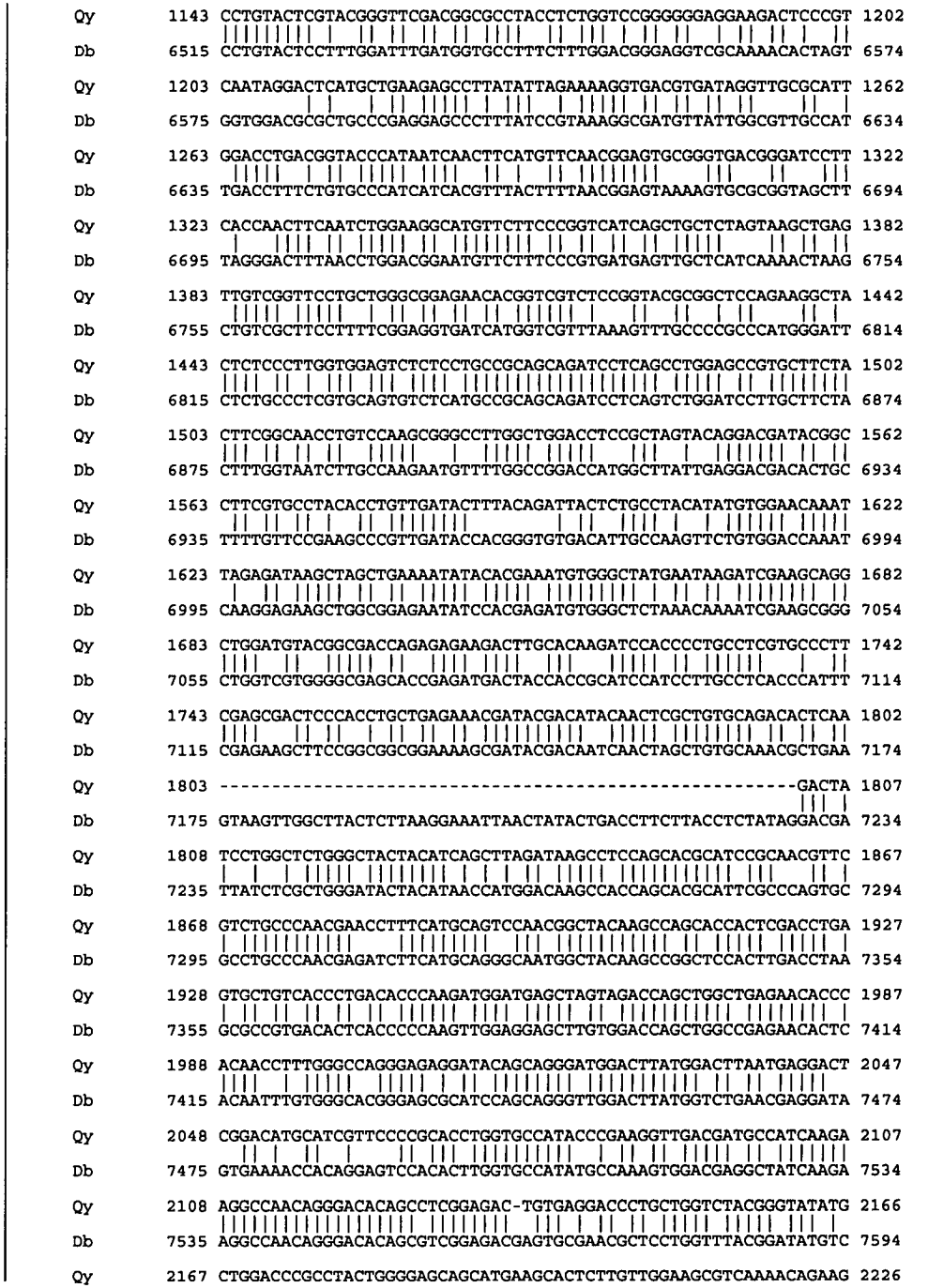
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  AUTHORS   Shiwa,M., Murayama,T. and Ogawa,Y.
  TITLE     Molecular cloning and characterization of ryanodine receptor from
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            (2002)
   PUBMED   11832393
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  AUTHORS   Murayama,T., Shiwa,M. and Ogawa,Y.
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  JOURNAL   Submitted (22-NOV-2000) Takashi Murayama, Juntendo University
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            (E-mail:takashim@med.juntendo.ac.jp, Tel:81-3-5802-1035,
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ORIGIN

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Qy          4 ATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAGACT 63
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Db       1699 ATGGGCAGCGCAGACATCAAATATGGAGATTCCACCGTCCTTATTCAACACATGAAGACG 1758

Qy         64 GGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTAGAA 123
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Qy        124 GAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCCAGG 183
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Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
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Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
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Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
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Qy       1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
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DEFINITION  S.scrofa mRNA for calcium release channel (CRC).
ACCESSION   X62880
VERSION     X62880.1  GI:1936
KEYWORDS    calcium channel; CRC (ryr1) gene; ryanodine receptor; sarcoplasmic
            reticulum protein; transmembrane protein.
SOURCE      Sus scrofa (pig)
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            Sus.
REFERENCE   1  (bases 1 to 15253)
  AUTHORS   Harbitz,I., Kristensen,T., Bosnes,M., Kran,S. and Davies,W.
  TITLE     DNA sequence of the skeletal muscle calcium release channel cDNA
            and verification of the Arg615---Cys615 mutation, associated with
            porcine malignant hyperthermia, in Norwegian landrace pigs
  JOURNAL   Anim. Genet. 23 (5), 395-402 (1992)
   PUBMED   1329581
REFERENCE   2  (bases 1 to 15253)
  AUTHORS   Harbitz,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-OCT-1991) I. Harbitz, Norwegian College of Veterinary
            Medicine, Dept of Biochemistry, P.O.Box 8146 Dep, 0033 Oslo 1,
            NORWAY
COMMENT     Related sequence: M32501.
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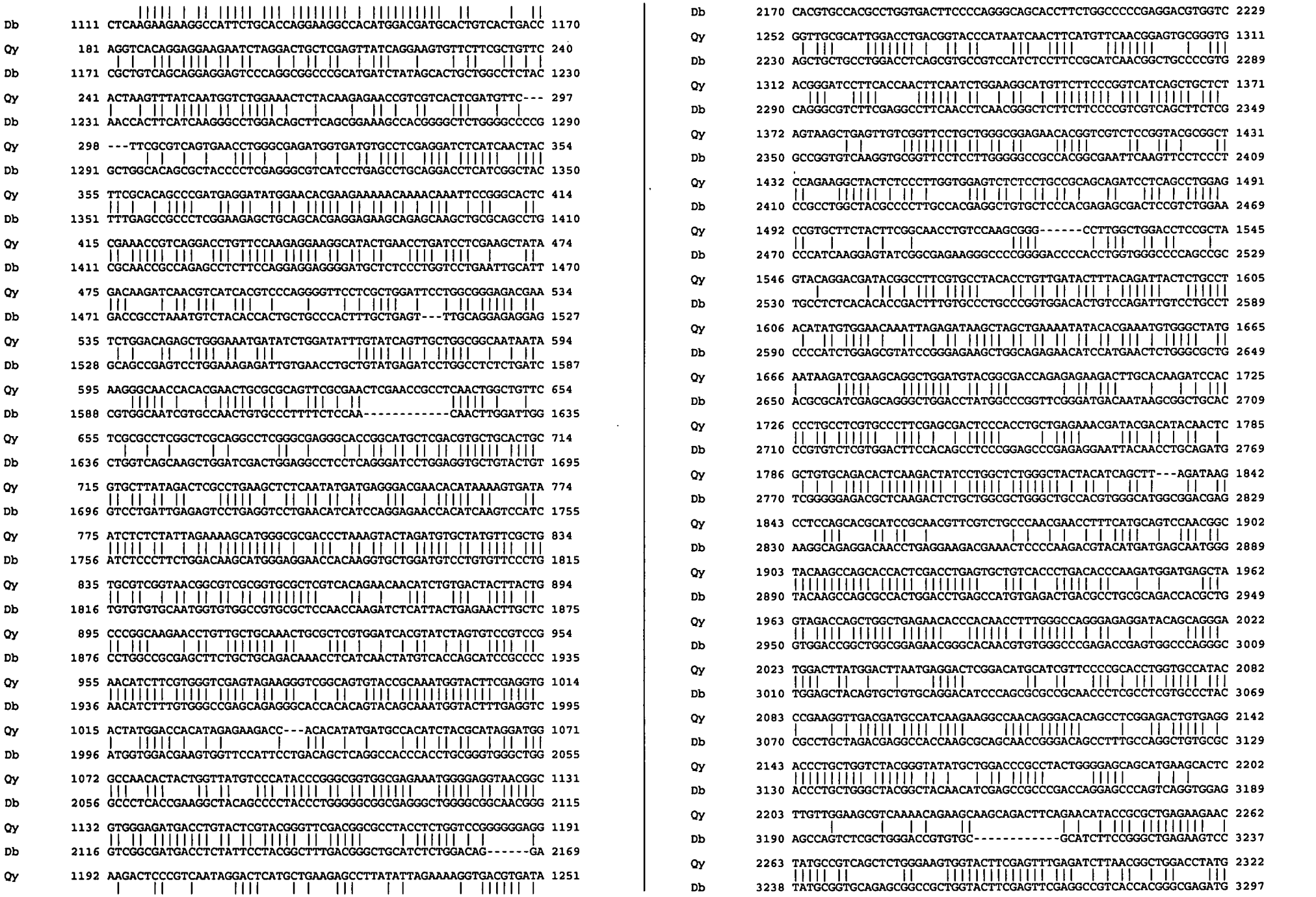
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RESULT 9
PIGRYRN
LOCUS       PIGRYRN                15378 bp    mRNA    linear   MAM 31-JUL-2001
DEFINITION  Sus scrofa Yorkshire ryanodine receptor (RYR1) mRNA, complete cds.
ACCESSION   M91452
VERSION     M91452.1  GI:164647
KEYWORDS    calcium release channel protein; foot protein; ryanodine receptor.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 15378)
  AUTHORS   Fujii,J., Otsu,K., Zorzato,F., de Leon,S., Khanna,V.K.,
            Weiler,J.E., O'Brien,P.J. and MacLennan,D.H.
  TITLE     Identification of a mutation in porcine ryanodine receptor
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  JOURNAL   Science 253 (5018), 448-451 (1991)
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ORIGIN

Query Match 22.5%; Score 674.2; DB 4; Length 15378;
Best Local Similarity 55.7%; Pred. No. 1.3e-159;
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Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
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Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTC--- 297
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Qy        298 ---TTCGCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTAC 354
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Qy        355 TTCGCACAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTC 414
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Qy        415 CGAAACCGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATA 474
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Qy        1312 ACGGGATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCT 1371
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RESULT 10
AF295105

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DEFINITION  Mus musculus cardiac Ca2+ release channel mRNA, complete cds.
ACCESSION   AF295105
VERSION     AF295105.1  GI:11321165
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
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  AUTHORS   Zhao,M., Li,P., Li,X., Zhang,L., Winkfein,R.J. and Chen,S.R.
  TITLE     Molecular identification of the ryanodine receptor pore-forming
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  JOURNAL   J. Biol. Chem. 274 (37), 25971-25974 (1999)
   PUBMED   10473538
REFERENCE   2  (bases 1 to 14904)
  AUTHORS   Chen,S.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2000) Physiology and Biophysics, University of
            Calgary, 3330 Hospital Drive N.W., Calgary, AB T2N 4N1, Canada
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ORIGIN

Query Match 22.4%; Score 671.4; DB 9; Length 14904;
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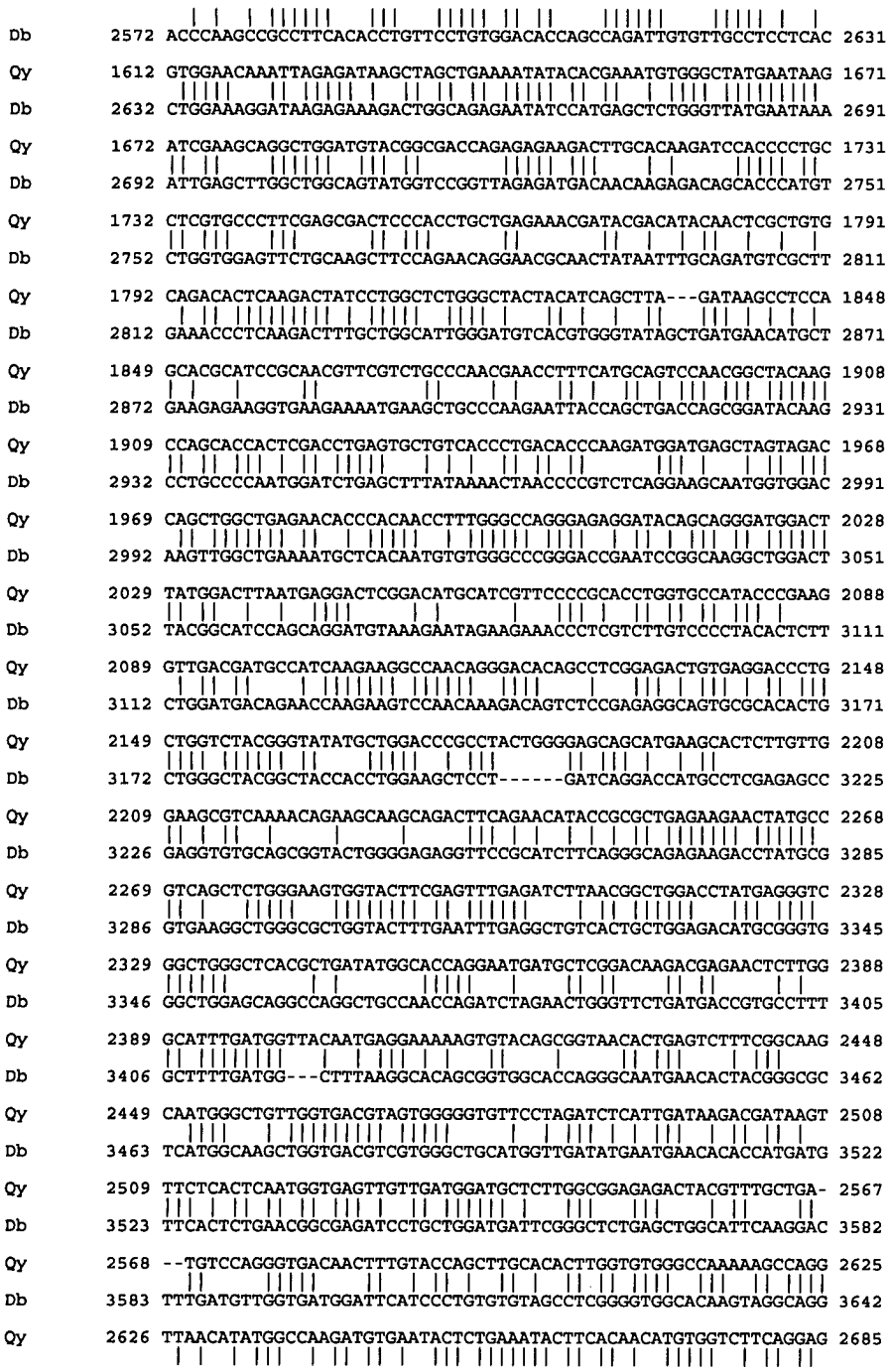
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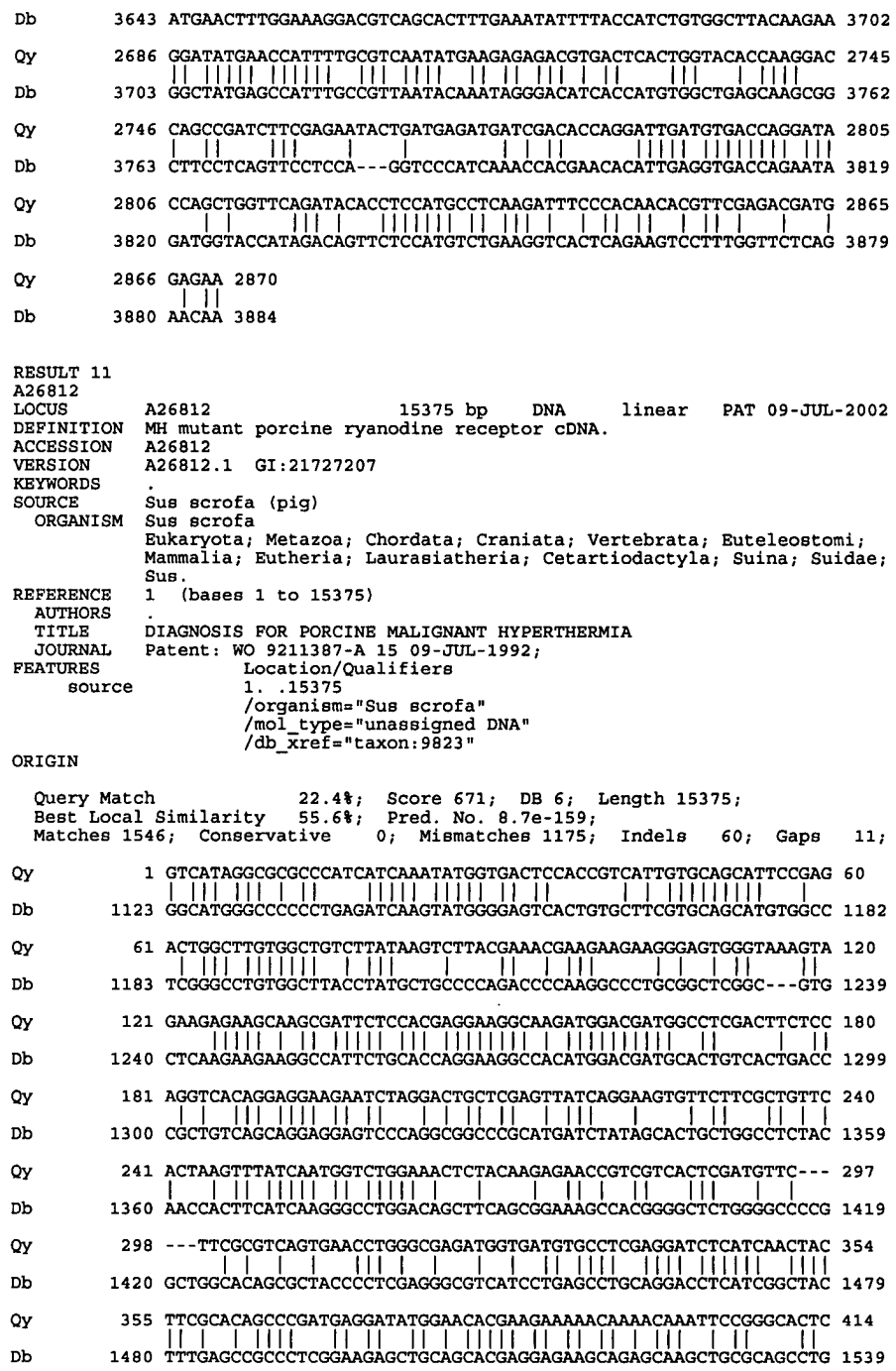
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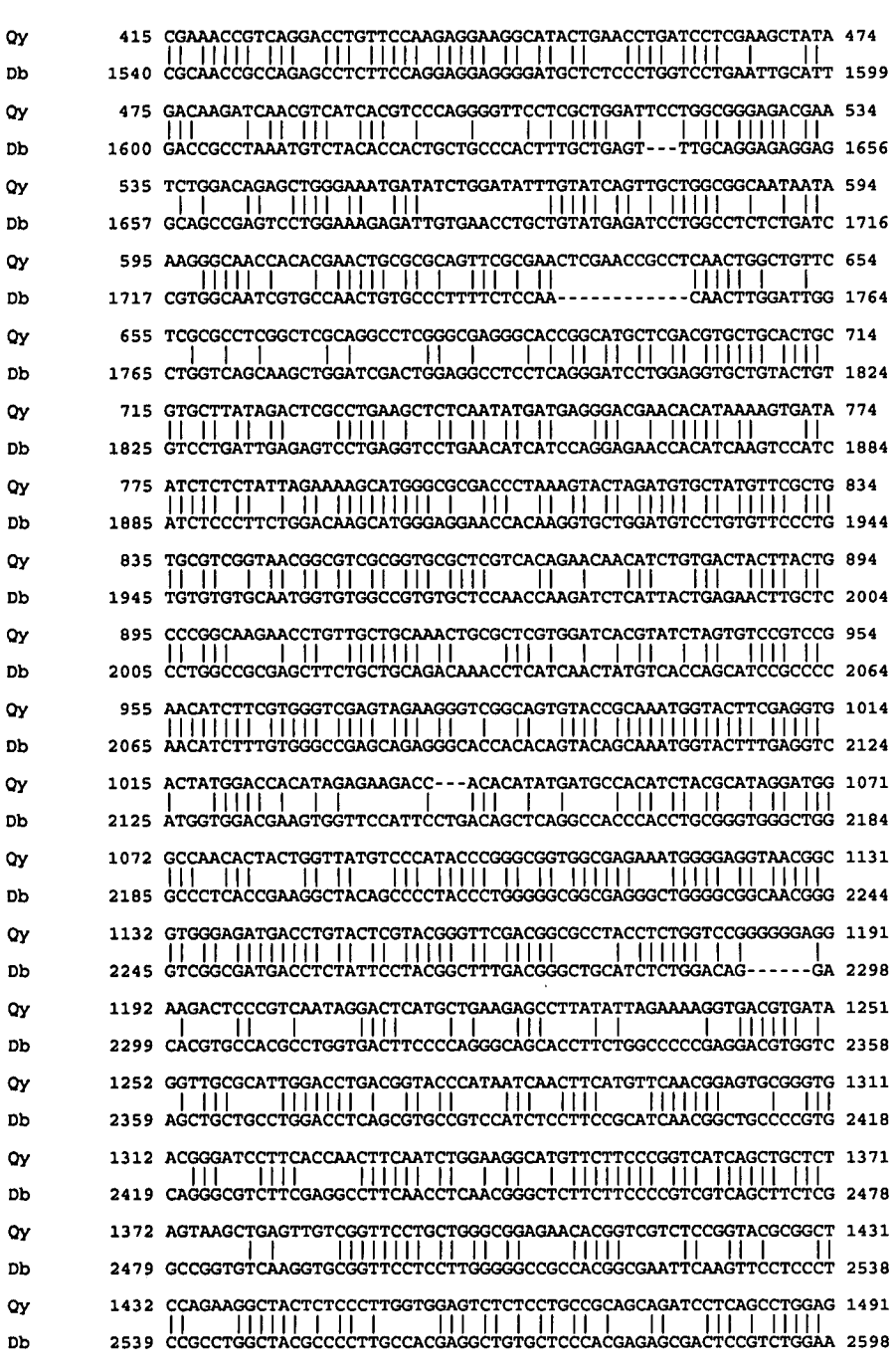
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DEFINITION MH mutant porcine ryanodine receptor cDNA.
ACCESSION A26812
VERSION A26812.1 GI:21727207
KEYWORDS .
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 15375)
AUTHORS .
TITLE DIAGNOSIS FOR PORCINE MALIGNANT HYPERTHERMIA
JOURNAL Patent: WO 9211387-A 15 09-JUL-1992;
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ORIGIN

Query Match 22.4%; Score 671; DB 6; Length 15375;
Best Local Similarity 55.6%; Pred. No. 8.7e-159;
Matches 1546; Conservative 0; Mismatches 1175; Indels 60; Gaps 11;


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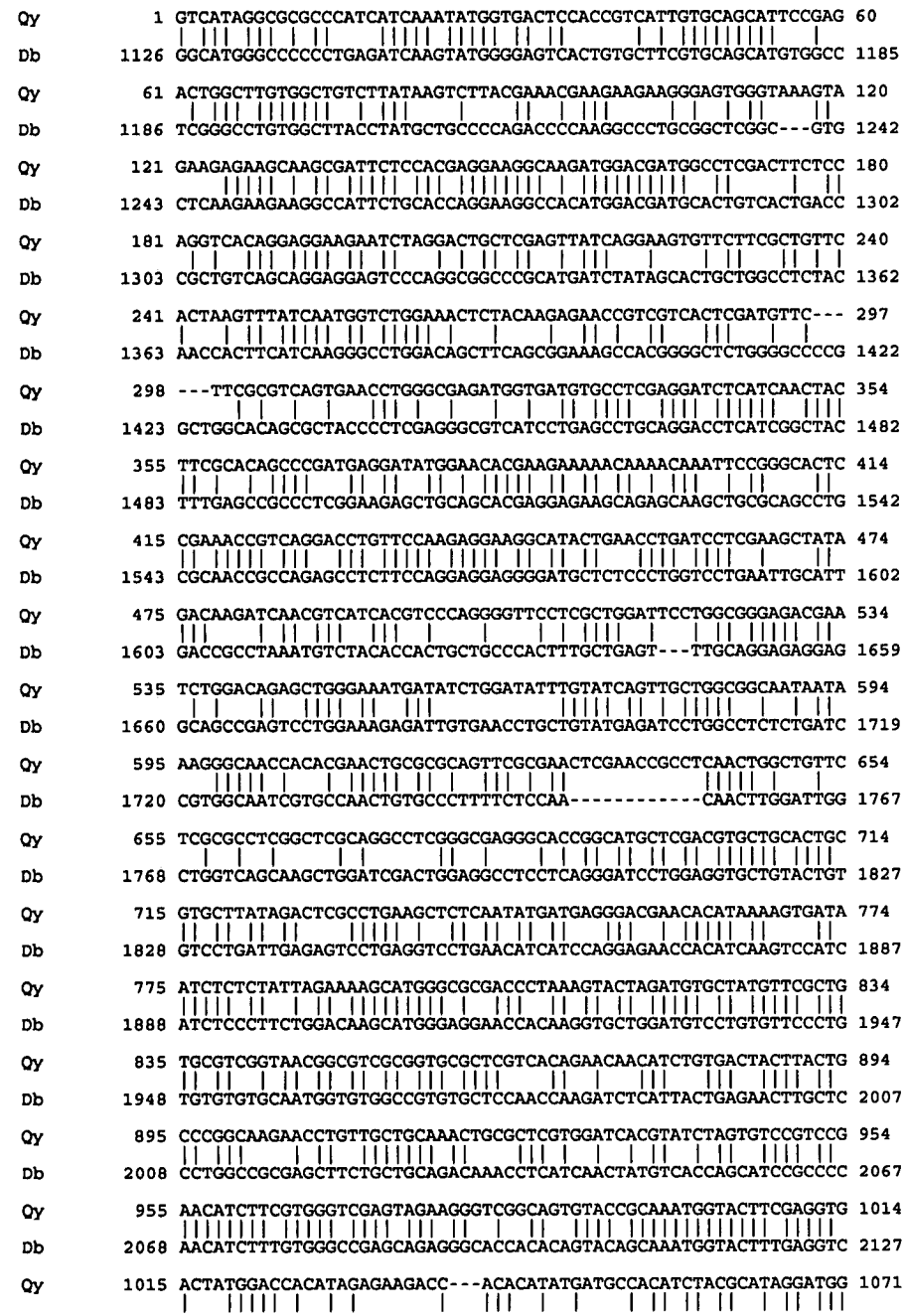
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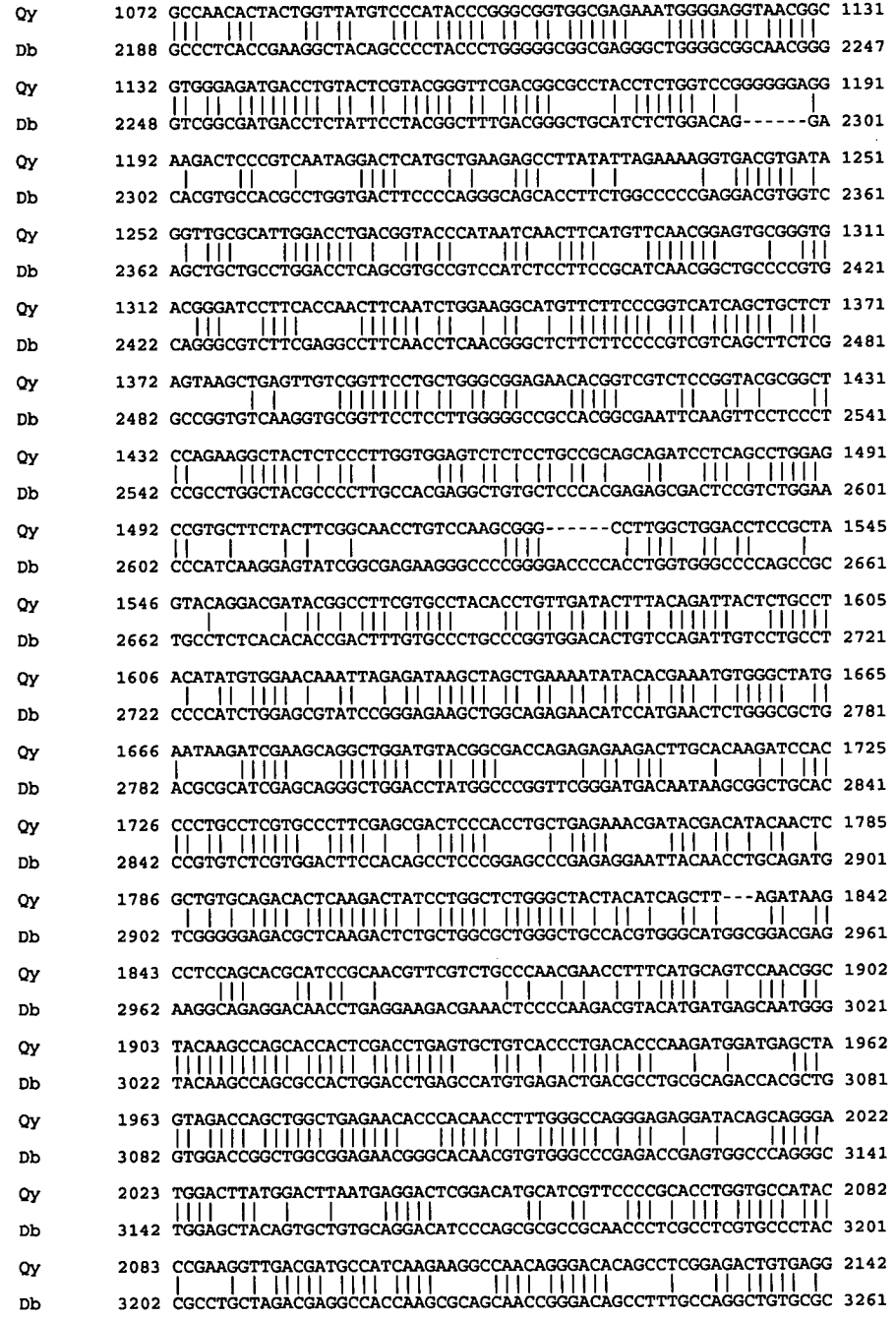
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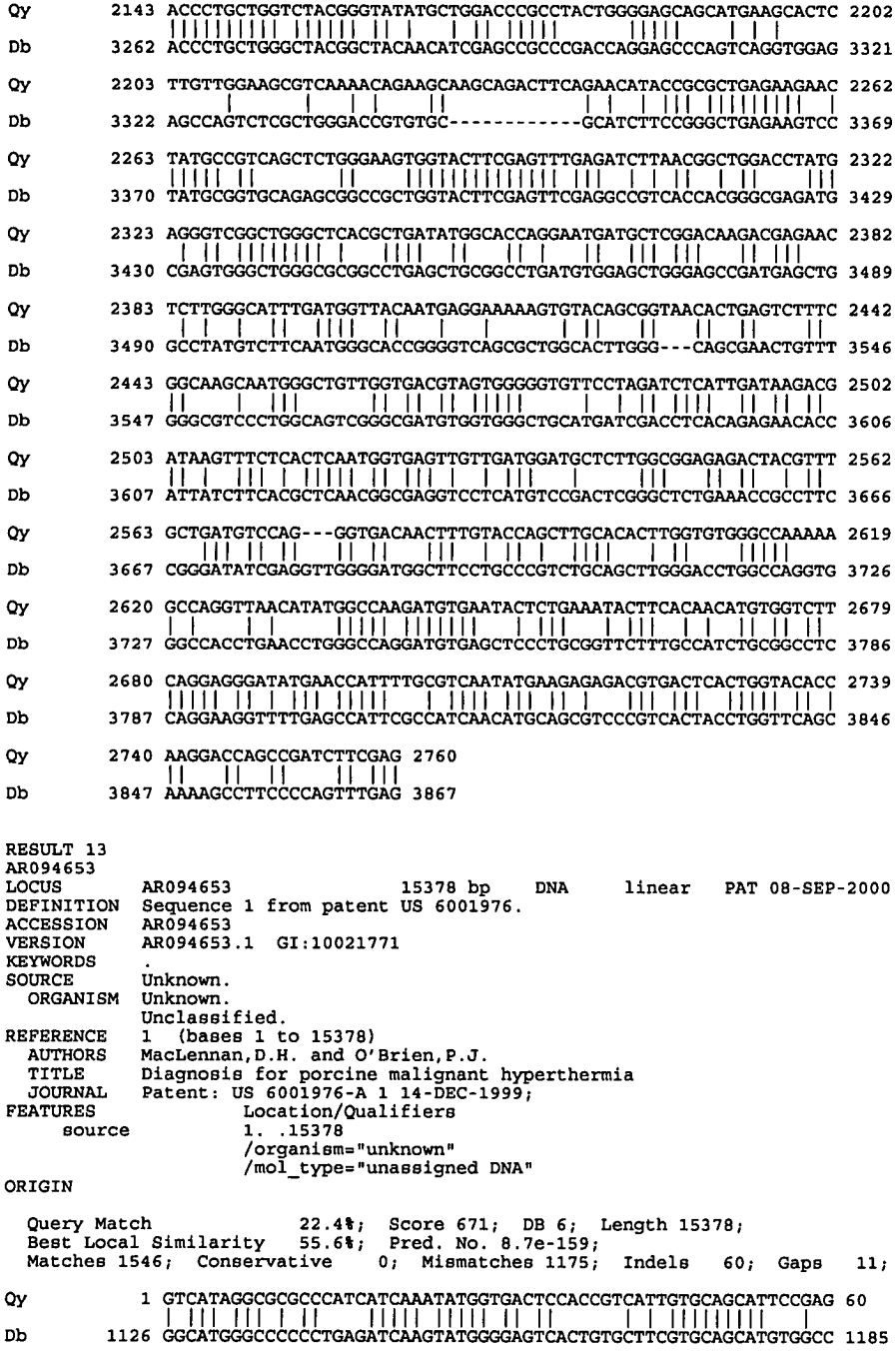
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DEFINITION  Sus scrofa Belgisch Landras/Pietrain ryanodine receptor (RYR1)
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ACCESSION   M91451
VERSION     M91451.1  GI:164645
KEYWORDS    calcium release channel protein; foot protein; malignant
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SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 15378)
  AUTHORS   Fujii,J., Otsu,K., Zorzato,F., de Leon,S., Khanna,V.K.,
            Weiler,J.E., O'Brien,P.J. and MacLennan,D.H.
  TITLE     Identification of a mutation in porcine ryanodine receptor
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  JOURNAL   Science 253 (5018), 448-451 (1991)
   PUBMED   1862346
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Best Local Similarity 55.6%; Pred. No. 8.7e-159;
Matches 1546; Conservative 0; Mismatches 1175; Indels 60; Gaps 11;

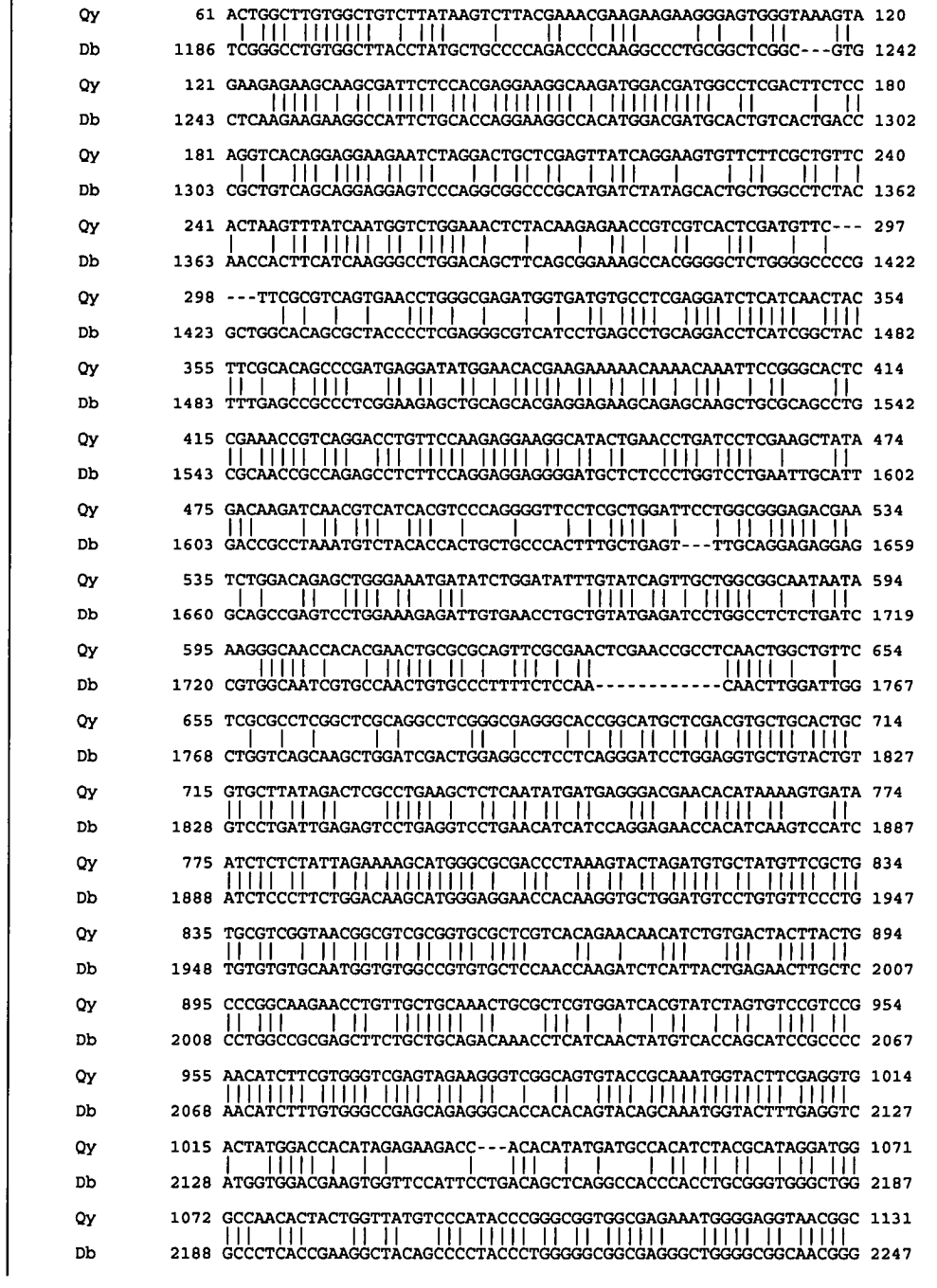






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ORGANISM Unknown.
Unclassified.
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AUTHORS MacLennan,D.H. and O'Brien,P.J.
TITLE Diagnosis for porcine malignant hyperthermia
JOURNAL Patent: US 6001976-A 1 14-DEC-1999;
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Qy       1192 AAGACTCCCGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATA 1251
Db       2302 CACGTGCCACGCCTGGTGACTTCCCCAGGGCAGCACCTTCTGGCCCCCGAGGACGTGGTC 2361

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Db       2362 AGCTGCTGCCTGGACCTCAGCGTGCCGTCCATCTCCTTCCGCATCAACGGCTGCCCCGTG 2421

Qy       1312 ACGGGATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCT 1371
Db       2422 CAGGGCGTCTTCGAGGCCTTCAACCTCAACGGGCTCTTCTTCCCCGTCGTCAGCTTCTCG 2481

Qy       1372 AGTAAGCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCT 1431
Db       2482 GCCGGTGTCAAGGTGCGGTTCCTCCTTGGGGGCCGCCACGGCGAATTCAAGTTCCTCCCT 2541

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Db       2542 CCGCCTGGCTACGCCCCTTGCCACGAGGCTGTGCTCCCACGAGAGCGACTCCGTCTGGAA 2601

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Db       2602 CCCATCAAGGAGTATCGGCGAGAAGGGCCCCGGGGACCCCACCTGGTGGGCCCCAGCCGC 2661

Qy       1546 GTACAGGACGATACGGCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCT 1605
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Db       3022 TACAAGCCAGCGCCACTGGACCTGAGCCATGTGAGACTGACGCCTGCGCAGACCACGCTG 3081

Qy       1963 GTAGACCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGA 2022
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Qy       2143 ACCCTGCTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTC 2202
Db       3262 ACCCTGCTGGGCTACGGCTACAACATCGAGCCGCCCGACCAGGAGCCCAGTCAGGTGGAG 3321

Qy       2203 TTGTTGGAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAAC 2262

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Qy       2263 TATGCCGTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATG 2322
Db       3370 TATGCGGTGCAGAGCGGCCGCTGGTACTTCGAGTTCGAGGCCGTCACCACGGGCGAGATG 3429

Qy       2323 AGGGTCGGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAAC 2382
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Qy       2443 GGCAAGCAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACG 2502
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Qy       2503 ATAAGTTTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTT 2562
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Qy       2563 GCTGATGTCCAG---GGTGACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAA 2619
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Qy       2620 GCCAGGTTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTT 2679
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Qy       2680 CAGGAGGGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACC 2739
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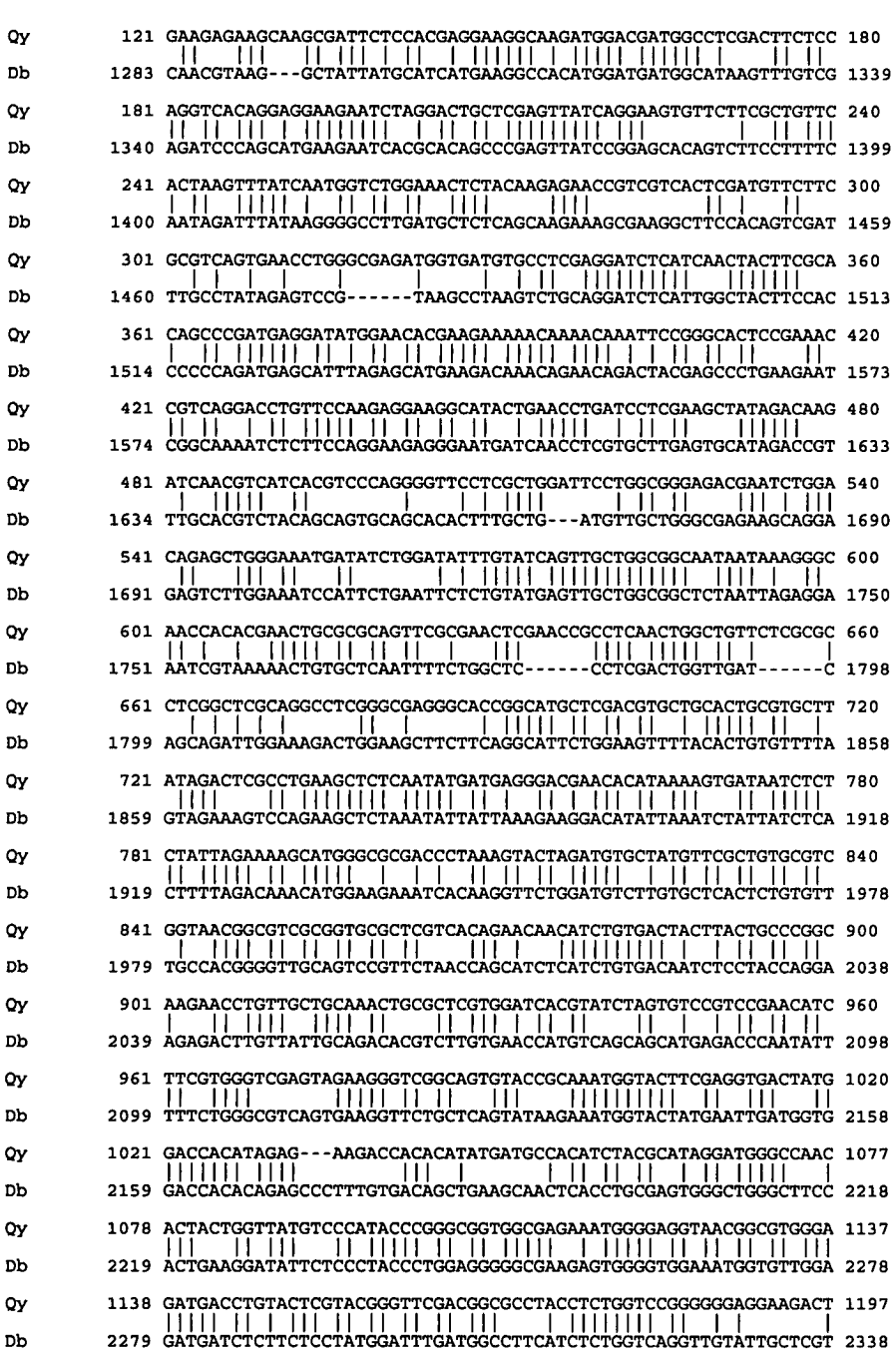
Qy       2740 AAGGACCAGCCGATCTTCGAG 2760
Db       3847 AAAAGCCTTCCCCAGTTTGAG 3867
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DEFINITION  Sequence 1154 from patent US 6500938.
ACCESSION   AR270591
VERSION     AR270591.1  GI:29701825
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 4078)
  AUTHORS   Au-Young,J. and Seilhamer,J.J.
  TITLE     Composition for the detection of signaling pathway gene expression
  JOURNAL   Patent: US 6500938-A 1154 31-DEC-2002;
            Incyte Genomics, Inc.; Palo Alto, CA;
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FEATURES             Location/Qualifiers
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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
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Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
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Qy 121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
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Qy 181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
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Qy 301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
Db 1460 TTGCCTATAGAGTCCG------TAAGCCTAAGTCTGCAGGATCTCATTGGCTACTTCCAC 1513
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Qy 961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
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Qy 1078 ACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGA 1137
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Qy 1138 GATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACT 1197
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Qy 2089 GTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTG 2148
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Qy 2209 GAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCC 2268
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Qy 2269 GTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTC 2328

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Db       3407 GTGAAGGCCGGACGGTGGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGGTT 3466

Qy       2329 GGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGG 2388
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Db       3467 GGTTGGAGTCGTCCTGGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTGCCTTT 3526

Qy       2389 GCATTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAG 2448
                || |||||||| |  |||  |   |       |  |     ||   || |||    |  ||
Db       3527 GCCTTTGATGGCTTCAAGGCCCAGCGGTGGCATCAGGG---CAATGAACACTATGGGCGC 3583

Qy       2449 CAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGT 2508
                 |||    |  || || || ||||||    |  | ||  | |  ||  | || || |
Db       3584 TCTTGGCAAGCAGGCGATGTCGTGGGGTGTATGGTTGACATGAACGAACACACCATGATG 3643

Qy       2509 TTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGAT 2568
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Db       3644 TTCACACTGAATGGTGAAATCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTCAAGGAC 3703

Qy       2569 GTCCAGGGTGACAA---CTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGG 2625
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Db       3704 TTTGATGTTGGCGATGGATTCATACCTGTGTGTAGCCTTGGAGTGGCTCAAGTGGGTAGG 3763

Qy       2626 TTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAG 2685
                | |  | |||  | |||||  |  ||  |||||||  |||||  |  |||||  | || |||
Db       3764 ATGAACTTTGGAAAGGATGTCAGCACCTTGAAATATTTCACCATCTGTGGCTTACAAGAG 3823

Qy       2686 GGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGAC 2745
                || ||||||||||||  |||  ||||  || || ||  | ||    |||   | ||||
Db       3824 GGCTATGAACCATTTGCCGTTAATACAAACAGGGATATTACCATGTGGCTGAGCAAGAGG 3883

Qy       2746 CAGCCGATCTTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATA 2805
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Db       3884 CTTCCTCAGTT---TCTTCAAGTTCCATCAAACCATGAACATATAGAGGTGACCAGAATA 3940

Qy       2806 CCAGCTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCG 2857
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RESULT 15
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DEFINITION  H.sapiens mRNA for ryanodine receptor 2.
ACCESSION   X98330
VERSION     X98330.1  GI:1526977
KEYWORDS    ryanodine receptor 2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Tunwell,R.E., Wickenden,C., Bertrand,B.M., Shevchenko,V.I.,
            Walsh,M.B., Allen,P.D. and Lai,F.A.
  TITLE     The human cardiac muscle ryanodine receptor-calcium release
            channel: identification, primary structure and topological analysis
  JOURNAL   Biochem. J. 318 (Pt 2), 477-487 (1996)
   PUBMED   8809036
REFERENCE   2  (bases 1 to 15731)
  AUTHORS   Lai,F.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-1996) T. Lai, National Institute for Medical
            Research, Neurophysiology, The Ridgeway, Mill Hill, London NW7 1AA,
            UK
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ORIGIN

Query Match 22.3%; Score 668; DB 8; Length 15731;
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Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
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Db       1223 ACAGGCCTATGGCTTACTTACCAGTCTGTGGACGTGAAATCCGTGAGAATGGGATCTATA 1282

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
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Db       1283 CAACGTAAG---GCTATTATGCATCATGAAGGCCACATGGATGATGGCATAAGTTTGTCG 1339

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
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Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
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Db       1691 GAGTCTTGGAAATCCATTCTGAATTCTCTGTATGAGTTGCTGGCGGCTCTAATTAGAGGA 1750

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
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Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
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Qy         841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
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Qy         901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
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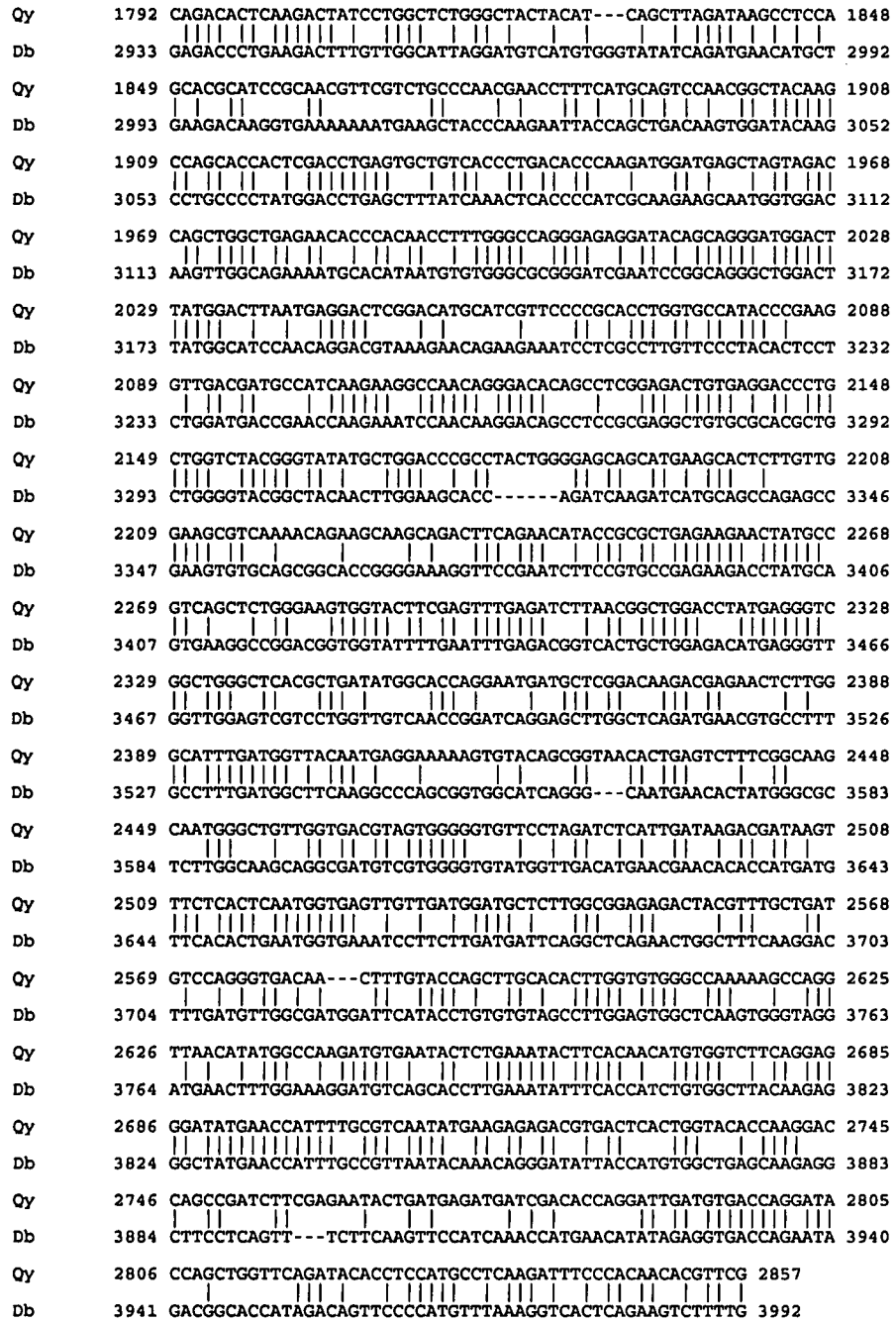
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 13:59:54 ; Search time 11349.5 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
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4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

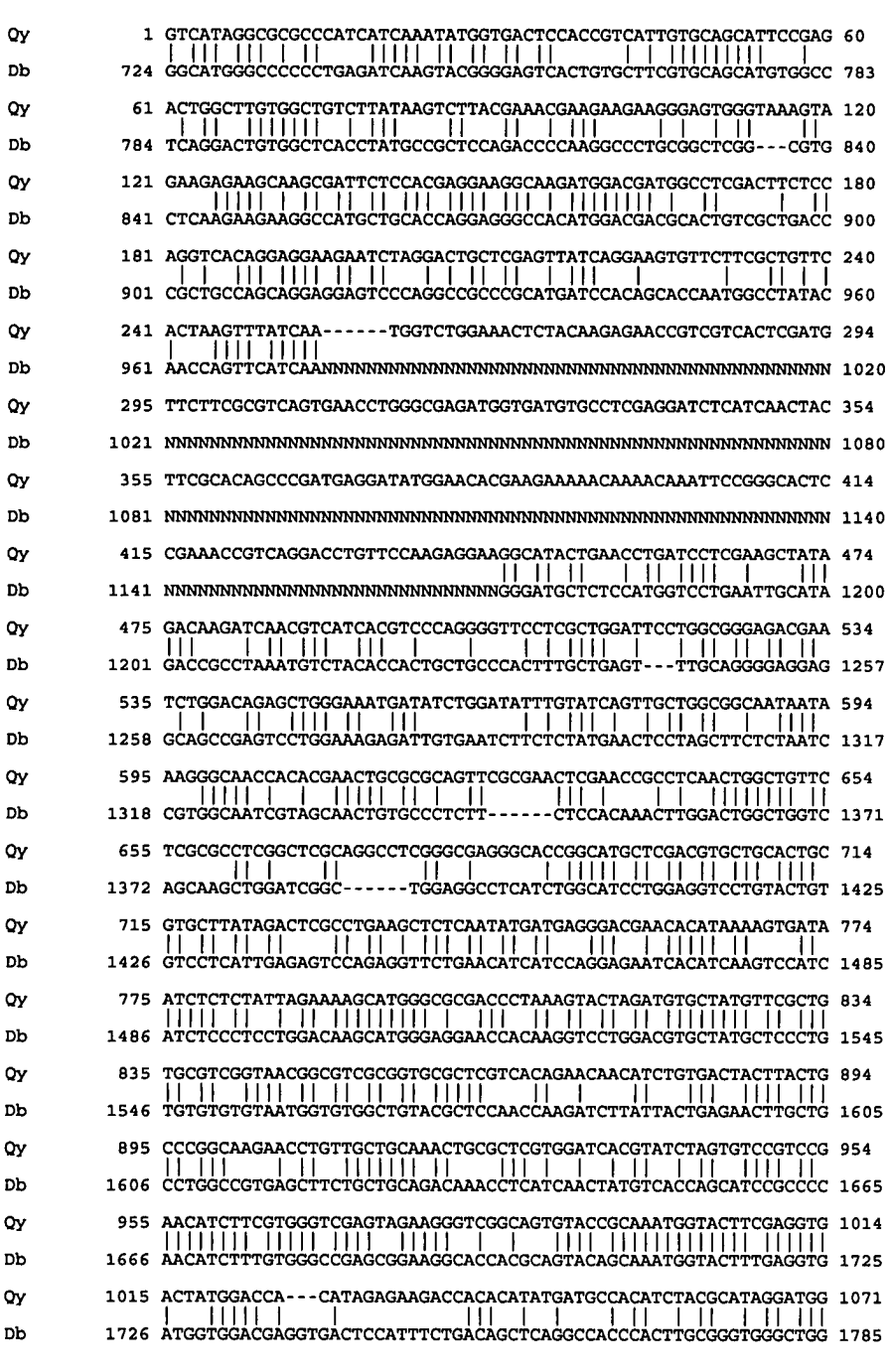
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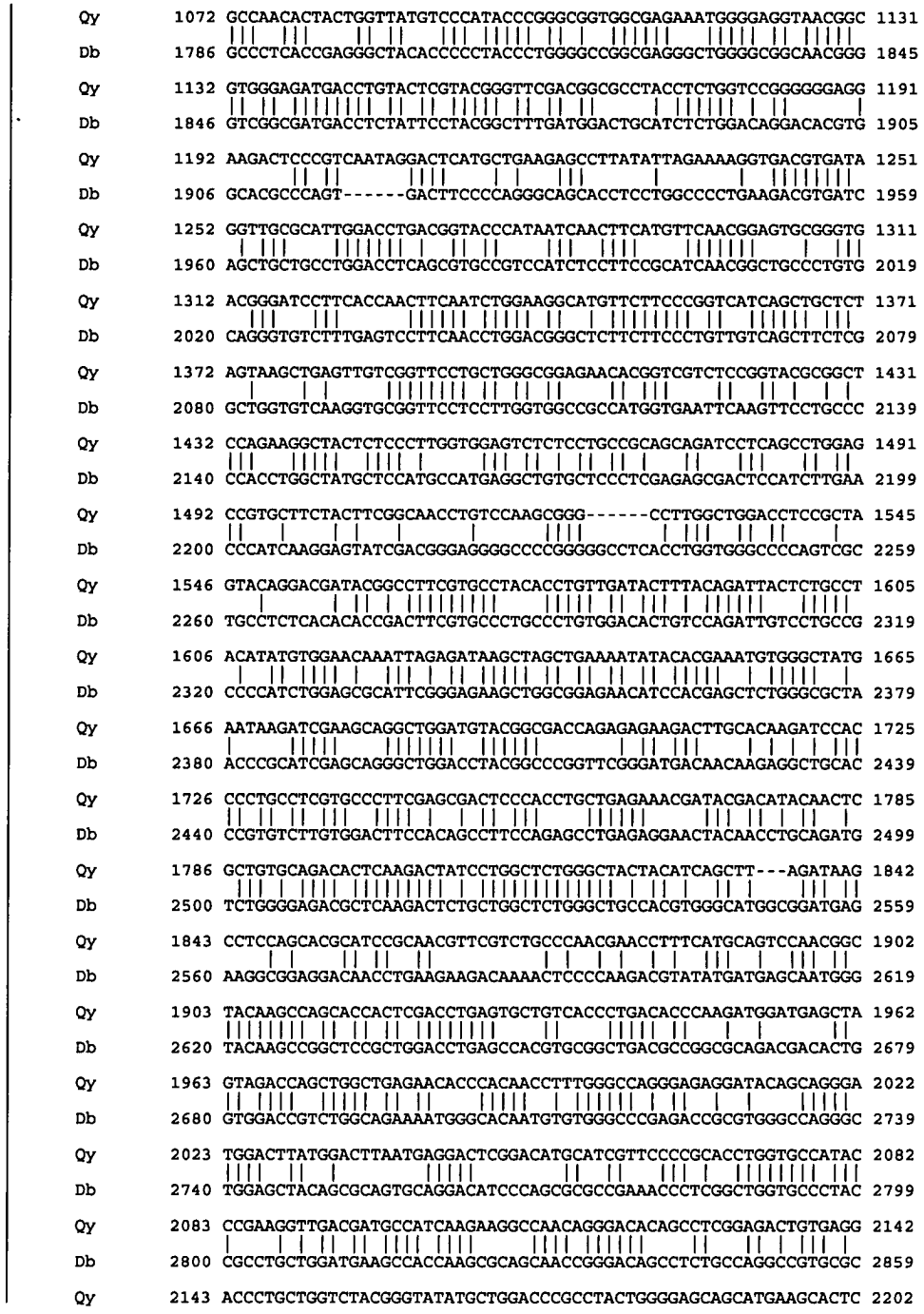
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c 27		119	4.0	535	2	BF420478	BF420478 UI-R-BJ2-
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ALIGNMENTS

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VERSION DQ052093.1 GI:66905537
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 14832)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 14832)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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ORIGIN

Query Match 19.3%; Score 578.2; DB 11; Length 14832;
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Matches 1423; Conservative 0; Mismatches 1298; Indels 60; Gaps 12;





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Qy       2323 AGGGTCGGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAAC 2382

Db       3028 CGCGTGGGCTGGGCGAGGCCCGAGCTGAGGCCTGATGTAGAGCTGGGAGCTGACGAGCTG 3087

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Qy       2563 GCTGATGTCCAG---GGTGACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAA 2619

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Qy       2620 GCCAGGTTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTT 2679

Db       3325 GGTCATCTGAACCTGGGCCAGGACGTGAGCTCTCTGAGGTTCTTTGCCATCTGTGGCCTC 3384

Qy       2680 CAGGAGGGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACC 2739

Db       3385 CAGGAAGGCTTCGAGCCATTTGCCATCAACATGCAGCGCCCAGTCACCACCTGGTTCAGC 3444

Qy       2740 AAGGACCAGCCGATCTTCGAG 2760

Db       3445 AAAGGCCTGCCCCAGTTTGAG 3465
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RESULT 2
DQ052094
LOCUS       DQ052094               14736 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes RYR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ052094
VERSION     DQ052094.1  GI:66905538
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 14736)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 14736)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source          1. .14736
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ORIGIN
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  Matches 1364;  Conservative    0;  Mismatches 1357;  Indels   60;  Gaps   12;

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Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120

Db        784 TCAGGACTGTGGCTCACCTATGCCGCTCCAGACCCCAAGGCCCTGCGGCTCGG---CGTG 840

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180

Db        841 CTCAAGAAGAAGGCCATGCTGCACCAGGAGGGCCACATGGACGACGCACTGTCGCTGACC 900

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240

Db        901 CGCTGCCAGCAGGAGGAGTCCCAGGCCGCCCGCATGATCCACAGCACCAATGGCCTATAC 960

Qy        241 ACTAAGTTTATCAA------TGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATG 294

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Db       1021 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1080

Qy        355 TTCGCACAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTC 414

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Qy        415 CGAAACCGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATA 474

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Qy        475 GACAAGATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAA 534

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Qy        535 TCTGGACAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATA 594

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Db       1372 AGCAAGCTGGATCGGC------TGGAGGCCTCGTCTGGCATCCTGGAGGTCCTGTACTGT 1425

Qy        715 GTGCTTATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATA 774

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Qy        835 TGCGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTG 894
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Db       1546 TGTGTGTGTAATGGTGTGGCTGTACGCTCCAACCAAGATCTTATTACTGAGAACTTGCTG 1605
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Qy        955 AACATCTTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTG 1014
Db       1666 AACATCTTTGTGGGCCGAGCGGAAGGCACCACGCAGTACAGCAAATGGTACTTTGAGGTG 1725
Qy       1015 ACTATGGACCA---CATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGG 1071
Db       1726 ATGGTGGACGAGGTGACTCCATTTCTGACAGCTCAGGCCACCCACTTGCGGGTGGGCTGG 1785
Qy       1072 GCCAACACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGC 1131
Db       1786 GCCCTCACCGAGGGCTACACCCCCTACCCTGGGGCCGGCGAGGGCTGGGGCGGCAACGGG 1845
Qy       1132 GTGGGAGATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGG 1191
Db       1846 GTCGGCGATGACCTCTATTCCTACGGCTTTGATGGACTGCATCTCTGGACAGGACACGTG 1905
Qy       1192 AAGACTCCCGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATA 1251
Db       1906 GCACGCCCGGT------GACTTCCCCAGGGCAGCACCTCTTGGCCCCTGAAGATGTGATC 1959
Qy       1252 GGTTGCGCATTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTG 1311
Db       1960 AGCTGCTGCCTGGACCTCAGTGTGCCGTCCATCTCCTTCCGCATCAACGGCTGCCCCGTG 2019
Qy       1312 ACGGGATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCT 1371
Db       2020 CAGGGTGTCTTTGAGTCCTTCAACCTGGACGGGCTCTTCTTCCCTGTTGTCAGCTTCTCG 2079
Qy       1372 AGTAAGCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCT 1431
Db       2080 GCTGGTGTCANGGTGCGGTTCCTCCTTGGTGGCCGCCATGGTGAATTCAAGTTCCTGCCC 2139
Qy       1432 CCAGAAGGCTACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAG 1491
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Qy       1492 CCGTGCTTCTACTTCGGCAACCTGTCCAAGCGGG------CCTTGGCTGGACCTCCGCTA 1545
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Qy       1546 GTACAGGACGATACGGCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCT 1605
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Qy       1606 ACATATGTGGAACAAATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATG 1665
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Qy       1786 GCTGTGCAGACACTCAAGACTATCCTGGCTCTGGGCTACTACATCAGCTT---AGATAAG 1842
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Qy       1843 CCTCCAGCACGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGC 1902
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Qy       1903 TACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTA 1962
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Db       2620 TACAAGCCGGCTCCGCTGGACCTGAGCCATGTGCGGCTGACACCGGCGCAGACGACACTG 2679
Qy       1963 GTAGACCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGA 2022
Db       2680 GTGGACCGTCTGGCAGAAAATGGGCACAACGTGTGGGCCCGAGACCGCGTGGGCCAGGGC 2739
Qy       2023 TGGACTTATGGACTTAATGAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATAC 2082
Db       2740 TGGAGCTACAGCGCAGTGCAGGACATCCCAGCGCGCCGAAACCCTCGGCTGGTGCCCTAC 2799
Qy       2083 CCGAAGGTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGG 2142
Db       2800 CGCCTGCTGGACGAAGCCACCAAGCGCAGCAACCGGGACAGCCTCTGCCAGGCCGTGCGC 2859
Qy       2143 ACCCTGCTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTC 2202
Db       2860 ACCCTCCTGGGCTACGGCTACAACATCGAGCCTCCTGACCAGGAGCCCAGTCAGGTGGAG 2919
Qy       2203 TTGTTGGAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAAC 2262
Db       2920 AACCAGTCTCGCTGTGACCGGGTGC------------GCATCTTCCGGGCAGAGAAATCC 2967
Qy       2263 TATGCCGTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATG 2322
Db       2968 TATACAGTGCAGAGCGGCCGCTGGTACTTCGAGTTTGAAGCAGTCACCACAGGCGAGATG 3027
Qy       2323 AGGGTCGGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAAC 2382
Db       3028 CGAGTGGGCTGGGCGAGGCCCGAGCTGAGGCCTGATGTAGAGCTGGGAGCTGACGAGCTG 3087
Qy       2383 TCTTGGGCATTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTC 2442
Db       3088 GCCTATGTCTTCAATGGGCACCGNGGCCAGCGCTGGCACTTGGG---CAGTGAACCATTT 3144
Qy       2443 GGCAAGCAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACG 2502
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Qy       2503 ATAAGTTTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTT 2562
Db       3205 ATTATCTTCACCCTCAATGGCGAGGTCCTCATGTCTGACTCAGGCTCCGAAACAGCCTTC 3264
Qy       2563 GCTGATGTCCAG---GGTGACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAA 2619
Db       3265 CGGGAGATTGAGATTGGGGACGGCTTCCTGCCCGTCTGCAGCTTGGGACCTGGCCAGGTG 3324
Qy       2620 GCCAGGTTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTT 2679
Db       3325 GGTCATCTGAACCTGGGCCAGGACGTGAGCTCTCTGAGGTTCTTTGCCATCTGTGGCCTC 3384
Qy       2680 CAGGAGGGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACC 2739
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Db       3445 AAAGGCCTGCCCCAGTTTGAG 3465
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DEFINITION  Homo sapiens RYR3 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   DQ034793
VERSION     DQ034793.1  GI:66886002
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 9562)
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  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2  (bases 1 to 9562)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.  Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 1484;  Conservative    0;  Mismatches 1248;  Indels  171;  Gaps   12;
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Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
Db        487 AGTGGTCTGTGGGTGACCTACAAAGCACAAGACGCCAAAACTTCCCGCCTGGGACCTCTA 546

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
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Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
Db        604 AGATGCCAGCGTGAGGAGTCCCAGGCTGCTCGGATCATCCGGAACACTACAGCCTTATTC 663

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
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Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
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Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
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Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
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Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
Db        883 TTAAATGTCTACAATAGCGTAGCACACTTTGCAGG---GATTGCAAGGGAAGAGAGTGGC 939

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
Db        940 ATGGCCTGGAAAGAAATTCTGAACCTCCTCTACAAATTGCTGGNNNNNNNNNNNNNNNN 999

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Qy        691 GGCATGCTCGACGTGCTGCACTGCGTGCTTATAGACTCGCCTGAAGCTCTCAATATGATG 750
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Qy        751 AGGGACGAACACATAAAAGTGATAATCTCTCTATTAGAAAAGCATGGGCGCGACCCTAAA 810
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Qy        811 GTACTAGATGTGCTATGTTCGCTGTGCGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAG 870
Db       1240 GTTCTGGATATCCTGTGCTCCCTCTGTCTCTGCAATGGGGTTGCAGTGAGAGCCAACCAG 1299

Qy        871 AACAACATCTGTGACTACTTACTGCCCGGCAAGAACCTGTTGCTGCAAACTGCGCTCGTG 930
Db       1300 AATCTGATCTGTGACAACTTGCTGCCCCGGAGAAACCTACTCCTGCAGACACGACTGATT 1359

Qy        931 GATCACGTATCTAGTGTCCGTCCGAACATCTTCGTGGGTCGAGTAGAAGGGTCGGCAGTG 990
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Qy        991 TACCGCAAATGGTACTTCGAGGTGACTATGGACCACATAGAGAAGACC---ACACATATG 1047
Db       1420 TACAAGAAGTGGTACTTCGAGCTGATTATCGACCAGGTGGACCCCTTCCTAACAGCAGAG 1479

Qy       1048 ATGCCACATCTACGCATAGGATGGGCCAACACTACTGGTTATGTCCCATACCCGGGCGGT 1107
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Qy       1108 GGCGAGAAATGGGGAGGTAACGGCGTGGGAGATGACCTGTACTCGTACGGGTTCGACGGC 1167
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Db       1600 CTTCACCTTTGGTCAGGCCG------GATACCCAGAGCTGTGGCTTCCATCAACCAGCAC 1653

Qy       1228 TATATTAGAAAAGGTGACGTGATAGGTTGCGCATTGGACCTGACGGTACCCATAATCAAC 1287
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Qy       1288 TTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACCAACTTCAATCTGGAAGGCATG 1347
Db       1714 TTCCGCATCAATGGGCAGCCCGTGCAGGGGATGTTTGAGAACTTCAACACAGACGGGCTC 1773

Qy       1348 TTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCCTGCTGGGCGGAGAA 1407
Db       1774 TTCTTCCCTGTGATGAGCTTTTCAGCAGGTGTCAAAGTACGTTTCCTGATGGGTGGACGT 1833

Qy       1408 CACGGTCGTCTCCGGTACGCGGCTCCAGAAGGCTACTCTCCCTTGGTGGAGTCTCTCCTG 1467
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Qy       1468 CCGCAGCAGATCCTCAGCCTGGAGCCGTGC------TTCTACTTCGGCAACCTGTCCAAG 1521
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Qy       1522 CGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACGGCCTTCGTGCCTACACCTGTT 1581
Db       1954 AGAGATCTCTTGGGTACCACCCAGTTCCTCTCCCAAGCCTCTTTCATCCCATGCCCCGTA 2013

Qy       1582 GATACTTTACAGATTACTCTGCCTACATATGTGGAACAAATTAGAGATAAGCTAGCTGAA 1641
Db       2014 GACACCAGTCAGGTTATTTTGCCACCTCACCTAGAAAAGATCCGAGACAGACTAGCTGAA 2073

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Qy       1762 GAGAAACGATACGACATACAACTCGCTGTGCAGACACTCAAGACTATCCTGGCTCTGGGC 1821

Db       2194 GAGAAGAACTATAACCTGCAAATGTCAACTGAAACCTTAAA---------- 2234

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Db       2235 ---------- 2234

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Qy       2002 AGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAATGAGGACTCGGACATGCATCGT 2061

Db       2353 AAAGACAGAATAAAACAAGGATGGACCTATGGCATCCAACAGGATTTGAAGAACAAAAGA 2412

Qy       2062 TCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCCATCAAGAAGGCCAACAGGGAC 2121

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Qy       2542 CTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGACAA---CTTTGTACCAGCTTGC 2598

Db       2881 AAAGGCTCTGAACTTGCCTTCGCTGACTACGAGATTGAGAATGGCTTCGTGCCCATCTGC 2940

Qy       2599 ACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAAGATGTGAATACTCTGAAA 2658

Db       2941 TGTCTGGGTCTATCTCAGATCGGCCGCATGAATCTCGGGACAGATGCCAGTACCTTCAAG 3000

Qy       2659 TACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTTTGCGTCAATATGAAGAGA 2718

Db       3001 TTTTATACCATGTGCGGTCTCCAAGAGGGCTTTGAGCCTTTTGCTGTCAACATGAACAGA 3060

Qy       2719 GACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAGAATACTGATGAGATGATC 2778

Db       3061 GATGTTGCTATGTGGTTCAGCAAGCGCCTCCCGACGTTTGTCAA---CGTGCCAAAGGAT 3117

Qy       2779 GACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGATACACCTCCATGCCTCAAG 2838

Db       3118 CATCCACACATAGAGGTCATGAGGATTGATGGCACCATGGACAGCCCTCCGTGTCTCAAG 3177

Qy       2839 ATTTCCCACAACACGTTCGAGAC 2861

Db       3178 GTGACGCATAAGACATTTGGCAC 3200
```

RESULT 4
DQ034794
LOCUS DQ034794 9526 bp DNA linear GSS 02-JUN-2005
DEFINITION Pan troglodytes RYR3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ034794
VERSION DQ034794.1 GI:66886003
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 9526)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 9526)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
source 1. .9526
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
gene <1. .>9526
/gene="RYR3"
/locus_tag="HC4229"
ORIGIN

Query Match 14.9%; Score 447.2; DB 11; Length 9526;
Best Local Similarity 48.3%; Pred. No. 4.9e-119;
Matches 1354; Conservative 0; Mismatches 1282; Indels 168; Gaps 11;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60

Db        391 GGCATGGGAGTTCCAGAAATCAAGTATGGAGATTCTGTCTGCTTTGTGCAGCATATAGCC 450

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120

Db        451 AGTGGTCTGTGGGTGACCTACAAAGCACAAGACGCCAAAACTTCCCGCCTGGGACCTCTA 510

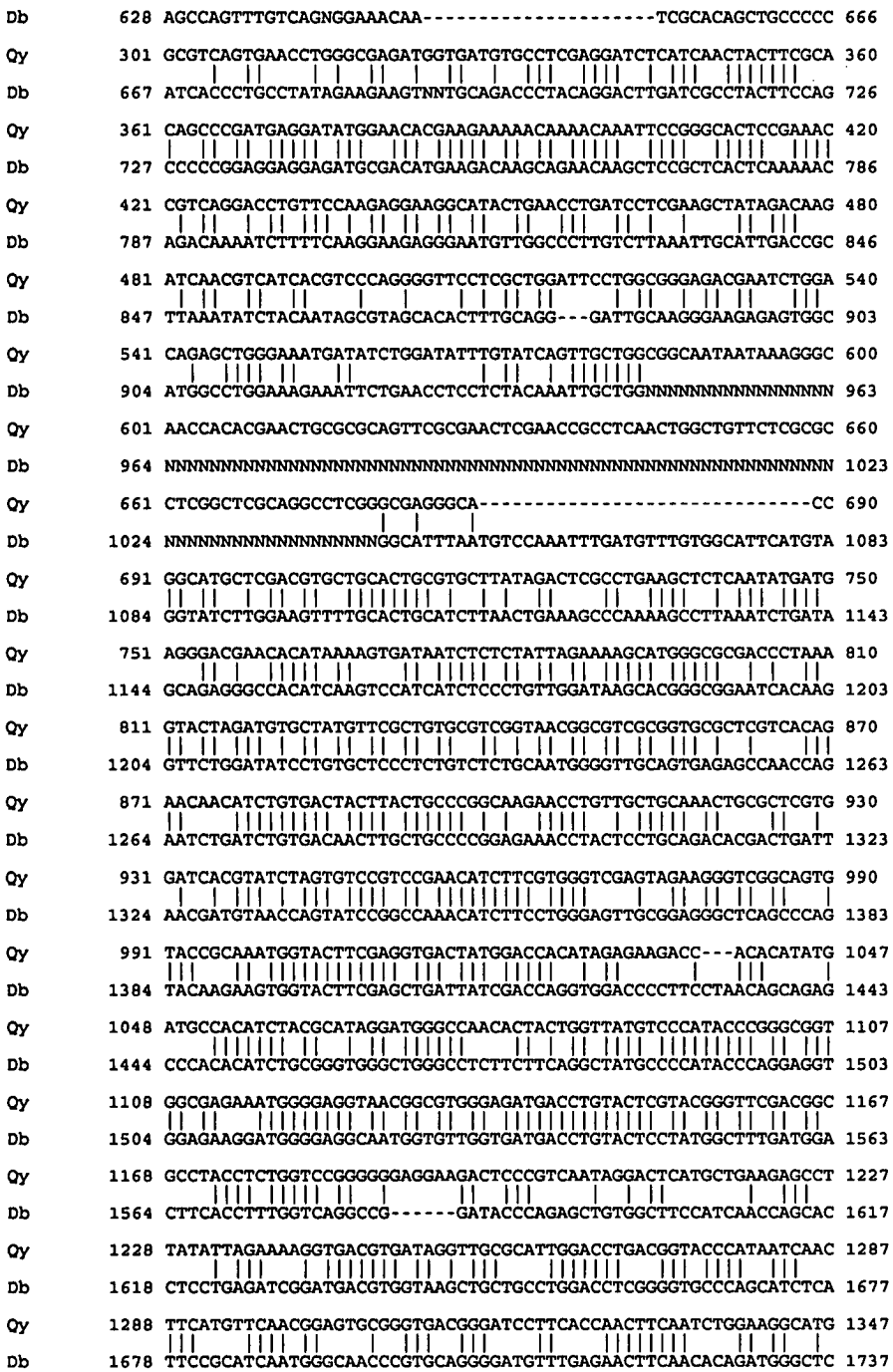
Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180

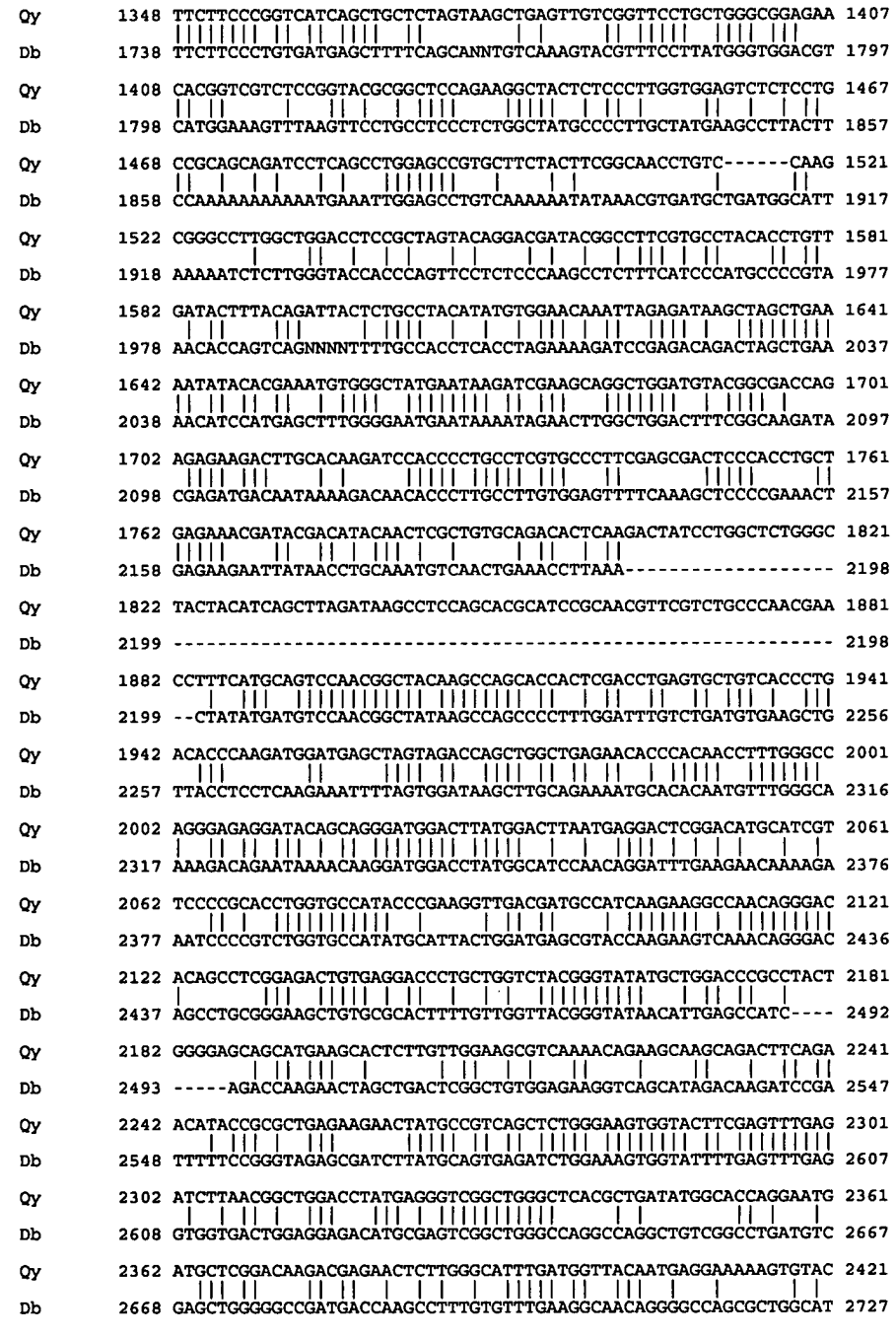
Db        511 AAAAGAAAG---GTCATACTCCATCAGGAAGGCCACATGGATGATGGATTAACACTGCAG 567

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240

Db        568 AGATGCCAGCGTGAGGAGTCCCAGGCTGCTCGGATCATCCGGAACACTACAGCCTTATTC 627

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
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Qy       2422 AGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTTGGTGACGTAGTGGGGGTGTTC 2481
Db       2728 CAAGG---AAGTGGGTATTTTGGGCGNNNCTGGCAGCCAGGGGATGTGGTCGGATGTATG 2784

Qy       2482 CTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAATGGTGAGTTGTTGATGGATGCT 2541
Db       2785 ATTAACCTGGATGATGCTTCAATGANNNTCACACTGAATGGGGANNNNNNGATCACCAAC 2844

Qy       2542 CTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGACAA---CTTTGTACCAGCTTGC 2598
Db       2845 AAAGGCTCNNNACTTGCCTTCGCTGACTACGAGATTGAGAATGNNNNNNNNNNNNNNNNN 2904

Qy       2599 ACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAAGATGTGAATACTCTGAAA 2658
Db       2905 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2964

Qy       2659 TACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTTTGCGTCAATATGAAGAGA 2718
Db       2965 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGAGCCTTNTNNNNTCAACATGAACAGA 3024

Qy       2719 GACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAGAA 2762
Db       3025 GATGTTGCNATGTGGTTCAGCAAGCGCCTCCCGACGTTNGTCAA 3068
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RESULT 5
CO307176
LOCUS CO307176 438 bp mRNA linear EST 25-JUN-2004
DEFINITION EK253833.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila melanogaster cDNA clone EK253833 5, mRNA sequence.
ACCESSION CO307176
VERSION CO307176.1 GI:49229019
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 438)
AUTHORS Kopczynski,C., Platt,D., Campbell,J., Muzong,C., Laufer,A., Peterson,E. and Swimmer,C.
TITLE Exelixis FlyTag EST Project CK01 Library
JOURNAL Unpublished (2004)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EK.2538 row: C column: 9
High quality sequence stop: 168.
FEATURES Location/Qualifiers
source 1. .438
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EK253833"
/clone_lib="Exelixis FlyTag CK01 pCDNA-SK+"
/note="Organ: mixed stage embryos, imaginal disks, and adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2: XhoI; Random primed, normalized library from mixed stage embryos, imaginal disks, and adult heads."
ORIGIN

Query Match 9.0%; Score 270.8; DB 7; Length 438;
Best Local Similarity 77.6%; Pred. No. 1.4e-67;
Matches 340; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

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Qy        472 ATAGACAAGATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGAC 531
Db          1 ATTGACAAGATCAACATAATCACCTCGCAGGGCTTCCTAGCCAGCTTCCTGGCCGGCGAC 60

Qy        532 GAATCTGGACAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATA 591
Db         61 GAGACCGGCCAGAGCTGGGATCTCATCTCCACCTATTTGTACCAACTCTTGGCCGCCATC 120

Qy        592 ATAAAGGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACT-GGCT 650
Db        121 ATCAAGGGCAACCACACGAACTGCGCCCAGTTCGCGAACAGTAACCGACTTAACTGGGTT 180

Qy        651 GTTCTCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCA 710
Db        181 ATTCTCCCGCCTCGGTTCCCAGGCCTCCAGCGAGGGTTCCGGCATGTTGGACGTACTTCA 240

Qy        711 CTGCGTGCTTATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGT 770
Db        241 CTGCGTGCTGATCGATTCGCCAGAGGCACTAAACATGATGCGGGATGAGCACATCAAGGT 300

Qy        771 GATAATCTCTCTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTC 830
Db        301 GATCATCTCCCTGCTGGAGAAGCACGGCAGGGACCCGAAAGTCCTAGACGTTCTGTGTTC 360

Qy        831 GCTGTGCGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTT 890
Db        361 CTTGTGCGTGGGTAATGGAGTGGCGGTGCGATCCTCCCAGAACAACATTTGCGACTTTTT 420

Qy        891 ACTGCCCGGCAAGAACCT 908
Db        421 GCTACCGGGCAAGAATCT 438
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RESULT 6
BI510684
LOCUS BI510684 506 bp mRNA linear EST 08-APR-2002
DEFINITION BB160003A20A12.5 Bee Brain Normalized Library, BB16 Apis mellifera cDNA clone BB160003A20A12 5', mRNA sequence.
ACCESSION BI510684
VERSION BI510684.1 GI:15361058
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
REFERENCE 1 (bases 1 to 506)
AUTHORS Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L., Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
TITLE Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee
JOURNAL Genome Res. 12 (4), 555-566 (2002)
PUBMED 11932240
COMMENT Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobi@life.uiuc.edu
This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
PCR PRimers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Plate: BB160003A20 row: A column: 12
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 506.
FEATURES Location/Qualifiers
source 1. .506
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB160003A20A12"

/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/clone_lib="Bee Brain Normalized Library, BB16"
/note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "

ORIGIN

Query Match 8.3%; Score 249.8; DB 3; Length 506;
Best Local Similarity 69.5%; Pred. No. 2.2e-61;
Matches 354; Conservative 0; Mismatches 152; Indels 3; Gaps 1;

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Qy       1165 GGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCCGTCAATAGGACTCATGCTGAAGAG 1224
             ||||||||| || ||| | || || || ||||| | ||  |       | |     |||
Db          1 GGCGCCTATCTGTGGACGGGCGGTAGAAAGACCCAAGT---TGTCCACAACGTGACGGAG 57

Qy       1225 CCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCATTGGACCTGACGGTACCCATAATC 1284
             ||||| || || ||| | |||||||| |||||||| ||||| || ||| ||||||||||||
Db         58 CCTTACATCAGGAAAAGCGACGTGATCGGTTGCGCGTTGGATCTCACGATACCCATAATC 117

Qy       1285 AACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACCAACTTCAATCTGGAAGGC 1344
             |  ||||  |||||||||| ||    | || ||||| |||   || ||||| ||||| ||
Db        118 ACGTTCACCTTCAACGGAGCGCCCATTACAGGATCGTTCCGAAATTTCAACCTGGACGGA 177

Qy       1345 ATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCCTGCTGGGCGGA 1404
             |||||||||| | ||||||||||||    ||  |    ||  | ||||||  | |||||
Db        178 ATGTTCTTCCCCGCCATCAGCTGCTCGTCCAAATTATCCTGCAGATTCCTGTTAGGCGGG 237

Qy       1405 GAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGCTACTCTCCCTTGGTGGAGTCTCTC 1464
             || ||||| || |||  || |    |||| ||||  | ||| || |||||||||   ||
Db        238 GACCACGGCCGGCTCAAGTTCCAACCTCCGGAAGAATTCTCACCGTTGGTGGAGAGCCTG 297

Qy       1465 CTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTCTACTTCGGCAACCTGTCCAAGCGG 1524
             || || || || ||  |   ||| || ||||||||||||||||| ||| ||  |||   |
Db        298 CTACCCCAACAAATTTTGTCCCTCGATCCGTGCTTCTACTTCGGGAACATGAACAAAGTG 357

Qy       1525 GCCTTGGCTGGACCTCCGCTAGTACAGGACGATACGGCCTTCGTGCCTACACCTGTTGAT 1584
             |  |||| || ||   ||| ||  ||||||| ||||| |||||  ||    || || ||
Db        358 GTGCTGGCCGGCCCCTGGCTGGTCGAGGACGACACGGCTTTCGTCCCGGGCCCGGTCGAC 417

Qy       1585 ACTTTACAGATTACTCTGCCTACATATGTGGAACAAATTAGAGATAAGCTAGCTGAAAAT 1644
             ||||    ||| | ||||||  | || || || ||||| || || |||||  || || ||
Db        418 ACTTCCATGATCAATCTGCCGTCCTACGTCGAGCAAATCAGGGACAAGCTGGCCGAGAAC 477

Qy       1645 ATACACGAAATGTGGGCTATGAATAAGAT 1673
             || ||||| |||||||| ||||| || ||
Db        478 ATCCACGAGATGTGGGCGATGAACAAAAT 506
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RESULT 7
DN394725
LOCUS DN394725 741 bp mRNA linear EST 07-MAR-2005
DEFINITION LIB3934-059-B1-K1-A11 LIB3934 Canis familiaris cDNA clone CLN12937360, mRNA sequence.
ACCESSION DN394725
VERSION DN394725.1 GI:60575946
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 741)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten

Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
FEATURES Location/Qualifiers
source 1. .741
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/clone="CLN12937360"
/tissue_type="brain"
/lab_host="DH10B"
/clone_lib="LIB3934"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; brain from normal dog"

ORIGIN

Query Match 7.3%; Score 220.2; DB 8; Length 741;
Best Local Similarity 58.6%; Pred. No. 1.3e-52;
Matches 422; Conservative 0; Mismatches 289; Indels 9; Gaps 2;

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Qy        777 CTCTCTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTG 836
              ||| ||  | || |||||||||| |  |||  || || || || ||||| ||||| |||||
Db         22 CTCCCTCCTGGACAAGCATGGGAGGAACCACAAGGTGCTGGACGTGCTGTGTTCCCTGTG 81

Qy        837 CGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCC 896
              ||  | || || || || |||||||||     || |   |||   |||  |||| || ||
Db         82 TGTGTGCAATGGTGTGGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACTTGCTCCC 141

Qy        897 CGGCAAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAA 956
              |||    | ||  ||||||||||     ||| |  |  | ||  | ||  |||| || ||
Db        142 TGGCCGTGAGCTTCTGCTGCAAACAAACCTCATCAACTATGTCACCAGCATCCGCCCCAA 201

Qy        957 CATCTTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGAC 1016
              |||||| ||||| |||| ||| || ||  |   ||| ||||||||||||| |||||||
Db        202 CATCTTTGTGGGCCGAGCAGAGGGCTCCACGCAATACGGCAAATGGTACTTTGAGGTGAT 261

Qy       1017 TATGGACCACATAGAGAAGACC---ACACATATGATGCCACATCTACGCATAGGATGGGC 1073
              |||||  |  | |          |  |||  |  |  | || || ||  | || |||||
Db        262 GGTGGACGAGGTGGCTCCATTCCTGACAGCTCAGGCCACCCACCTGCGGGTGGGCTGGGC 321

Qy       1074 CAACACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGT 1133
              |  ||||   || ||   ||| ||||| || || ||||||   |||| || || || ||
Db        322 CCTCACTGAGGGCTACAGCCCCTACCCAGGGGGCGGCGAGGGCTGGGGCGGCAATGGGGT 381

Qy       1134 GGGAGATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAA 1193
              || || ||||| || || ||||| || || ||    | |||||| | ||      |
Db        382 CGGCGACGACCTCTATTCCTACGGCTTTGATGGGCTGCATCTCTGGACAGGACACGTGGC 441

Qy       1194 GACTCCCGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGG 1253
              |  ||      ||||    | | | |||       |       | |||||  |  |
Db        442 ACGCCTGGT------GACTTCCCCAGGACAGCACCTCCTGGCCCCTGAGGACGTGGTCAG 495

Qy       1254 TTGCGCATTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGAC 1313
              |||    |||||| |  |||||    |||  ||||    |||| ||    |  |||
Db        496 CTGCTGCCTGGACCTCAGTGTACCGTCCATCTCCTTCCGCATCAATGGCTGTCCTGTGCA 555

Qy       1314 GGGATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAG 1373
              |||  |||     ||||||  |||||  ||  | ||||||| ||  ||||| |||
Db        556 GGGTGTCTTTGAGGCCTTCAACCTGGATGGGCTCTTCTTCCCTGTTGTCAGCTTCTCAGC 615

Qy       1374 TAAGCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCC 1433
              |   | |     |||||||| || || ||  || |||   ||  || |    ||||
Db        616 TGGTGTCAAGGTGCGGTTCCTCCTTGGTGGCCGCCATGGTGAATTCAAGTTCCTCCCTCC 675

Qy       1434 AGAAGGCTACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCC 1493
              |   | |||  | || |     ||| || | || || |   |    ||    ||||||||
Db        676 ACCTGNCTATGCCCCATGTCATGAGGCTGTGCTCCCTCGAGAACGACTTCATCTGGAGCC 735
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RESULT 8
BB619828
LOCUS BB619828 686 bp mRNA linear EST 26-OCT-2001
DEFINITION BB619828 RIKEN full-length enriched, adult male thymus Mus musculus

cDNA clone 5830433B05 5', mRNA sequence.
ACCESSION BB619828
VERSION BB619828.1 GI:16459075
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 686)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.
FEATURES Location/Qualifiers
source 1. .686
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5830433B05"
/sex="male"
/tissue_type="thymus"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male thymus"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
ORIGIN

Query Match 6.7%; Score 202; DB 2; Length 686;
Best Local Similarity 59.5%; Pred. No. 2.9e-47;
Matches 381; Conservative 0; Mismatches 250; Indels 9; Gaps 2;

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Qy        707 TGCACTGCGTGCTTATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAA 766
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Db          3 TGCACTGCATCTTGATTGAAAGCCCAGAAGCCTTAAACCTAATAGCAGAGGGCCACATCA 62

Qy        767 AAGTGATAATCTCTCTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTAT 826
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Db         63 AGTCTATCATCTCCCTACTGGATAAGCATGGGCGGAATCACAAGGTTCTCGATGTCCTGT 122

Qy        827 GTTCGCTGTGCGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACT 886
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RESULT 9
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LOCUS BY717863 610 bp mRNA linear EST 17-DEC-2002
DEFINITION BY717863 RIKEN full-length enriched, adult male thymus Mus musculus cDNA clone 5830431J16 5', mRNA sequence.
ACCESSION BY717863
VERSION BY717863.1 GI:27130980
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
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            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
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            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
   PUBMED   12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
             cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
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                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI."
ORIGIN

  Query Match             6.7%;  Score 200.6;  DB 5;  Length 610;
  Best Local Similarity   60.4%;  Pred. No. 7.2e-47;
  Matches  370;  Conservative    0;  Mismatches  234;  Indels    9;  Gaps    2;

Qy        707 TGCACTGCGTGCTTATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAA 766
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Db          3 TGCACTGCATCTTGATTGAAAGCCCAGAAGCCTTAAACCTAATAGCAGAGGGCCACATCA 62

Qy        767 AAGTGATAATCTCTCTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTAT 826
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Db         63 AGTCTATCATCTCCCTACTGGATAAGCATGGGCGGAATCACAAGGTTCTCGATGTCCTGT 122

Qy        827 GTTCGCTGTGCGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACT 886
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Db        123 GCTCCCTCTGTCTCTGCAATGGGGTTGCAGTAAGAGCCAACCAGAATCTGATCTGTGACA 182

Qy        887 ACTTACTGCCCGGCAAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTG 946
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Db        183 ACCTACTACCCCGAAGGAACCTGCTTCTGCAGACACGACTAATTAATGATGTCACCAGCA 242

Qy        947 TCCGTCCGAACATCTTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACT 1006
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Db        243 TCCGGCCAAACATCTTCCTGGGAGTTGCTGAAGGTTCACCACAGTACAAGAAGTGGTACT 302

Qy       1007 TCGAGGTGACTATGGACCACATAGAGAAGACC---ACACATATGATGCCACATCTACGCA 1063
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Db        303 TTGAGTTAATTATCGACCAGGTGGAGCCTTTCCTAACAGCAGAGCCTACACATCTGCGAG 362

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Db        363 TGGGCTGGGCCTCCTCTTCAGGCTATGCCCCGTACCCTGGTGGTGGAGAAGGATGGGGAG 422

Qy       1124 GTAACGGCGTGGGAGATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCG 1183
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Db        423 GCAATGGTGTCGGTGATGATCTGTACTCCTATGGCTTTGATGGGCTTCATCTGTGGTCAG 482

Qy       1184 GGGGGAGGAAGACTCCCGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTG 1243
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Db        483 GACG------GATACCCAGAGCTGTGGCTTCCATCAACCAGCATCTGCTCAAGTCAGACG 536

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Qy       1304 TGCGGGTGACGGG 1316
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RESULT 10
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LOCUS       AL919721                523 bp    mRNA    linear   EST 06-JUL-2004
DEFINITION  AL919721 PJR-Z1+Z2 Danio rerio cDNA clone 067-G09-2, mRNA sequence.
ACCESSION   AL919721
VERSION     AL919721.1  GI:23185019
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W.,
            Wang,W., Wen,Z. and Peng,J.
  TITLE     15000 unique zebrafish EST clusters and their future use in
            microarray for profiling gene expression patterns during
            embryogenesis
  JOURNAL   Genome Res. 13 (3), 455-466 (2003)
   PUBMED   12618376
COMMENT     Contact: Peng J
            Lab of Functional Genomics
            Institute of Molecular and Cell Biology
            30 Medical Drive, Singapore, 117609, Singapore
            Email: pengjr@imcb.a-star.edu.sg
            Clone requests: info@openbiosystems.com
            Open Biosystems,
            6705 Odyssey Drive, Huntsville, AL 35806.
FEATURES             Location/Qualifiers
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ORIGIN

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Db        343 AATTTCATCTGTGACCACCTGCTTCCAAGGAGAGACCTGCTGCTCCAAACACGACTGGTC 284

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RESULT 11
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LOCUS       BB251214                652 bp    mRNA    linear   EST 23-OCT-2001
DEFINITION  BB251214 RIKEN full-length enriched, 7 days neonate cerebellum Mus
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ACCESSION   BB251214
VERSION     BB251214.2  GI:16355849
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 652)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
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            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     On Jul 6, 2000 this sequence version replaced gi:8943960.
            Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
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            and Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
            Sugahara,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
            Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
FEATURES             Location/Qualifiers
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 6.5%; Score 194.2; DB 2; Length 652;
Best Local Similarity 59.1%; Pred. No. 5.7e-45;
Matches 372; Conservative 0; Mismatches 248; Indels 9; Gaps 2;

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Qy       806 CTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTCGGTAACGGCGTCGCGGTGCGCTCGT 865
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Qy       926 TCGTGGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTGGGTCGAGTAGAAGGGTCGG 985
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Db       301 CAGAAGCCACTCACCTGCGAGTGGGCTGGGCTTCCACTGAAGGGTATTCTCCATACCCAG 360

Qy      1103 GCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGATGACCTGTACTCGTACGGGTTCG 1162
Db       361 GTGGGGGTGAAGAGTGGGGTGGCAATGGCGTTGGTGACGACCTCTTCTCCTATGGGTTTG 420

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Db       421 ATGGCCTTCACCTCTGGTCAGGTTGTATAGCTCGGACCGT------GAGCTCCCCCAACC 474

Qy      1223 AGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCATTGGACCTGACGGTACCCATAA 1282
Db       475 AGATCCTGCTGAGAACTGACGATGTCATCAGTTGTTGTTTAGATCTAAGTGCCCCCAGCA 534

Qy      1283 TCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACCAACTTCAATCTGGAAG 1342
Db       535 TCTCGTTTCGCATTAATGGACAACCGGTGCAAGGGATGTTTGAGAACTTCAATATCGATG 594

Qy      1343 GCATGTTCTTCCCGGTCATCAGCTGCTCT 1371
Db       595 GCCTGTTCTTTCCAGTTGTCAGTTTCTCT 623
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RESULT 12
BJ753908
LOCUS BJ753908 665 bp mRNA linear EST 24-MAY-2004
DEFINITION BJ753908 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone yk1396b07 5', mRNA sequence.
ACCESSION BJ753908
VERSION BJ753908.1 GI:47593670
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 665)
AUTHORS Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES Location/Qualifiers
source 1. .665
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1396b07"
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ORIGIN

Query Match 6.3%; Score 189.4; DB 3; Length 665;
Best Local Similarity 57.6%; Pred. No. 1.5e-43;
Matches 359; Conservative 0; Mismatches 261; Indels 3; Gaps 1;

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Qy         4 ATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAGACT 63
Db        39 ATGGGAAATGCTACAATCAGATATGGAGAGACAAATGCTTTTATTCAACACGTGAAAACT 98

Qy        64 GGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTAGAA 123
Db        99 CAGCTCTGGTTGTCCTATCAAACAACTGAAGTTACAAAGAAAGGACTTGGAAAGGTGGAA 158

Qy       124 GAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCCAGG 183
Db       159 GAGAAGAAAGCAGTTGCTCTGAAAGATGGTCACATGGATGACTGTTACACTTTCTTTATG 218

Qy       184 TCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACT 243
Db       219 GCTTTAGAAGAAGAATCCAAATCAGCTAGAGTCATTAGGAAATGTTCATCGGTTCTCAAT 278

Qy       244 AAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTCGCG 303
Db       279 AAATTCTTGAAAGGAATCGATGCATTGCAACTTGAAGGAAACCAATCAACGGATTGGACA 338

Qy       304 TCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCACAG 363
Db       339 AGAGTCGATCTCAATGAAGTTTTAAAATTGATGGAAGATCTCATTGAATACTTTGCACAA 398

Qy       364 CCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAACCGT 423
Db       399 CCAAATGATGAGCAAGACTTTGAGGAGAAACAGAATCACTTGAGAGCTCTTCGTAGTCGG 458
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Qy        424 CAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATC 483
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Db        459 CAAGATCTTTTCCAAGAAGAAGGAGTTCTTAATATGATTCTTGACACTATCGACAAATTC 518

Qy        484 AACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGACAG 543
                ||   | | |          ||||||||||  |    |||||  ||  ||      |
Db        519 TCTCAAATGGAGGCGCTTCCTGATTTCGCTGGATTAAT---CGGAGAAGAGACTCATGTG 575

Qy        544 AGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGCAAC 603
              |  |||||   ||| |||   ||| ||||||  ||| | || || || || ||||| ||
Db        576 AAATGGGAGCAGATCTCTACTTATCTGTATCTTTTGGTAGCTGCTATGATTAAGGGAAAT 635

Qy        604 CACACGAACTGCGCGCAGTTCGC 626
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Db        636 CATTATAATTGTGCCCAATTTGC 658


RESULT 13
BJ104437
LOCUS       BJ104437                610 bp    mRNA    linear   EST 18-JAN-2002
DEFINITION  BJ104437 unpublished oligo-capped cDNA library, C. elegans L1 stage
            Caenorhabditis elegans cDNA clone yk1061g01 5', mRNA sequence.
ACCESSION   BJ104437
VERSION     BJ104437.1  GI:18247107
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             6.2%;  Score 186.2;  DB 3;  Length 610;
  Best Local Similarity   57.8%;  Pred. No. 1.3e-42;
  Matches  351;  Conservative    0;  Mismatches  253;  Indels    3;  Gaps    1;

Qy         14 CCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAGACTGGCTTGTGGC 73
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Db          7 CTACAATCAGATATGGAGAGACAAATGCTTTTATTCAACACGTGAAAACTCAGCTCTGGT 66

Qy         74 TGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTAGAAGAGAAGCAAG 133
              |||| ||| |  |    |||   |  ||||| ||| | || || || |||||||| |||
Db         67 TGTCCTATCAAACAACTGAAGTTACAAAGAAAGGACTTGGAAAGGTGGAAGAGAAGAAAG 126

Qy        134 CGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCCAGGTCACAGGAGG 193
              |  ||   |  | || ||  | ||||| ||  |   |  ||||  | | |    || |
Db        127 CAGTTGCTCTGAAAGATGGTCACATGGATGACTGTTACACTTTCTTTATGGCTTTAGAAG 186

Qy        194 AAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAGTTTATCA 253
              ||||||| |   | ||| |||| || ||||| ||||| ||| |  ||| ||| ||  | |

Db        187 AAGAATCCAAATCAGCTAGAGTCATTAGGAAATGTTCATCGGTTCTCAATAAATTCTTGA 246

Qy        254 ATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCAGTGAACC 313
              | ||  | ||  |  | |||     |  |    || || | |   |   |  ||| | |
Db        247 AAGGAATCGATGCATTGCAACTTGAAGGAAACCAATCAACGGATTGGACAAGAGTCGATC 306

Qy        314 TGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCACAGCCCGATGAGG 373
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Db        307 TCAATGAAGTTTTAAAATTGATGGAAGATCTCATTGAATACTTTGCACAACCAAATGATG 366

Qy        374 ATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAACCGTCAGGACCTGT 433
              |    ||    || || ||||| ||  | ||  | || || || |  || || || || |
Db        367 AGCAAGACTTTGAGGAGAAACAGAATCACTTGAGAGCTCTTCGTAGTCGGCAAGATCTTT 426

Qy        434 TCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAACGTCATCA 493
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Db        427 TCCAAGAAGAAGGAGTTCTTAATATGATTCTTGACACTATCGACAAATTCTCTCAAATGG 486

Qy        494 CGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGCTGGGAAA 553
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Db        487 AGGCGCTTCCTGATTTCGCTGGATTAAT---CGGAGAAGAGACTCATGTGAAATGGGAGC 543

Qy        554 TGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGCAACCACACGAACT 613
              ||| |||   ||| ||||||  ||| | || || || || ||||| || ||    || |
Db        544 AGATCTCTACTTATCTGTATCTTTTGGTAGCTGCTATGATTAAGGGAAATCATTATAATT 603

Qy        614 GCGCGCA 620
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Db        604 GTGCCCA 610


RESULT 14
BU313121
LOCUS       BU313121                692 bp    mRNA    linear   EST 28-NOV-2002
DEFINITION  603405539F1 CSEQCHN61 Gallus gallus cDNA clone ChEST309m9 5', mRNA
            sequence.
ACCESSION   BU313121
VERSION     BU313121.1  GI:25821122
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .692
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                     /strain="Compton Line 15I"
                     /db_xref="taxon:9031"
                     /clone="ChEST309m9"
                     /sex="Female"
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                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN61"
                     /note="Organ: heart; Vector: pBluescript II KS(+); Site_1:
                     EcoRI; Site_2: Not1; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
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methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 6.2%; Score 186; DB 5; Length 692;
Best Local Similarity 57.2%; Pred. No. 1.5e-42;
Matches 380; Conservative 0; Mismatches 275; Indels 9; Gaps 2;

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Db         22 TAAACATTATTAAGGAAGGACATATTAAATCAATCATCTGTCTTTTGGACAAACATGGAA 81

Qy        800 GCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTCGGTAACGGCGTCGCGGTGC 859
              |  ||| ||| ||  | |||||  ||||||| || || ||  || | || || || ||||
Db         82 GAAACCATAAGGTTTTGGATGTCTTATGTTCTCTCTGTGTATGTCATGGAGTAGCTGTGC 141

Qy        860 GCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGCAAGAACCTGTTGCTGCAAA 919
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Db        142 GGTCCAATCAACATCTAATCTGTGATAATCTCCTGCCAGGAAGAGATCTGCTCTTACAGA 201

Qy        920 CTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATCTTCGTGGGTCGAGTAGAAG 979
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Db        202 CCCGCCTTGTGAACCATGTGAGCAGCATGCGACCTAATATTTTCTTGGGAATTAGTGAAG 261

Qy        980 GGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATGGACCACATAGAG---AAGA 1036
              | || ||   |||| | ||||||||||  ||  | |   |||||||  |||||
Db        262 GCTCTGCTCAGTACAGAAAATGGTACTATGAACTTATGGTGGACCATCTAGAGCCTTTTG 321

Qy       1037 CCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACTACTGGTTATGTCCCAT 1096
                ||           | || |||||  |||| |||||     ||    || ||    || |
Db        322 TGACTGCAGAATCAACTCACCTACGAGTAGGCTGGGCTTCAACAGAGGGCTACTCACCGT 381

Qy       1097 ACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGATGACCTGTACTCGTACG 1156
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Db        382 ATCCAGGGGGAGGAGCAGAGTGGGGAGGAAATGGTGTTGGTGATGACTTGTATTCTTATG 441

Qy       1157 GGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCCGTCAATAGGACTCATG 1216
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Db        442 GCTTCGATGGTCTGCATCTGTGGTCAGGCTGTGTAGCTCGAACAGTAAATTC------TC 495

Qy       1217 CTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCATTGGACCTGACGGTAC 1276
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Db        496 CAAACCAACATCTGCTGAGAACTGAAGATGTTATTAGTTGCTGTTTGGATCTGAGCGCCC 555

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Db        556 CCAGCATCTCTTTTCGGATAAATGGACAGCCAGTTCAAGGAATGTTTGAGAATTTCAACA 615

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RESULT 15
BU341628
LOCUS BU341628 777 bp mRNA linear EST 28-NOV-2002
DEFINITION 603520327F1 CSEQCHN67 Gallus gallus cDNA clone ChEST462f8 5', mRNA sequence.
ACCESSION BU341628
VERSION BU341628.1 GI:25849629
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 777)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
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/lab_host="DH10B"
/clone_lib="CSEQCHN67"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 5.3%; Score 160; DB 5; Length 777;
Best Local Similarity 55.2%; Pred. No. 7.1e-35;
Matches 421; Conservative 0; Mismatches 325; Indels 16; Gaps 5;

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Qy       1047 GATGCCACATCTACGCATAGGATGGGCCAACACTACTGGTTATGTCCCATACCCGGGCGG 1106
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Db         65 ATCAACTCACCTACGAGTAGGCTGGGCTTCAACAGAGGGCTACTCACCGTATCCAGG-GG 123

Qy       1107 TGGCGAGAAATGGGGAGGTAACGGCGTGGGAGATGACCTGTACTCGTACGGGTTCGACGG 1166
                || |   | |||||||| || || |  || |||||| |||| || || || ||||| ||
Db        124 AGGAGCAGAGTGGGGAGGAAATGGTGCTGGTGATGACTTGTATTCTTATGGCTTCGATGG 183

Qy       1167 CGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCCGTCAATAGGACTCATGCTGAAGAGCC 1226
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Db        184 TCTGCATCTGTGGTCAGGCTGTGTAGCTCGAACAGTAAATTC------TCCAAACCAACA 237

Qy       1227 TTATATTAGAAAAGGTGACGTGATAGGTTGCGCATTGGACCTGACGGTACCCATAATCAA 1286
                |    | ||||  |  || || ||  |||||  ||||| ||||  |  ||||  |||
Db        238 TCTGCTGAGAACTGAAGATGTTATTAGTTGCTGTTTGGATCTGAGCGCCCCCAGCATCTC 297

Qy       1287 CTTCATGTTCAACGGAGTGCGGGTGACGGGATCCTTCACCAACTTCAATCTGGAAGGCAT 1346
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Db        298 TTTTCGGATAAATGGACAGCCAGTTCAAGGAATGTTTGAGAATTTCAACATAGATGGCCT 357
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Qy       1347 GTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTGAGTTGTCGGTTCCTGCTGGGCGGAGA 1406
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Db        358 TTTCTTCCCAGTTGTCAGCTTCTCTGCAGGAATAAAGGTACGTTTCTTGCTTGGAGGTCG 417

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Qy       1467 GCCGCAGCAGATCCTCAGCCTGGAG-----CCGTGCTTCTACTTCGGCAACCTGTCCAAG 1521
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Search completed: April 14, 2006, 20:56:05
Job time : 11368.5 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 14:01:15 ; Search time 499.5 Seconds
(without alignments)
10679.605 Million cell updates/sec

Title: US-10-668-767-127_COPY_1000_4000
Perfect score: 3001
Sequence: 1 gtcataggcgcgcccatcat.....cctaatgaaagaggcagttg 3001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	671	22.4	15378	3	US-08-785-420-1	Sequence 1, Appli
	2	668	22.3	4078	3	US-09-016-434-1154	Sequence 1154, Ap
	3	597	19.9	15572	3	US-09-424-783-1	Sequence 1, Appli
	4	61.8	2.1	1050	2	US-08-480-481-4	Sequence 4, Appli
	5	60.2	2.0	1050	2	US-08-480-481-3	Sequence 3, Appli
	6	58	1.9	1598	3	US-08-785-420-3	Sequence 3, Appli
	7	46.2	1.5	900	2	US-08-480-481-6	Sequence 6, Appli
c	8	43	1.4	7218	2	US-08-232-463-14	Sequence 14, Appl
	9	38.6	1.3	2125	3	US-09-485-529-14	Sequence 14, Appl
	10	38	1.3	832	3	US-09-621-976-2813	Sequence 2813, Ap
	11	38	1.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	12	38	1.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	13	37.8	1.3	294	3	US-09-252-991A-11838	Sequence 11838, A
	14	37.6	1.3	1334	3	US-09-668-097A-35	Sequence 35, Appl
c	15	37.4	1.2	299	3	US-09-513-999C-35034	Sequence 35034, A
	16	37	1.2	1768	3	US-09-485-529-13	Sequence 13, Appl
c	17	36.8	1.2	2387	3	US-09-831-683B-17	Sequence 17, Appl
	18	36.6	1.2	3778	3	US-09-799-451-160	Sequence 160, App
	19	36.6	1.2	4376	3	US-10-200-012-15	Sequence 15, Appl
c	20	36.4	1.2	650	3	US-09-533-559-306	Sequence 306, App
c	21	36	1.2	399	3	US-09-621-976-8976	Sequence 8976, Ap
	22	36	1.2	1738	3	US-10-164-595-31	Sequence 31, Appl
	23	35.6	1.2	1389	3	US-09-252-991A-3839	Sequence 3839, Ap
	24	35.6	1.2	1398	3	US-09-252-991A-3757	Sequence 3757, Ap
c	25	35.6	1.2	1710	3	US-09-252-991A-3623	Sequence 3623, Ap
c	26	35.6	1.2	2490	3	US-10-104-047-65	Sequence 65, Appl
	27	35.6	1.2	10528	3	US-09-902-540-945	Sequence 945, App
	28	35.6	1.2	61913	3	US-09-949-016-15338	Sequence 15338, A
	29	35.6	1.2	61922	3	US-09-949-016-11772	Sequence 11772, A
	30	35.4	1.2	1122	3	US-09-252-991A-7810	Sequence 7810, Ap
	31	35.4	1.2	1389	3	US-09-252-991A-7948	Sequence 7948, Ap
c	32	35.4	1.2	1947	3	US-09-252-991A-7533	Sequence 7533, Ap
	33	35.2	1.2	870	3	US-09-902-540-5914	Sequence 5914, Ap
	34	35.2	1.2	1289	3	US-09-902-540-175	Sequence 175, App
	35	35	1.2	1269	3	US-09-252-991A-9164	Sequence 9164, Ap
	36	35	1.2	1446	3	US-09-252-991A-10586	Sequence 10586, A
	37	35	1.2	3222	3	US-09-252-991A-10770	Sequence 10770, A
c	38	34.8	1.2	19954	3	US-09-902-540-1150	Sequence 1150, Ap
	39	34.4	1.1	430	3	US-09-621-976-16656	Sequence 16656, A
c	40	34.4	1.1	1323	3	US-09-489-039A-5432	Sequence 5432, Ap
c	41	34.4	1.1	2016	3	US-09-252-991A-7070	Sequence 7070, Ap
c	42	34.4	1.1	2422	3	US-09-369-247-53	Sequence 53, Appl
c	43	34.4	1.1	2422	3	US-10-062-548-53	Sequence 53, Appl
c	44	34.4	1.1	4112	3	US-09-799-451-706	Sequence 706, App
	45	34.4	1.1	6855	3	US-09-252-991A-6976	Sequence 6976, Ap

ALIGNMENTS

RESULT 1
US-08-785-420-1
; Sequence 1, Application US/08785420
; Patent No. 6001976
; GENERAL INFORMATION:
; APPLICANT: MacLennan, David H
; APPLICANT: O'Brien, Peter J.
; TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
; TITLE OF INVENTION: HYPERTHERMIA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte,
; STATE: No. 6001976th Carolina 28234
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,388
; FILING DATE:
; APPLICATION NUMBER: US 08/030,159
; FILING DATE: 15-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Layton,Jr., Samuel G.
; REGISTRATION NUMBER: 22807
; REFERENCE/DOCKET NUMBER: 3477-73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 704-377-1561
; TELEFAX: 704-334-2014
; TELEX: 57-5102
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

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;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  Porcine RYR1 Gene
;    POSITION IN GENOME:
;      UNITS:  bp
US-08-785-420-1

  Query Match             22.4%;  Score 671;  DB 3;  Length 15378;
  Best Local Similarity   55.6%;  Pred. No. 3.2e-185;
  Matches 1546;  Conservative    0;  Mismatches 1175;  Indels   60;  Gaps   11;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              | ||| ||| | ||    ||||| ||||| || ||       | | |||||||||   |
Db       1126 GGCATGGGCCCCCCTGAGATCAAGTATGGGGAGTCACTGTGCTTCGTGCAGCATGTGGCC 1185

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              | ||| |||||||  | |||     ||  | |||     | |  | ||    ||
Db       1186 TCGGGCCTGTGGCTTACCTATGCTGCCCCAGACCCCAAGGCCCTGCGGCTCGGC---GTG 1242

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
               |||||  | || |||||  ||| |||||||| | ||||||||||  ||      |  ||
Db       1243 CTCAAGAAGAAGGCCATTCTGCACCAGGAAGGCCACATGGACGATGCACTGTCACTGACC 1302

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              | |  ||| |||| || ||    | | || ||  | |||     |    | ||   || | |
Db       1303 CGCTGTCAGCAGGAGGAGTCCCAGGCGGCCCGCATGATCTATAGCACTGCTGGCCTCTAC 1362

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTC--- 297
              |  | || ||||| || ||||| | |   |  || |  ||  |||  |  |
Db       1363 AACCACTTCATCAAGGGCCTGGACAGCTTCAGCGGAAAGCCACGGGGCTCTGGGGCCCCG 1422

Qy        298 ---TTCGCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTAC 354
                 | |  |   |  ||| |  |   |  |  || ||||  |||| |||||  ||||
Db       1423 GCTGGCACAGCGCTACCCCTCGAGGGCGTCATCCTGAGCCTGCAGGACCTCATCGGCTAC 1482

Qy        355 TTCGCACAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTC 414
              || |  | ||||   || ||  || | ||||| || || ||  |||  | ||     ||
Db       1483 TTTGAGCCGCCCTCGGAAGAGCTGCAGCACGAGGAGAAGCAGAGCAAGCTGCGCAGCCTG 1542

Qy        415 CGAAACCGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATA 474
              || ||||| |||  ||| ||||| ||||| || ||  ||   |||| ||||  |   ||
Db       1543 CGCAACCGCCAGAGCCTCTTCCAGGAGGAGGGGATGCTCTCCCTGGTCCTGAATTGCATT 1602

Qy        475 GACAAGATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAA 534
              |||    | || |||  |||  |    |    | | ||||  |   | || ||||| ||
Db       1603 GACCGCCTAAATGTCTACACCACTGCTGCCCACTTTGCTGAGT---TTGCAGGAGAGGAG 1659

Qy        535 TCTGGACAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATA 594
              | |   ||  |||| ||  |||           ||||| || | ||||  |  | ||
Db       1660 GCAGCCGAGTCCTGGAAAGAGATTGTGAACCTGCTGTATGAGATCCTGGCCTCTCTGATC 1719

Qy        595 AAGGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTC 654
                |||||  |   | |||||  || |  |||  | ||          |||||  |   |
Db       1720 CGTGGCAATCGTGCCAACTGTGCCCTTTTCTCCAA-----------CAACTTGGATTGG 1767

Qy        655 TCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGC 714
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Db       1768 CTGGTCAGCAAGCTGGATCGACTGGAGGCCTCCTCAGGGATCCTGGAGGTGCTGTACTGT 1827

Qy        715 GTGCTTATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATA 774
              || || || ||     ||||| |  || || || ||    |||  | |||||  ||
Db       1828 GTCCTGATTGAGAGTCCTGAGGTCCTGAACATCATCCAGGAGAACCACATCAAGTCCATC 1887

Qy        775 ATCTCTCTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTG 834
              |||||  ||  | || |||||||||  |  |||  ||  || || ||||| || ||||| |||
Db       1888 ATCTCCCTTCTGGACAAGCATGGGAGGAACCACAAGGTGCTGGATGTCCTGTGTTCCCTG 1947

Qy        835 TGCGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTG 894
              || ||  | || || || || ||| ||||    ||  |   |||   |||  |||| ||
Db       1948 TGTGTGTGCAATGGTGTGGCCGTGTGCTCCAACCAAGATCTCATTACTGAGAACTTGCTC 2007

Qy        895 CCCGGCAAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCG 954
              || |||    | ||  ||||||| ||    ||| |  |  | ||  | ||  |||| ||

Db       2008 CCTGGCCGCGAGCTTCTGCTGCAGACAAACCTCATCAACTATGTCACCAGCATCCGCCCC 2067

Qy        955 AACATCTTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTG 1014
              |||||||| ||||| |||| ||| ||  |  ||  |||| |||||||||||||| |||||
Db       2068 AACATCTTTGTGGGCCGAGCAGAGGGCACCACACAGTACAGCAAATGGTACTTTGAGGTC 2127

Qy       1015 ACTATGGACCACATAGAGAAGACC---ACACATATGATGCCACATCTACGCATAGGATGG 1071
              |  ||||| |  | |    |   ||| |  |   | || || ||  | || |||
Db       2128 ATGGTGGACGAAGTGGTTCCATTCCTGACAGCTCAGGCCACCCACCTGCGGGTGGGCTGG 2187

Qy       1072 GCCAACACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGC 1131
              |||  |||     || ||   ||| ||||| || || ||||||   ||||| || |||||
Db       2188 GCCCTCACCGAAGGCTACAGCCCCTACCCTGGGGGCGGCGAGGGCTGGGGCGGCAACGGG 2247

Qy       1132 GTGGGAGATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGG 1191
              || || |||||||| || || |||| || ||||      | ||||| | |    |
Db       2248 GTCGGCGATGACCTCTATTCCTACGGCTTTGACGGGCTGCATCTCTGGACAG------GA 2301

Qy       1192 AAGACTCCCGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATA 1251
              |  ||  |   |||| | |  |||  | |    |  |||||| |
Db       2302 CACGTGCCACGCCTGGTGACTTCCCCAGGGCAGCACCTTCTGGCCCCCGAGGACGTGGTC 2361

Qy       1252 GGTTGCGCATTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTG 1311
              | |||   |||||||  |  || ||   |||  ||||   |||||||    |  |||
Db       2362 AGCTGCTGCCTGGACCTCAGCGTGCCGTCCATCTCCTTCCGCATCAACGGCTGCCCCGTG 2421

Qy       1312 ACGGGATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCT 1371
               |||   ||||          |||  | ||  | |||||||| |||  |||||| |||
Db       2422 CAGGGCGTCTTCGAGGCCTTCAACCTCAACGGGCTCTTCTTCCCCGTCGTCAGCTTCTCG 2481

Qy       1372 AGTAAGCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCT 1431
                | |  |||||||| || || ||   ||||     ||  || |   ||
Db       2482 GCCGGTGTCAAGGTGCGGTTCCTCCTTGGGGGCCGCCACGGCGAATTCAAGTTCCTCCCT 2541

Qy       1432 CCAGAAGGCTACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAG 1491
              ||    |||||| | || |    ||| || | || || |   ||   ||| | |||||
Db       2542 CCGCCTGGCTACGCCCCTTGCCACGAGGCTGTGCTCCCACGAGAGCGACTCCGTCTGGAA 2601

Qy       1492 CCGTGCTTCTACTTCGGCAACCTGTCCAAGCGGG------CCTTGGCTGGACCTCCGCTA 1545
              ||   |   | | |          ||||        | |||   || ||    |
Db       2602 CCCATCAAGGAGTATCGGCGAGAAGGGCCCCGGGGACCCCACCTGGTGGGCCCCAGCCGC 2661

Qy       1546 GTACAGGACGATACGGCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCT 1605
              |      | || | ||| |||||    || || || ||| | ||||||   ||||||
Db       2662 TGCCTCTCACACACCGACTTTGTGCCCTGCCCGGTGGACACTGTCCAGATTGTCCTGCCT 2721

Qy       1606 ACATATGTGGAACAAATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATG 1665
              | || |||| |  || | || ||||| || || || || || ||| | |||||  ||
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Qy       1666 AATAAGATCGAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCAC 1725
              |      |||||          ||||||  || |||        | || |||    | | |||
Db       2782 ACGCGCATCGAGCAGGGCTGGACCTATGGCCCGGTTCGGGATGACAATAAGCGGCTGCAC 2841

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              || || ||||||  |||| |  | |||||     | ||||     ||| || | ||  |
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Qy       1843 CCTCCAGCACGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGC 1902
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Db       2962 AAGGCAGAGGACAACCTGAGGAAGACGAAACTCCCCAAGACGTACATGATGAGCAATGGG 3021

Qy       1903 TACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTA 1962
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Db       3082 GTGGACCGGCTGGCGGAGAACGGGCACAACGTGTGGGCCCGAGACCGAGTGGCCCAGGGC 3141
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Qy       2023 TGGACTTATGGACTTAATGAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATAC 2082
Db       3142 TGGAGCTACAGTGCTGTGCAGGACATCCCAGCGCGCCGCAACCCTCGCCTCGTGCCCTAC 3201

Qy       2083 CCGAAGGTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGG 2142
Db       3202 CGCCTGCTAGACGAGGCCACCAAGCGCAGCAACCGGGACAGCCTTTGCCAGGCTGTGCGC 3261

Qy       2143 ACCCTGCTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTC 2202
Db       3262 ACCCTGCTGGGCTACGGCTACAACATCGAGCCGCCCGACCAGGAGCCCAGTCAGGTGGAG 3321

Qy       2203 TTGTTGGAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAAC 2262
Db       3322 AGCCAGTCTCGCTGGGACCGTGTGC-----------GCATCTTCCGGGCTGAGAAGTCC 3369

Qy       2263 TATGCCGTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATG 2322
Db       3370 TATGCGGTGCAGAGCGGCCGCTGGTACTTCGAGTTCGAGGCCGTCACCACGGGCGAGATG 3429

Qy       2323 AGGGTCGGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAAC 2382
Db       3430 CGAGTGGGCTGGGCGCGGCCTGAGCTGCGGCCTGATGTGGAGCTGGGAGCCGATGAGCTG 3489

Qy       2383 TCTTGGGCATTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTC 2442
Db       3490 GCCTATGTCTTCAATGGGCACCGGGGTCAGCGCTGGCACTTGGG---CAGCGAACTGTTT 3546

Qy       2443 GGCAAGCAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACG 2502
Db       3547 GGGCGTCCCTGGCAGTCGGGCGATGTGGTGGGCTGCATGATCGACCTCACAGAGAACACC 3606

Qy       2503 ATAAGTTTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTT 2562
Db       3607 ATTATCTTCACGCTCAACGGCGAGGTCCTCATGTCCGACTCGGGCTCTGAAACCGCCTTC 3666

Qy       2563 GCTGATGTCCAG---GGTGACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAA 2619
Db       3667 CGGGATATCGAGGTTGGGGATGGCTTCCTGCCCGTCTGCAGCTTGGGACCTGGCCAGGTG 3726

Qy       2620 GCCAGGTTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTT 2679
Db       3727 GGCCACCTGAACCTGGGCCAGGATGTGAGCTCCCTGCGGTTCTTTGCCATCTGCGGCCTC 3786

Qy       2680 CAGGAGGGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACC 2739
Db       3787 CAGGAAGGTTTTGAGCCATTCGCCATCAACATGCAGCGTCCCGTCACTACCTGGTTCAGC 3846

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RESULT 2
US-09-016-434-1154
; Sequence 1154, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1154:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4078 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1526977
US-09-016-434-1154

  Query Match             22.3%;  Score 668;  DB 3;  Length 4078;
  Best Local Similarity   55.4%;  Pred. No. 1.2e-184;
  Matches 1590;  Conservative    0;  Mismatches 1225;  Indels   57;  Gaps   13;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
Db       1163 GGCATGGGAACATCTGAAATAAAATACGGTGACTCAGTATGCTATATACAACATGTAGAC 1222

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
Db       1223 ACAGGCCTATGGCTTACTTACCAGTCTGTGGACGTGAAATCCGTGAGAATGGGATCTATA 1282

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
Db       1283 CAACGTAAG---GCTATTATGCATCATGAAGGCCACATGGATGATGGCATAAGTTTGTCG 1339

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
Db       1340 AGATCCCAGCATGAAGAATCACGCACAGCCCGAGTTATCCGGAGCACAGTCTTCCTTTTC 1399

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
Db       1400 AATAGATTTATAAGGGGCCTTGATGCTCTCAGCAAGAAAGCGAAGGCTTCCACAGTCGAT 1459

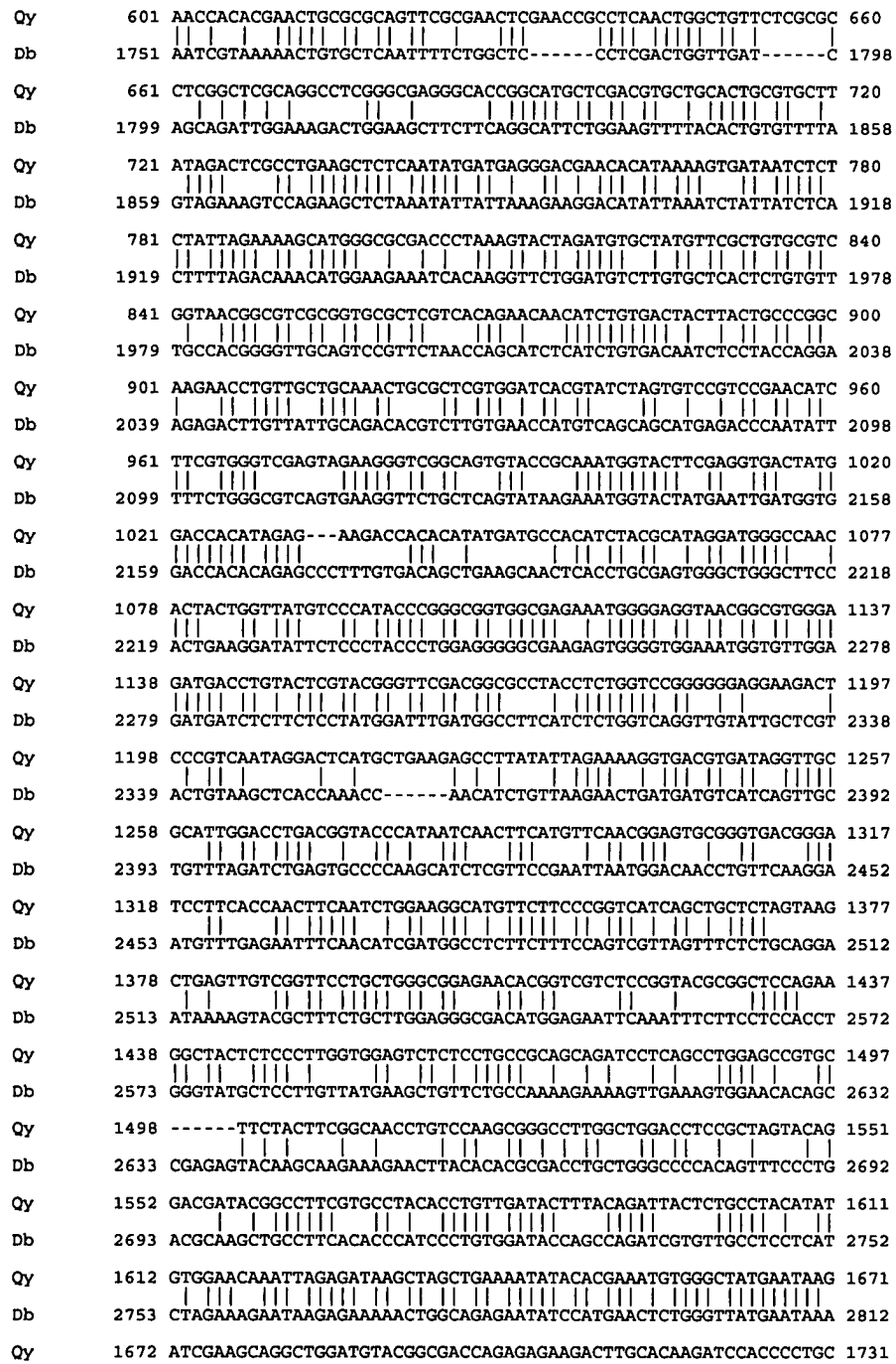
Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
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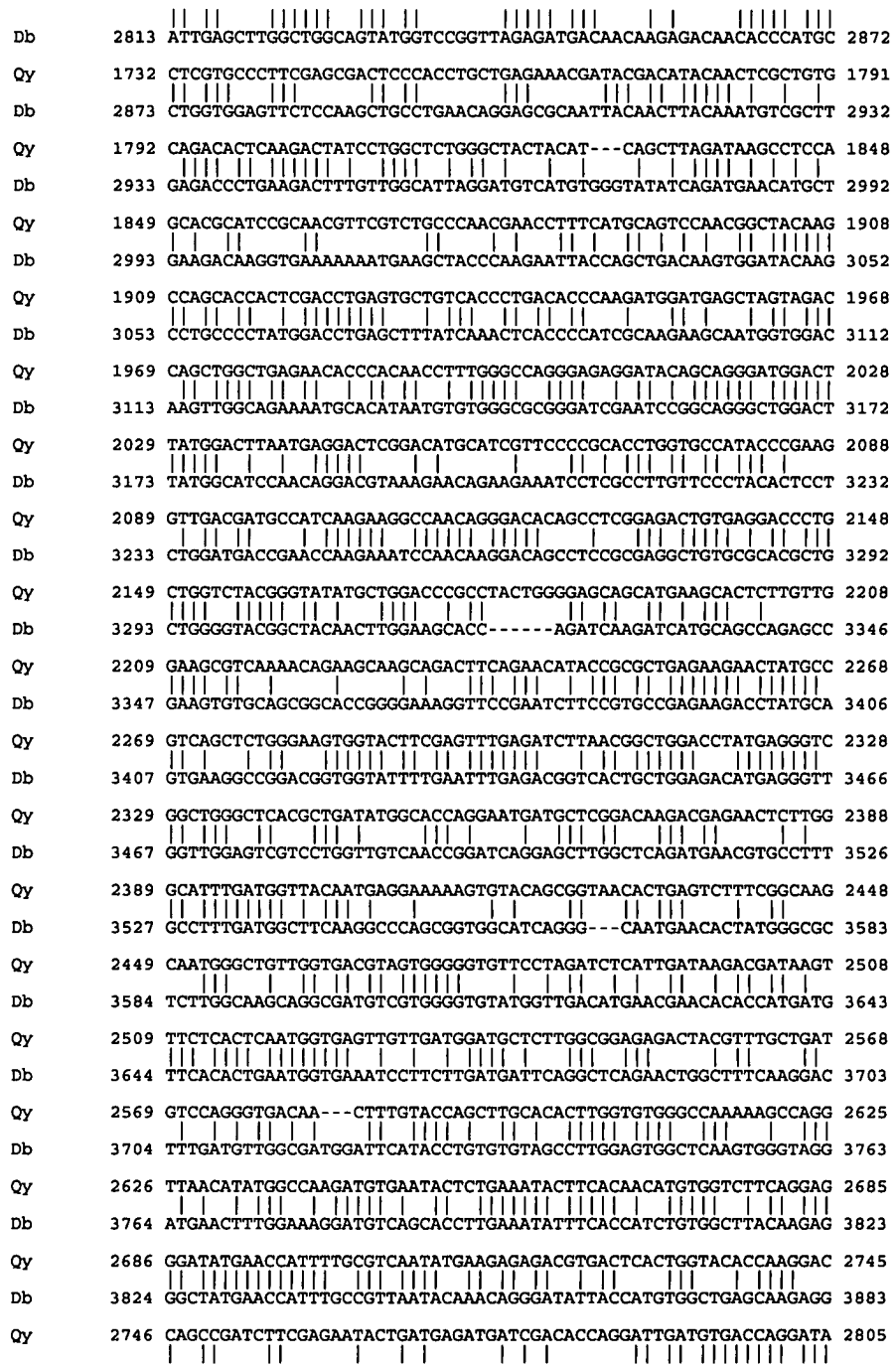
Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
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Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
Db       1574 CGGCAAAATCTCTTCCAGGAAGAGGGAATGATCAACCTCGTGCTTGAGTGCATAGACCGT 1633

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
Db       1634 TTGCACGTCTACAGCAGTGCAGCACACTTTGCTG---ATGTTGCTGGGCGAGAAGCAGGA 1690

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
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Db       3884 CTTCCTCAGTT---TCTTCAAGTTCCATCAAACCATGAACATATAGAGGTGACCAGAATA 3940

Qy       2806 CCAGCTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCG 2857

Db       3941 GACGGCACCATAGACAGTTCCCCATGTTTAAAGGTCACTCAGAAGTCTTTTG 3992


RESULT 3
US-09-424-783-1
; Sequence 1, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
;  APPLICANT: Hakamata, Yasuhiro
;  APPLICANT:  Nishimura, Seiichiro
;  APPLICANT:  Barsoumian, Edward Leon
;  TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
;  TITLE OF INVENTION:  and DNA Molecules Coding Therefor
;  FILE REFERENCE: 0652.2000000
;  CURRENT APPLICATION NUMBER: US/09/424,783
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: PCT/EP98/02926
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: DE 197 22 317.6
;  PRIOR FILING DATE: 1997-05-28
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 15572
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-424-783-1

  Query Match             19.9%;  Score 597;  DB 3;  Length 15572;
  Best Local Similarity   54.1%;  Pred. No. 1.5e-163;
  Matches 1561;  Conservative    0;  Mismatches 1250;  Indels   74;  Gaps   14;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60

Db       1104 GGCATGGGAGTTCCAGAAATCAAGTATGGAGATTCTGTCTGCTTTGTGCAGCATATAGCC 1163

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120

Db       1164 AGTGGTCTGTGGGTGACCTACAAAGCACAAGACGCCAAAACTTCCCGCCTGGGACCTCTA 1223

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180

Db       1224 AAAAGAAAG---GTCATACTCCATCAGGAAGGCCACATGGATGATGGATTAACACTGCAG 1280

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240

Db       1281 AGATGCCAACGTGAGGAGTCCCAGGCTGCTCGGATCATCCGGAACACTACAGCCTTATTC 1340

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300

Db       1341 AGCCAGTTTGTCAGTGGAAACAA--------------------TCGCACAGCTGCCCCC 1379

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360

Db       1380 ATCACCCTGCCTATAGAAGAAGTCCTGCAGACCCTACAGGACTTGATCGCCTACTTCCAG 1439

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420

Db       1440 CCCCCAGAGGAGGAGATGCGACATGAAGACAAGCAGAACAAGCTCCGCTCACTCAAAAAC 1499

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480

Db       1500 AGACAAAATCTTTTCAAGGAAGAGGGAATGTTGGCCCTTGTCTTAAATTGCATTGACCGC 1559

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540

Db       1560 TTAAATGTCTACAATAGCGTAGCACACTTTGCAGGGATT---GCAAGGGAAGAGAGTGGC 1616

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600

Db       1617 ATGGCCTGGAAAGAAATTCTGAACCTCCTCTACAAATTGCTGGCTGCTCTCATTCGCGGA 1676

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660

Db       1677 AACAGAAACAATTGCGCTCAATT------CTCCAATAACCTTGATTGGCTCATCAGTAAA 1730

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720

Db       1731 TTGGACAGACTAGAATCTTCCT------CAGGTATCTTGGAAGTTTTGCACTGCATCTTA 1784

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780

Db       1785 ACTGAAAGCCCAGAAGCCTTAAATCTGATAGCGGAGGGCCACATCAAGTCGATCATCTCC 1844

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840

Db       1845 CTGTTGGATAAGCACGGGCGGAATCACAAGGTTCTGGATATCCTGTGCTCCCTCTGTCTC 1904

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900

Db       1905 TGCAATGGGGTTGCAGTGAGAGCCAACCAGAATCTGATCTGTGACAACTTGCTGCCCCGG 1964

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960

Db       1965 AGAAACCTACTCCTGCAGACACGACTGATTAACGATGTAACCAGTATCCGGCCAAACATC 2024

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020

Db       2025 TTCCTGGGAGTCGCGGAGGGCTCAGCCCAGTACAAGAAGTGGTACTTCGAGCTGATTATC 2084

Qy       1021 GACCACATAGAGAAGACC---ACACATATGATGCCACATCTACGCATAGGATGGGCCAAC 1077

Db       2085 GACCAGGTGGACCCCTTCCTAACAGCAGAGCCCACACATCTGCGGGTGGGCTGGGCCTCT 2144

Qy       1078 ACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGA 1137

Db       2145 TCTTCAGGCTATGCCCCATACCCAGGAGGTGGAGAAGGATGGGGAGGCAATGGTGTTGGT 2204

Qy       1138 GATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACT 1197

Db       2205 GACGACCTGTACTCCTATGGCTTTGATGGACTTCACCTTTGGTCAGGCCGG----ATACC 2260

Qy       1198 CCCGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGC 1257

Db       2261 CAGAGCTGTGGCTTCCATCAACCAGCACCTCCTGAGATCGGATGACGTGGGTAAGCTGCT 2320

Qy       1258 GCATTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTG-ACGGG 1316

Db       2321 GCCTGGACCTCGGGGGTGCCCAGCATCTCATTCCGCATCAATGGGCAGCCCGTGCAGGGG 2380

Qy       1317 ATCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAA 1376

Db       2381 ATGTTTGGAGAACTTCAACACAGACGGGCTCTTCTTCCCTGTGATGAGCTTTTCAGCAGG 2440

Qy       1377 GCTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGA 1436

Db       2441 TGTCAAAGTACGTTTCCTGATGGGTGGACGTCATGGAGAGTTTAAGTTCCTGCCTCCCTC 2500

Qy       1437 AGGCTACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTG 1496

Db       2501 TGGCTATGCCCCTTGCTATGAAGCCTTACTTCCAAAAGAGAAGATGAGATTGGAGCCTGT 2560

Qy       1497 C------TTCTACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACA 1550

Db       2561 CAAAGAATATAAACGTGATGCTGATGGCATTAGAGATCTCTTGGGTACCACCCAGTTCCT 2620

Qy       1551 GGACGATACGGCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATA 1610

Db       2621 CTCCCAAGCCTCTTTCATCCCATGCCCCGTAGACACCAGTCAGGTTATTTTGCCACCTCA 2680

Qy       1611 TGTGGAACAAATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAA 1670
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Db       2681 CCTAGAAAAGATCCGAGACAGACTAGCTGAAAACATCCATGAGCTTTGGGGAATGAATAA 2740

Qy       1671 GATCGAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTG 1730

Db       2741 AATAGAACTTGGCTGGACTTTCGGCAAGATACGAGATGACAATAAAAGACAACACCCTTG 2800

Qy       1731 CCTCGTGCCCTTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGT 1790

Db       2801 CCTTGTGGAGTTTTCAAAGCTCCCAGAAACTGAGAAGAACTATAACCTGCAAATGTCAAC 2860

Qy       1791 GCAGACACTCAAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGC---CTCC 1847

Db       2861 TGAAACCTTAAAAACCCTCTTGACCCTGGGTTGCCACATTGCTCATGTTAACCCAGCTGC 2920

Qy       1848 AGCACGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAA 1907

Db       2921 TGAGGAGGATCTCAAGAAGGTCAAACTGCCCAAAAACTATATGATGTCCAACGGCTATAA 2980

Qy       1908 GCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGA 1967

Db       2981 GCCAGCCCCTTTGGATTTGTCTGATGTGAAGCTGTTACCTCCTCAAGAAATTTTAGTGGA 3040

Qy       1968 CCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGAC 2027

Db       3041 TAAGCTTGCAGAAAATGCACACAATGTTTGGGCAAAAGACAGAATAAAACAAGGATGGAC 3100

Qy       2028 TTATGGACTTAATGAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAA 2087

Db       3101 CTATGGCATCCAACAGGATTTGAAGAACAAAAGAAATCCCCGTCTGGTGCCATATGCATT 3160

Qy       2088 GGTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCT 2147

Db       3161 ACTGGATGAGCGTACCAAGAAGTCAAACAGGGACAGCCTGCGGGAAGCTGTGCGCACTTT 3220

Qy       2148 GCTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTT 2207

Db       3221 TGTTGGTTACGGGTATAACATTGAGCCATCAGACCAAGAACTAGCTGACTCGGCTGTGGA 3280

Qy       2208 GGAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGC 2267

Db       3281 GAAGGTCAGCATAGACAAG---------ATCCGATTTTTCCGGGTAGAGCGATCTTATCC 3331

Qy       2268 CGTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGT 2327

Db       3332 AGTGAGATCTGGAAAGTGGTATTTTGAGTTTGAAGTGGTGACTGGAGGAGACATGCGAGT 3391

Qy       2328 CGGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTG 2387

Db       3392 CGGCTGGGCGAGGCCAGGCTGTCGACCTGATGTCGAGCTGGGGGCCGATGACCAAGCCTT 3451

Qy       2388 GGCATTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAA 2447

Db       3452 TGTGTTTGAAGGCAACAGGGGCCAGCGTTGGCATCAAGGAAG---TGGGTATTTTGGGCG 3508

Qy       2448 GCAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAG 2507

Db       3509 TACCTGGCAGCCAGGGGATGTGGTCGGATGTATGATTAACCTGGATGATGCTTCAATGAT 3568

Qy       2508 TTTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGA 2567

Db       3569 CTTCACACTGAATGGGGAGCTGCTGATCACCAACAAAGGCTCTGAACTTGCCTTCGCTGA 3628

Qy       2568 TGTCCAGGGTGACAA---CTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAG 2624

Db       3629 CTACGAGATTGAGAATGGCTTCGTGCCCATCTGCTGTCTGGGTCTATCTCAGATCGGCCG 3688

Qy       2625 GTTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGA 2684

Db       3689 CATGAATCTCGGGACAGATGCCAGTACCTTCAAGTTTTATACCATGTGCGGTCTCCAAGA 3748

Qy       2685 GGGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGA 2744

Db       3749 GGGCTTTGAGCCTTTTGCTGTCAACATGAACAGAGATGTTGCTATGTGGTTCAGCAAGCG 3808

Qy       2745 CCAGCCGATCTTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGAT 2804

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Qy       2805 ACCAGCTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGAT 2864

Db       3866 TGATGGCACCATGGACAGCCCTCCGTGTCTCAAGGTGACGCATAAGACATTTGGCACACA 3925

Qy       2865 GGAGA 2869

Db       3926 GAATA 3930
```

```
RESULT 4
US-08-480-481-4
; Sequence 4, Application US/08480481
; Patent No. 5639614
;  GENERAL INFORMATION:
;    APPLICANT:  Sen, Luyi
;    APPLICANT:  Philipson, Kenneth D.
;    APPLICANT:  Lusis, Aldons J.
;    TITLE OF INVENTION:  GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,481
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  UCLA012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1050 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  380...380
;      OTHER INFORMATION:  Position distinguishes idiopathic
;      OTHER INFORMATION:  dilated cardiomyopathy
;      NAME/KEY:  Other
;      LOCATION:  776...776
;      OTHER INFORMATION:  Position distinguishes idiopathic
;      OTHER INFORMATION:  dilated cardiomyopathy
;      NAME/KEY:  Other
;      LOCATION:  1...1
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;      OTHER INFORMATION:  Position 1 corresponds to
;      OTHER INFORMATION:  7987 of the rabbit cDNA homolog
US-08-480-481-4

  Query Match             2.1%;  Score 61.8;  DB 2;  Length 1050;
  Best Local Similarity   47.7%;  Pred. No. 2.2e-07;
  Matches  235;  Conservative    0;  Mismatches  237;  Indels   21;  Gaps    1;

Qy       1563 CTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAAT 1622
              |||    ||   |||||||||||| | | | ||||   | |||    |  ||||| | |
Db        117 CTTTAACCCACAACCTGTTGATACCTCAAATATTATAATTCCTGAGAAGTTGGAATACTT 176

Qy       1623 TAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCAGG 1682
              |   | ||    || ||| ||   || || |  ||| | ||| | ||| | | |   ||
Db        177 CATTAACAAATATGCAGAACATTCTCATGACAAATGGTCAATGGACAAGTTAGCAAATGG 236

Qy       1683 CTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTT 1742
              ||||| || || ||          |||||    |||||| || ||||   |    || |
Db        237 ATGGATTTATGGAGAAATATATTCAGACTCCTCCAAGATTCAACCCTTGATGAAACCATA 296

Qy       1743 CGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTCAA 1802
              | | | |  |      || |||  |    |        |          |  | |||||
Db        297 TAAACTATTATCTGAAAAGGAAAAAGAAATTTATCGCTGGCCAATCAAAGAATCTCTCAA 356

Qy       1803 GACTATCCTGGCTCTGGGCTACTACAT----------------------CAGCTTAGATAA 1841
              |||||  |||||  |||  |    | ||                      |||| | |
Db        357 AACTATGTTGGCTTGGGGTTGGAAGATTGAAAGAACCCCAGAAGGAGACAGCATGGCCCT 416

Qy       1842 GCCTCCAGCACGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGG 1901
              |    |      || |    ||       | | |   || |       || | ||
Db        417 TTATAACCGAACTCGTCGTATTTCTCAGACAAGCCAGGTTTCTGTAGATGCTGCCCATGG 476

Qy       1902 CTACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCT 1961
              || |  ||   | |  | ||| ||||   ||| || ||  |      |  || |||   |
Db        477 TTATAGTCCCCGAGCCATTGACATGAGCAATGTTACACTATCCAGAGACCTGCATGCTAT 536

Qy       1962 AGTAGACCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGG 2021
              | |||   | ||||||| |||   || ||| | ||||| | | | | || || | ||
Db        537 GGCAGAAATGATGGCTGAAAACTATCATAACATATGGGCAAAGAAAAAGAAACTGGAGTT 596

Qy       2022 ATGGACTTATGGA 2034
              |  || | |||
Db        597 GGAGTCTAAAGGA 609


RESULT 5
US-08-480-481-3
; Sequence 3, Application US/08480481
; Patent No. 5639614
;  GENERAL INFORMATION:
;    APPLICANT:  Sen, Luyi
;    APPLICANT:  Philipson, Kenneth D.
;    APPLICANT:  Lusis, Aldons J.
;    TITLE OF INVENTION:  GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,481
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  UCLA012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1050 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...1
;      OTHER INFORMATION:  Position 1 corresponds to
;      OTHER INFORMATION:  7987 of the rabbit cDNA homolog
US-08-480-481-3

  Query Match             2.0%;  Score 60.2;  DB 2;  Length 1050;
  Best Local Similarity   47.5%;  Pred. No. 6.4e-07;
  Matches  234;  Conservative    0;  Mismatches  238;  Indels   21;  Gaps    1;

Qy       1563 CTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAAAT 1622
              |||    ||   |||||||||||| | | | ||||   | |||    |  ||||| | |
Db        117 CTTTAACCCACAACCTGTTGATACCTCAAATATTATAATTCCTGAGAAGTTGGAATACTT 176

Qy       1623 TAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCAGG 1682
              |   | ||    || ||| ||   || || |  ||| | ||| | ||| | | |   ||
Db        177 CATTAACAAATATGCAGAACATTCTCATGACAAATGGTCAATGGACAAGTTAGCAAATGG 236

Qy       1683 CTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCCTT 1742
              ||||| || || ||          |||||    |||||| || ||||   |    || |
Db        237 ATGGATTTATGGAGAAATATATTCAGACTCCTCCAAGATTCAACCCTTGATGAAACCATA 296

Qy       1743 CGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTCAA 1802
              | | | |  |      || |||  |    |        |          |  | |||||
Db        297 TAAACTATTATCTGAAAAGGAAAAAGAAATTTATCGCTGGCCAATCAAAGAATCTCTCAA 356

Qy       1803 GACTATCCTGGCTCTGGGCTACTACAT----------------------CAGCTTAGATAA 1841
              |||||  |||||  |||  |    ||                      |||| | |
Db        357 AACTATGTTGGCTTGGGGTTGGAGGATTGAAAGAACCCCAGAAGGAGACAGCATGGCCCT 416

Qy       1842 GCCTCCAGCACGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGG 1901
              |    |      || |    ||       | | |   || |       || | ||
Db        417 TTATAACCGAACTCGTCGTATTTCTCAGACAAGCCAGGTTTCTGTAGATGCTGCCCATGG 476

Qy       1902 CTACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCT 1961
              || |  ||   | |  | ||| ||||   ||| || ||  |      |  || |||   |
Db        477 TTATAGTCCCCGAGCCATTGACATGAGCAATGTTACACTATCCAGAGACCTGCATGCTAT 536

Qy       1962 AGTAGACCAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGG 2021
              | |||   | ||||||| |||   || ||| | ||||| | | | | || || | ||
Db        537 GGCAGAAATGATGGCTGAAAACTATCATAACATATGGGCAAAGAAAAAGAAACTGGAGTT 596

Qy       2022 ATGGACTTATGGA 2034
              |  || | |||
Db        597 GGAGTCTAAAGGA 609


RESULT 6
US-08-785-420-3
; Sequence 3, Application US/08785420
; Patent No. 6001976
;  GENERAL INFORMATION:
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;    APPLICANT:  MacLennan, David H
;    APPLICANT:  O'Brien, Peter J.
;    TITLE OF INVENTION:  DIAGNOSIS FOR PORCINE MALIGNANT
;    TITLE OF INVENTION:  HYPERTHERMIA
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte,
;      STATE:  No. 6001976th Carolina 28234
;      COUNTRY:  U.S.A.
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/785,420
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/249,388
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/030,159
;      FILING DATE:  15-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Layton,Jr., Samuel G.
;      REGISTRATION NUMBER:  22807
;      REFERENCE/DOCKET NUMBER:  3477-73
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  704-377-1561
;      TELEFAX:  704-334-2014
;      TELEX:  57-5102
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1598 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  Pig RYR1 gene
;    POSITION IN GENOME:
;      UNITS:  bp
US-08-785-420-3

  Query Match             1.9%;  Score 58;  DB 3;  Length 1598;
  Best Local Similarity   58.8%;  Pred. No. 3.5e-06;
  Matches  100;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy        795 TGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTCGGTAACGGCGTCGC 854
              ||   |  |||||  | ||  || ||||| || ||||| |||||  ||  | ||  || || ||
Db        929 TGACCTTGACCCCTAGGTGCTGGATGTCCTGTGTTCCCTGTGTGTGTGCAATGGTGTGGC 988

Qy        855 GGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGCAAGAACCTGTTGCT 914
               ||||||||    ||  |   |||  |||  |||| || || |||    | ||  ||||
Db        989 CGTGCGCTCCAACCAAGATCTCATTACTGAGAACTTGCTCCCTGGCCGCGAGCTTCTGCT 1048

Qy        915 GCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATCTTCG 964
              |||  ||    |||  |  |  | ||  | ||     | ||    | |||  |
Db       1049 GCAGACAAACCTCATCAACTATGTCACCAGGTCTGGCCCCCCAACCTTTG 1098


RESULT 7
US-08-480-481-6
; Sequence 6, Application US/08480481
; Patent No. 5639614
;  GENERAL INFORMATION:
;    APPLICANT:  Sen, Luyi
;    APPLICANT:  Philipson, Kenneth D.
;    APPLICANT:  Lusis, Aldons J.
;    TITLE OF INVENTION:  GENE MUTATION IN PATIENTS WITH IDIOPATHIC DILATED CARD
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,481
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  UCLA012.001A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  900 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...1
;      OTHER INFORMATION:  Position 1 corresponds to
;      OTHER INFORMATION:  8137 of the rabbit cDNA homolog
;      NAME/KEY:  Other
;      LOCATION:  230...230
;      OTHER INFORMATION:  Position distinguishes idiopathic
;      OTHER INFORMATION:  dilated cardiomyopathy
;      NAME/KEY:  Other
;      LOCATION:  626...626
;      OTHER INFORMATION:  Position distinguishes idiopathic
;      OTHER INFORMATION:  dilated cardiomyopathy
US-08-480-481-6

  Query Match             1.5%;  Score 46.2;  DB 2;  Length 900;
  Best Local Similarity   46.4%;  Pred. No. 0.0074;
  Matches  211;  Conservative    0;  Mismatches  223;  Indels   21;  Gaps    1;

Qy       1601 TGCCTACATATGTGGAACAAATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGG 1660
              | |||    |  ||||| |  | |   | ||    || ||| ||   || || |  |||
Db          5 TTCCTGAGAAGTTGGAATACTTCATTAACAAATATGCAGAACATTCTCATGACAAATGGT 64

Qy       1661 CTATGAATAAGATCGAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGA 1720
              | ||| | ||| | | |   || ||||| || || ||          |||||    |||||
Db         65 CAATGGACAAGTTAGCAAATGGATGGATTTATGGAGAAATATATTCAGACTCCTCCAAGA 124

Qy       1721 TCCACCCCTGCCTCGTGCCCTTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATAC 1780
              | || ||||    |    || |   | | | |        || |||  |    |
Db        125 TTCAACCCTTGATGAAACCATATAAACTATTATCTGAAAAGGAAAAAGAAATTTATCGCT 184

Qy       1781 AACTCGCTGTGCAGACACTCAAGACTATCCTGGCTCTGGGCTACTACAT---------- 1829
```

```
Db        185 GGCCAATCAAAGAATCTCTCAAAACTATGTTGGCTTGGGGTTGGAAGATTGAAAGAACCC 244

Qy       1830 ----------CAGCTTAGATAAGCCTCCAGCACGCATCCGCAACGTTCGTCTGCCCAACG 1879

Db        245 CAGAAGGAGACAGCATGGCCCTTTATAACCGAACTCGTCGTATTTCTCAGACAAGCCAGG 304

Qy       1880 AACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTCGACCTGAGTGCTGTCACCC 1939

Db        305 TTTCTGTAGATGCTGCCCATGGTTATAGTCCCCGAGCCATTGACATGAGCAATGTTACAC 364

Qy       1940 TGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAGAACACCCACAACCTTTGGG 1999

Db        365 TATCCAGAGACCTGCATGCTATGGCAGAAATGATGGCTGAAAACTATCATAACATATGGG 424

Qy       2000 CCAGGGAGAGGATACAGCAGGGATGGACTTATGGA 2034

Db        425 CAAAGAAAAAGAAACTGGAGTTGGAGTCTAAAGGA 459


RESULT 8
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             1.4%;  Score 43;  DB 2;  Length 7218;
  Best Local Similarity   4.1%;  Pred. No. 0.2;
  Matches   16;  Conservative  211;  Mismatches  166;  Indels    0;  Gaps    0;

Qy         91 GAAACGAAGAAGAAGGGAGTGGGTAAAGTAGAAGAGAAGCAAGCGATTCTCCACGAGGAA 150

Db       1427 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1368

Qy        151 GGCAAGATGGACGATGGCCTCGACTTCTCCAGGTCACAGGAGGAAGAATCTAGGACTGCT 210

Db       1367 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1308

Qy        211 CGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAGTTTATCAATGGTCTGGAAACTCTA 270

Db       1307 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1248

Qy        271 CAAGAGAACCGTCGTCACTCGATGTTCTTCGCGTCAGTGAACCTGGGCGAGATGGTGATG 330

Db       1247 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1188

Qy        331 TGCCTCGAGGATCTCATCAACTACTTCGCACAGCCCGATGAGGATATGGAACACGAAGAA 390

Db       1187 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1128

Qy        391 AAACAAAACAAATTCCGGGCACTCCGAAACCGTCAGGACCTGTTCCAAGAGGAAGGCATA 450

Db       1127 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1068

Qy        451 CTGAACCTGATCCTCGAAGCTATAGACAAGATC 483

Db       1067 RATCGCAAGCTCCCTCGACCTGCAGCCAAGCTC 1035


RESULT 9
US-09-485-529-14
; Sequence 14, Application US/09485529
; Patent No. 6762348
; GENERAL INFORMATION:
;  APPLICANT: Harberd, Nicholas P
;  APPLICANT:  Richards, Donald E
;  APPLICANT:  Peng, Jinrong
;  TITLE OF INVENTION: Genetic Control of Plant Growth and Development
;  FILE REFERENCE: 620-91
;  CURRENT APPLICATION NUMBER: US/09/485,529
;  CURRENT FILING DATE:  2000-03-01
;  PRIOR APPLICATION NUMBER: PCT/GB98/02383
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: GB 9717192.0
;  PRIOR FILING DATE: 1997-08-13
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 2125
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-485-529-14

  Query Match             1.3%;  Score 38.6;  DB 3;  Length 2125;
  Best Local Similarity   47.6%;  Pred. No. .2;
  Matches  147;  Conservative    0;  Mismatches  159;  Indels    3;  Gaps    1;

Qy        609 GAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGCCTCGGCTC 668

Db       1194 GAAGCTCGCCCAGTTCGCGCACACCATCCGCGTCGACTTCCAGTACCGCGGCCTCGTCGC 1253

Qy        669 GCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTTATAGACTC 728

Db       1254 ---CGCCACGCTCGCGGACCTGGAGCCGTTCATGCTGCAGCCGGAGGGCGAGGAAGACCC 1310

Qy        729 GCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTAGA 788

Db       1311 GAACGAGGAGCCCGAGGTAATCGCCGTCAACTCAGTCTTCGAGATGCACCGGCTGCTCGC 1370

Qy        789 AAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTCGGTAACGG 848

Db       1371 GCAGCCCGGCGCCCTGGAGAAGGTCCTGGGCACCGTGCGCGCCGTGCGGCCCAGGATCGT 1430
```

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Qy        849 CGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGCAAGAACCT 908
              |  || ||||     |      |||  ||| ||  | |   || |||  | ||   | |
Db       1431 CACCGTGGTGGAGCAGGAGGCGAATCACAACTCCGGCACATTCCTGGACCGCTTCACCGA 1490

Qy        909 GTTGCTGCA 917
              ||  |||||
Db       1491 GTCTCTGCA 1499


RESULT 10
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 2813
;   LENGTH: 832
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 235..399
US-09-621-976-2813

  Query Match             1.3%;  Score 38;  DB 3;  Length 832;
  Best Local Similarity   9.4%;  Pred. No. 1.8;
  Matches   31;  Conservative  164;  Mismatches  134;  Indels    1;  Gaps    1;

Qy       2495 ATAAGACGATAAGTTTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGA 2554
              :| ::::  ::: ::::::  : :: ::::  :::::: :  ::  :  :| :::  : :
Db         16 WTKWKWSWSYWMYWKWYYMKTYWRWRRKKKKAWWKYWKTWTWWYWRYAMWGTYKKKAMCR 75

Qy       2555 CTACGTTTGCTGATGTCCAGGGTGACAACTTTGTACCAGCTTGCACACTTGGTGTGG-GC 2613
               :  ::::: : :  :  ::::: |::  |:|||:|::::: :  :::|::::  :::  |
Db         76 TKTKKKKKKGYMWMWYWGWRRSYMAMWTRTWTGYAYYRSMMYWWRYRCWKKKAYYRKTTC 135

Qy       2614 CAAAAAGCCAGGTTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGT 2673
              :    :    : ::|:  ::::: : : ||:: ::    |   :| ::: : :  |  ::|
Db        136 YSSKGWTWWKRWKKAWTTWWWKKTYYWAATRYWWMMCWTKRWRASWWYCWWWGKARKWST 195

Qy       2674 GGTCTTCAGGAGGGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGG 2733
              :::  :|: :: ::  ::    |  :: :  :::::  | |||::| : : :  : : |
Db        196 WRKSRSYASARSAKRCCYSCSWGAMSWKYMWRMWRWRGWATGAGMKAWRASCMMRRKYAG 255

Qy       2734 TACACCAAGGACCAGCCGATCTTCGAGAATACTGATGAGATGATCGACACCAGGATTGAT 2793
              :   ::    :|  :: :  :|: ::   : : :   :|  |:::    :::::::: :
Db        256 KSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKKYMWKRWWWCWA 315

Qy       2794 GTGACCAGGATACCAGCTGGTTCAGATACA 2823
              :  ::: | :  : :: :  | ::::: :|
Db        316 RMYRYSTGTRASMWWRRWYYTMMMKWWKYA 345


RESULT 11
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             1.3%;  Score 38;  DB 3;  Length 4403765;
  Best Local Similarity   55.2%;  Pred. No. 1.4e+02;
  Matches   74;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy       1070 GGGCCAACACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACG 1129
              | |  |||   || |||   ||     ||   || |  |||| |||  | || |    ||
Db    3793768 GCGGAAACCAAACCGGTGGCGTGGGCAACGGCGGGGCCGGCGGGAACGGCGGCGCCGGCG 3793827

Qy       1130 GCGTGGGAGATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGA 1189
              | |  || | | | ||||||    ||||    |||||||| | ||  | || ||||  |||
Db    3793828 GGGCCGGTGGTCAGCTGTACGGCAACGGCGGGGACGGCGGCAACGGCGGGGCCGGCGGGG 3793887

Qy       1190 GGAAGACTCCCGTC 1203
                || |   ||| |
Db    3793888 CCAACATCGCCGGC 3793901


RESULT 12
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             1.3%;  Score 38;  DB 3;  Length 4411529;
  Best Local Similarity   55.2%;  Pred. No. 1.4e+02;
  Matches   74;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy       1070 GGGCCAACACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACG 1129
              | |  |||   || |||   ||     ||   || |  |||| |||  | || |    ||
Db    3802946 GCGGAAACCAAACCGGTGGCGTGGGCAACGGCGGGGCCGGCGGGAACGGCGGCGCCGGCG 3803005

Qy       1130 GCGTGGGAGATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGA 1189
              | |  || | | | ||||||    ||||    |||||||| | ||  | || ||||  |||
Db    3803006 GGGCCGGTGGTCAGCTGTACGGCAACGGCGGGGACGGCGGCAACGGCGGGGCCGGCGGGG 3803065

Qy       1190 GGAAGACTCCCGTC 1203
                || |   ||| |
Db    3803066 CCAACATCGCCGGC 3803079


RESULT 13
US-09-252-991A-11838
```

```
; Sequence 11838, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 11838
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11838

  Query Match             1.3%;  Score 37.8;  DB 3;  Length 294;
  Best Local Similarity   52.2%;  Pred. No. 1.2;
  Matches   84;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy       2016 GCAGGGATGGACTTATGGACTTAATGAGGACTCGGACATGCATCGTTCCCCGCACCTGGT 2075
              ||||     | | || |||| ||   |||||||| |   ||  ||     |   || |||
Db         84 GCAGCAGCAGCCCTACGGACCCAACCCGGACTCGAAATCGCTCCGCCAGCACTACGTGGA 143

Qy       2076 GCCATACCCGAAGGTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGAC 2135
              || | |  | | |   | ||| | ||| || ||  |   |  ||||  | ||
Db        144 AGGGCGCCTGGACATCGCCCGGGTGATCTACAAGACCGACCTGTGGAGCGCCTGTGGGAT 203

Qy       2136 TGTGAGGACCCTGCTGGTCTACGGGTATATGCTGGACCCGC 2176
              ||   | | |  |||||||||| | |   || || |  ||
Db        204 CGTCCCGGCGCGCCTGGTCTACGAGGACTCGCAGGGCGAGC 244


RESULT 14
US-09-668-097A-35
; Sequence 35, Application US/09668097A
; Patent No. 6673988
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Edgar B.
;  APPLICANT:  Cahoon, Rebecca E.
;  APPLICANT:  Klein, Ted
;  APPLICANT:  Shen, Jennie
;  TITLE OF INVENTION: Plant Lipases
;  FILE REFERENCE: BB1401 US NA
;  CURRENT APPLICATION NUMBER: US/09/668,097A
;  CURRENT FILING DATE:  2000-09-22
;  PRIOR APPLICATION NUMBER: 60/157309
;  PRIOR FILING DATE: 1999-10-01
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
;   LENGTH: 1334
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-09-668-097A-35

  Query Match             1.3%;  Score 37.6;  DB 3;  Length 1334;
  Best Local Similarity   57.8%;  Pred. No. 3;
  Matches   67;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy        600 CAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCG 659
              ||||  |   ||| ||  |||| ||    |  ||| ||  |||||  |||||   | ||
Db        728 CAACGCCGGCGACTACGACCAGTACGGCTGCCTGAAGCGGTTCAACGCGCTGTCGGCCCG 787

Qy        660 CCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCG 715
              || |  ||||| |  |  | || |||  ||| || |||  | |  |   | || ||
Db        788 CCACAACTCGCTGCTCCAGAGCAAGGTGACCAGCCTGCAGGGCAAGTACCCCTACG 843


RESULT 15
US-09-513-999C-35034/c
; Sequence 35034, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 35034
;   LENGTH: 299
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 80
;   OTHER INFORMATION: s=g or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 124
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 126
;   OTHER INFORMATION: r=a or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 131
;   OTHER INFORMATION: r=a or g
US-09-513-999C-35034

  Query Match             1.2%;  Score 37.4;  DB 3;  Length 299;
  Best Local Similarity   60.8%;  Pred. No. 1.5;
  Matches   90;  Conservative    2;  Mismatches   54;  Indels    2;  Gaps    2;

Qy        314 TGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA-CAGCCCGATGAG 372
              | |  ||  |  ||  |  |||  ||||  | |||  |:||||:  | |  || || |||
Db        169 TAGAAGAAGTCCTGCAGACCCTACAGGACTTGATCGCCYACTTYCNAGCCCCCAGAGGAG 110

Qy        373 GATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAACCGTCAGGACCTG 432
              || |||  ||| ||||| || || ||| || ||||  |||||  |||| | ||  | ||
Db        109 GAGATGCGACATGAAGACAAGCAGAAC-AASTCCGCTCACTCAAAAACAGACAAAATCTT 51

Qy        433 TTCCAAGAGGAAGGCATACTGAACCTGA 460
              ||| | || || |  |  |  ||  |||
Db         50 TTCAAGGAAGAGGTAAGTCGAAAAATGA 23


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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 13:51:25 ; Search time 1686.5 Seconds
(without alignments)
11859.320 Million cell updates/sec

Title: US-10-668-767-127_COPY_1000_4000
Perfect score: 3001
Sequence: 1 gtcataggcgcgcccatcat.....cctaatgaaagaggcagttg 3001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3001	100.0	15387	12	ADM68883	Adm68883 Heliothis
2	2857	95.2	15303	12	ADM68901	Adm68901 Heliothis
3	2847.4	94.9	15679	12	ADM68757	Adm68757 Heliothis
4	2841	94.7	15405	12	ADM68885	Adm68885 Heliothis
5	2839.4	94.6	15429	12	ADM68899	Adm68899 Heliothis
6	1620.4	54.0	15606	4	ABL16881	Abl16881 Drosophil
7	1617.2	53.9	16363	12	ADM68765	Adm68765 Drosophil
8	1542.2	51.4	15413	12	ADM68763	Adm68763 Peregrinu
9	1335.4	44.5	15315	12	ADM68761	Adm68761 Periplane
10	1319	44.0	15845	12	ADM68759	Adm68759 Myzus per
c 11	1150	38.3	24236	4	ABL16880	Abl16880 Drosophil
12	673.4	22.4	15377	2	AAQ25975	Aaq25975 MH mutant
13	668	22.3	4078	10	ACA56556	Aca56556 Human sig
14	668	22.3	4078	12	ADI56352	Adi56352 Human pol
15	668	22.3	14302	4	ABA08776	Aba08776 Human rya
16	668	22.3	15731	4	AAH98746	Aah98746 Human EST
17	668	22.3	15731	12	ADP21411	Adp21411 Gene RYR2
18	668	22.3	15731	14	ADZ49161	Adz49161 Insulin s
19	651.4	21.7	15672	2	AAQ10613	Aaq10613 Rianodin
20	648.2	21.6	15355	4	AAH57405	Aah57405 Human ske
21	648.2	21.6	15464	2	AAQ11415	Aaq11415 Ryanodine
22	646.6	21.5	15359	4	ABA08724	Aba08724 Human rya
23	646.6	21.5	15359	5	AAS69156	Aas69156 DNA encod
24	646.6	21.5	15359	12	ADQ85750	Adq85750 Human tum
25	646.6	21.5	15359	12	ADQ86825	Adq86825 Human tum
26	646.6	21.5	15359	13	ADQ84285	Adq84285 Human tum
27	646.6	21.5	15359	13	ADQ83605	Adq83605 Human tum
28	646.6	21.5	15359	13	ACN40554	Acn40554 Tumour-as
29	646.6	21.5	15359	14	ADY19485	Ady19485 DNA encod
30	646.6	21.5	15359	14	ADY15561	Ady15561 DNA encod
31	646.6	21.5	15359	14	ADZ49160	Adz49160 Insulin s
32	622.8	20.8	15453	12	ADQ22976	Adq22976 Human sof
33	618.4	20.6	15563	12	ADP21412	Adp21412 Gene RYR3
34	618.4	20.6	15563	14	ADZ49162	Adz49162 Insulin s
35	617.6	20.6	14800	5	AAS06039	Aas06039 Angiotens
36	597	19.9	15512	2	AAV59470	Aav59470 Human rya
37	597	19.9	15583	5	AAS76501	Aas76501 DNA encod
38	597	19.9	15583	10	ADF59841	Adf59841 Human con
39	597	19.9	15820	5	AAS87533	Aas87533 DNA encod
40	104.8	3.5	321	12	ACH82910	Ach82910 Human gen
41	104.8	3.5	597	12	ACH69210	Ach69210 Human gen
42	99.4	3.3	1440	3	ABL58201	Abl58201 CRC1gene
43	71	2.4	1800	5	AAS87530	Aas87530 DNA encod
44	70	2.3	994	13	ADQ81023	Adq81023 Human phe
45	66.8	2.2	474	14	ADY64973	Ady64973 S. manson

ALIGNMENTS

RESULT 1
ADM68883
ID ADM68883 standard; DNA; 15387 BP.
XX
AC ADM68883;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:127.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Heliothis virescens.
XX
FH Key Location/Qualifiers
FT CDS 1. .15387
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68884.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 127; 687pp; English.

XX
CC The present invention describes an isolated nucleotide fragment (I) comprising: (a) a nucleic acid sequence encoding a ryanodine receptor having an amino acid sequence identity of at least 80% when compared to a polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8, 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO. 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant construct comprising (I) operably linked to at least one regulatory sequence; (2) a transformed host cell comprising the recombinant construct; (3) a method to isolate (I) encoding ryanodine receptors and related polypeptides; (4) an isolated polypeptide having ryanodine receptor activity; (5) a method for evaluating at least one compound for its ability to modulate calcium homeostasis; (6) a method for evaluating at least one compound which modulates ryanodine receptor activity; (7) an isolated nucleic acid fragment encoding an insect ion channel comprising at least two fully defined polypeptide sequences selected from SEQ ID NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56, 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant construct comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. The isolated nucleotide fragment (I) encoding a ryanodine receptor is useful for the isolation of other pest ryanodine receptors and developing of screens to identify insecticidally active compounds. The nucleic acid fragments are useful as pesticides, fragments of protein for antibody production, fragments of protein for determination of the structure of insecticide binding sites and in the identification of insecticides that disrupt the calcium balance in cells through other messengers that interact with the receptor calcium release mechanism. The present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15387 BP; 4065 A; 3845 C; 4182 G; 3295 T; 0 U; 0 Other;

Query Match 100.0%; Score 3001; DB 12; Length 15387;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 1059

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 1119

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1120 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 1179

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 1239

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 1299

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 1359

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1360 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 1419

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1420 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 1479

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1480 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 1539

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1540 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 1599

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1600 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 1659

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1660 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 1719

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1720 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 1779

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1780 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 1839

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1840 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 1899

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1900 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 1959

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1960 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 2019

Qy       1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2020 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 2079

Qy       1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2080 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 2139

Qy       1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2140 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 2199

Qy       1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2200 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 2259

Qy       1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2260 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 2319

Qy       1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2320 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 2379

Qy       1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2380 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 2439

Qy       1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2440 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 2499

Qy       1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2500 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 2559

Qy       1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2560 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 2619
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Qy       1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2620 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 2679

Qy       1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2680 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 2739

Qy       1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2740 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 2799

Qy       1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2800 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 2859

Qy       1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2860 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 2919

Qy       1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2920 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 2979

Qy       1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2980 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 3039

Qy       2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3040 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 3099

Qy       2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3100 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 3159

Qy       2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3160 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 3219

Qy       2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3220 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 3279

Qy       2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3280 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 3339

Qy       2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3340 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 3399

Qy       2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3400 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 3459

Qy       2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3460 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 3519

Qy       2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3520 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 3579

Qy       2581 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3580 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 3639

Qy       2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3640 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 3699

Qy       2701 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3700 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 3759

Qy       2761 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3760 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 3819

Qy       2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3820 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 3879

Qy       2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3880 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 3939

Qy       2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3940 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTT 3999

Qy       3001 G 3001
              |
Db       4000 G 4000
```

RESULT 2
ADM68901
ID ADM68901 standard; DNA; 15303 BP.
XX
AC ADM68901;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:145.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Heliothis virescens.
XX
FH Key Location/Qualifiers
FT CDS 1. .15303
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68902.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 145; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a

CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO. 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant construct comprising (I) operably linked to at least one regulatory sequence; (2) a transformed host cell comprising the recombinant construct; (3) a method to isolate (I) encoding ryanodine receptors and related polypeptides; (4) an isolated polypeptide having ryanodine receptor activity; (5) a method for evaluating at least one compound for its ability to modulate calcium homeostasis; (6) a method for evaluating at least one compound which modulates ryanodine receptor activity; (7) an isolated nucleic acid fragment encoding an insect ion channel comprising at least two fully defined polypeptide sequences selected from SEQ ID NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56, 120-126; (8) a method for identifying a nucleic acid sequence encoding an insect ion channel; (9) a method for expressing an isolated nucleic acid fragment encoding a toxic insect ion channel; and (10) recombinant construct comprising in the 5' to 3' direction a promoter operably linked to an isolated nucleic acid fragment encoding a toxic insect ion channel. The isolated nucleotide fragment (I) encoding a ryanodine receptor is useful for the isolation of other pest ryanodine receptors and developing of screens to identify insecticidally active compounds. The nucleic acid fragments are useful as pesticides, fragments of protein for antibody production, fragments of protein for determination of the structure of insecticide binding sites and in the identification of insecticides that disrupt the calcium balance in cells through other messengers that interact with the receptor calcium release mechanism. The present sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15303 BP; 4036 A; 3822 C; 4161 G; 3284 T; 0 U; 0 Other;

Query Match 95.2%; Score 2857; DB 12; Length 15303;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 2911; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1015 GTCATAGGCGCTCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 1074

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 1134

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1135 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 1194

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1195 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 1254

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              |||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||
Db       1255 ACTAAGTTTATCAATGGGCTTGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 1314

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1315 GCGTCAGTGAACCTGGGTGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 1374

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              ||||| ||||| |||||||||||||||||||| |||||||||||||| || ||||| |||
Db       1375 CAGCCAGATGAAGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAAC 1434

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1435 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 1494

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              |||||||||||||| |||||||||||||||||||| |||||||| ||||||||||||||
Db       1495 ATCAACGTCATCACATCCCAGGGGTTCCTCGCTGGTTTCCTGGCAGGAGACGAATCTGGA 1554

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       1555 CAAAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGC 1614
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Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1615 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGCTCAACTGGCTGTTCTCGCGC 1674

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1675 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTCCTC 1734

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
              |||||||||||||||| |||||||||| |||||||||||||||||||||||||||| |||
Db       1735 ATAGACTCGCCTGAAGCGCTCAATATGATGCGGGACGAACACATAAAAGTGATAATTTCT 1794

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
              |||||||||||||||||||||||||| |||||||||||||||||||| || ||||||||
Db       1795 CTATTAGAAAAGCATGGGCGCGACCCAAAAGTACTAGATGTGCTATGTTCACTCTGCGTC 1854

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
              |||||||||||||||||||||||||||||||||||||||||||| |||||||| |||||||||
Db       1855 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTACTTGCTGCCCGGC 1914

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
              |||||||||||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db       1915 AAGAACCTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATC 1974

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
              |||||||||||||||||||| || || |||||||||||||||||||||| |||||||||
Db       1975 TTCGTGGGTCGAGTAGAAGGTTCAGCCGTGTACCGCAAATGGTACTTCGAAGTGACTATG 2034

Qy       1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       2035 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAACACT 2094

Qy       1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
              ||||| || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2095 ACTGGCTACGTCCCATACCCGGGCGGTGGCGAGAAGTGGGGAGGTAACGGCGTGGGAGAC 2154

Qy       1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGGAGGAAGACTCCC 1200
              |||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||||
Db       2155 GACCTGTACTCGTACGGGCTCGACGGCGCCTACCTCTGGTCCGGCGGGAGGAAGACTCCC 2214

Qy       1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
              || |||||||||||||||||||||||||||||||||| |||||||||||||||||||| |||
Db       2215 GTTAATAGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCA 2274

Qy       1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2275 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 2334

Qy       1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
              |||||||||||||| |||||||||||||||||||||||||||||| ||||||||||  ||
Db       2335 TTCACCAACTTCAACCTGGAAGGCATGTTCTTCCCGGTCATCAGTTGCTCTAGTAAATTG 2394

Qy       1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
              |||||||||||||||| ||||| ||||||||| | ||||||||||||||||||||||||
Db       2395 AGTTGTCGGTTCCTGCTAGGCGGGGAACACGGTAGACTCCGGTACGCGGCTCCAGAAGGC 2454

Qy       1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
              ||||| ||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2455 TACTCCCCACTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 2514

Qy       1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
              |||||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||
Db       2515 TACTTCGGCAACCTGTCCAAGCGGGCCCTGGCTGGACCCCCGCTAGTACAGGACGATACG 2574

Qy       1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
              || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2575 GCTTTTGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 2634

Qy       1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2635 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 2694

Qy       1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
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Db       2695 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 2754

Qy       1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800

Db       2755 TTCGAGCGTCTCCCGCCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 2814

Qy       1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860

Db       2815 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 2874

Qy       1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920

Db       2875 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 2934

Qy       1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980

Db       2935 GATCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 2994

Qy       1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040

Db       2995 AACACACACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAAT 3054

Qy       2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100

Db       3055 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCGTACCCGAAGGTTGACGATGCC 3114

Qy       2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160

Db       3115 ATCAAGAAAGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 3174

Qy       2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 2220

Db       3175 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 3234

Qy       2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280

Db       3235 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAAAAGAACTATGCCGTCAGCTCTGGG 3294

Qy       2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340

Db       3295 AAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 3354

Qy       2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400

Db       3355 GCTGATATGGCACCAGGAATGATGCTCGGACAAGATGAGAACTCTTGGGCATTTGATGGT 3414

Qy       2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460

Db       3415 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 3474

Qy       2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520

Db       3475 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAC 3534

Qy       2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 2580

Db       3535 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 3594

Qy       2581 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 2640

Db       3595 AACTTTGTACCTGCTTGCACGCTTGGTGTGGGCCAAAAAGCCAGGTTAACATACGGTCAG 3654

Qy       2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700

Db       3655 GACGTGAACACGTTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTT 3714

Qy       2701 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 2760

Db       3715 TGTGTCAATATGAAGAGAGACGTGACTCACTGGTATACTAAAGATCAGCCAATCTTCGAG 3774

Qy       2761 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 2820

Db       3775 AATACTGATGAGATGATCGACACCAGAATTGATGTCACCAGGATACCAGCTGGTTCAGAT 3834

Qy       2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880

Db       3835 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 3894

Qy       2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940

Db       3895 GAGTTCTTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAA 3954

Qy       2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTT 3000

Db       3955 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGCCAACAGATTTTAATGAAAGAGGCAGTT 4014

Qy       3001 G 3001

Db       4015 G 4015
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RESULT 3
ADM68757
ID ADM68757 standard; DNA; 15679 BP.
XX
AC ADM68757;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:1.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Heliothis virescens.
XX
FH Key Location/Qualifiers
FT CDS 251. .15679
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68758.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 1; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine

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CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 15679 BP; 4148 A; 3911 C; 4252 G; 3366 T; 0 U; 2 Other;

  Query Match             94.9%;  Score 2847.4;  DB 12;  Length 15679;
  Best Local Similarity   96.8%;  Pred. No. 0;
  Matches 2905;  Conservative    0;  Mismatches   96;  Indels    0;  Gaps    0;

Qy          1 GTCATAGGCGCGCCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              ||||||||||||||||||||||| || |||||||||||||||||||||||||||||| |||
Db       1265 GTCATAGGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCGGAG 1324

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              |||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1325 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAAGGCGTGGGTAAAGTA 1384

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1385 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACCTCTCC 1444

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1445 AGGTCACAGGAGGAAGAATCTATGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 1504

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              |||||||||||||||| |||||||||| ||||||||||||||||||||||||||||||||
Db       1505 ACTAAGTTTATCAATGGCCTGGAAACTCTTCAAGAGAACCGTCGTCACTCGATGTTCTTC 1564

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              |||||||||||||||||||||||||||||||||| || || ||||||| |||||||||||||
Db       1565 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGTCTTGAAGATCTCACCAACTACTTCGCA 1624

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              |||||||||||||||||||||||||||||||| ||||||||||||| || ||||| |||||
Db       1625 CAGCCCGATGAGGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAAC 1684

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1685 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 1744

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              |||||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1745 ATCAACGTCGTCACGTCCCAGGGGTTCCTGGCTGGATTCCTGGCGGGAGACGAATCTGGA 1804

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       1805 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAAGGC 1864

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db       1865 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGTTCAACTGGCTGTTCTCGCGC 1924

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||

Db       1925 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCATCCTC 1984

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
              || |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       1985 ATCGACTCGCCTGAAGCGCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 2044

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
              |||||||||||||| || |||||||||||||||||||||||||||||| || ||||||
Db       2045 CTATTAGAAAAGCACGGACGCGACCCTAAAGTACTAGATGTGCTATGTTCACTCTGCGTC 2104

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| || |||||||||
Db       2105 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGCGACTATTTGCTGCCCGGC 2164

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
              |||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||||
Db       2165 AAGAACCTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATC 2224

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2225 TTCGTGGGCCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 2284

Qy       1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       2285 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAACACT 2344

Qy       1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
              |||||||||||||||||||||||||| ||||| |||||||||||||||||||||||||||||
Db       2345 ACTGGTTATGTCCCATACCCGGGTGGTGGTGAGAAGTGGGGAGGTAACGGCGTGGGAGAC 2404

Qy       1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
              |||||||||||||||||| || |||||||||||||||||||| |||||||||| ||
Db       2405 GACCTGTACTCGTACGGGTTTGATGGCGCCTACCTCTGGTCCGGCGGGAGGAAGACCCCG 2464

Qy       1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
              |||||||||||||||||||||||||||||||| |||||||||||||||||||| |||
Db       2465 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCA 2524

Qy       1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       2525 TTGGACCTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 2584

Qy       1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2585 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 2644

Qy       1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
              |||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Db       2645 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTAGACTCCGGTACGCGGCTCCAGAAGGC 2704

Qy       1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
              ||||| ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2705 TACTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 2764

Qy       1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       2765 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCCCCGCTAGTACAGGACGATACG 2824

Qy       1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
              || || |||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db       2825 GCTTTTGTGCCTACGCCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 2884

Qy       1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
              || ||||| |||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       2885 ATCAGAGACAAGCTAGCTGAAAATATTCACGAAATGTGGGCTATGAATAAGATCGAAGCA 2944

Qy       1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2945 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 3004

Qy       1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
              |||||||||||||| || |||||||||||||||| |||||||| ||||||||||||||||
Db       3005 TTCGAGCGACTCCCGCCCGCTGAGAAACGATACGATATACAACTTGCTGTGCAGACACTC 3064
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Qy       1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3065 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 3124

Qy       1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3125 AACGTTCGTCTGCCCAATGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 3184

Qy       1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       3185 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGGCCAGCTGGCTGAG 3244

Qy       1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       3245 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAAT 3304

Qy       2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       3305 GAGGACTCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 3364

Qy       2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3365 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 3424

Qy       2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 2220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3425 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 3484

Qy       2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3485 CAGAAGCAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 3544

Qy       2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       3545 AAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 3604

Qy       2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400
             |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||||
Db       3605 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCTTTTGATGGT 3664

Qy       2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3665 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 3724

Qy       2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3725 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAC 3784

Qy       2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 2580
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3785 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 3844

Qy       2581 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 2640
             |||||||||||| |||||||| |||||||| ||||||||||||||||||||||| || ||
Db       3845 AACTTTGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAG 3904

Qy       2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700
             || ||||| || ||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3905 GACGTGAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTC 3964

Qy       2701 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 2760
             || ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3965 TGTGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAG 4024

Qy       2761 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 2820
             ||||| |||||||||||||||||||| || ||||||||||||||||||||||||||||||
Db       4025 AATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGAT 4084

Qy       2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       4085 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGG 4144

Qy       2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       4145 GAGTTCTTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAA 4204

Qy       2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTT 3000
             |||||||| ||||||||||||||||||||||| |||| ||||||||||||||||||||||
Db       4205 AAAGCCAGGCGTTGGGTAGAAATCAAGGACCGCCAACGGATCCTAATGAAAGAGGCAGTT 4264

Qy       3001 G 3001
             |
Db       4265 G 4265
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RESULT 4
ADM68885
ID   ADM68885 standard; DNA; 15405 BP.
XX
AC   ADM68885;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:129.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS   Heliothis virescens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15405
FT                   /*tag= a
FT                   /product= "ryanodine receptor"
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
DR   P-PSDB; ADM68895.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Claim 6; SEQ ID NO 129; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
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CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15405 BP; 4086 A; 3850 C; 4173 G; 3296 T; 0 U; 0 Other;

Query Match 94.7%; Score 2841; DB 12; Length 15405;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 2901; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              |||||||||||||||||||||| || ||||||||||||||||||||||||||||||||||
Db       1000 GTCATAGGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 1059

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1060 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGGAGGGAGTGGGTAAAGTA 1119

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1120 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGACGGCCTCGACTTCTCC 1179

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1180 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGAAAGTGTTCTTCGCTGTTC 1239

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 1299

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 1359

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              || |||||||| |||||||||||||||||||| |||||||||||||| || ||||| |||
Db       1360 CAACCCGATGAAGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAAC 1419

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1420 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 1479

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              |||||||||||||||| |||||||||||| ||||| ||||||||||||||||||||||||||
Db       1480 ATCAACGTCATCACGTCTCAGGGGTTCCTGGCTGGTTTCCTGGCGGGAGACGAATCTGGA 1539

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1540 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGTTGGCGGCAATAATAAAGGGC 1599

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||||
Db       1600 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGCTGAACTGGCTGTTCTCGCGC 1659

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1660 CTCGGCTCGCAGGCCTCGGGCGAGGGCACTGGCATGCTCGACGTGCTGCACTGCGTGCTC 1719

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
              || |||||||||||||  | ||||||||||||||||||||||||||||||||||||||||
Db       1720 ATCGACTCGCCTGAAGCGTTGAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 1779

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
              |||||||||||||| |||||||||||||||||||||||||||||| ||||||| || ||||||
Db       1780 CTATTAGAAAAGCACGGGCGCGACCCTAAAGTACTAGATGTGTTATGTTCACTCTGCGTC 1839

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
              |||||||||||||||||||||||||||||||||||||||||||||||||| || |||||||||
Db       1840 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTATTTGCTGCCCGGC 1899

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
              |||||||||||||||||||||||||||||||| || ||||||||||||||||||||||||||||
Db       1900 AAGAACCTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATC 1959

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       1960 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAAGTGACTATG 2019

Qy       1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
              |||||||||||||||||||||||||||||| |||||||||||||||||||||| ||||||
Db       2020 GACCACATAGAGAAGACCACACATATGATACCACATCTACGCATAGGATGGGCTAACACT 2079

Qy       1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
              ||||| || |||||||||||||| ||||| || || ||||||||||||||||||||||||
Db       2080 ACTGGCTACGTCCCATACCCGGGTGGTGGTGAAAAGTGGGGAGGTAACGGCGTGGGAGAC 2139

Qy       1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
              |||||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||
Db       2140 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGCGGGAGGAAAACTCCC 2199

Qy       1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||| ||
Db       2200 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCG 2259

Qy       1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
              || |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       2260 TTAGACCTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 2319

Qy       1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db       2320 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAATTG 2379

Qy       1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
              ||||| |||||||||||||||| ||||| ||| | ||||||||||||||||||||||||
Db       2380 AGTTGCCGGTTCCTGCTGGGCGGGGAACATGGTAGACTCCGGTACGCGGCTCCAGAAGGC 2439

Qy       1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
              ||||| ||  ||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       2440 TACTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCTTGCTTC 2499

Qy       1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
              |||||||||||||||||||| ||| |||||||||| ||||||||||||||||||||||||
Db       2500 TACTTCGGCAACCTGTCCAAGCGCGCCCTGGCTGGACCCCCGCTAGTACAGGACGATACG 2559

Qy       1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
              || || |||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       2560 GCTTTTGTGCCTACACCTGTTGACACTTTACAGATTACTCTGCCTACATATGTGGAACAA 2619

Qy       1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
              || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2620 ATCAGAGACAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 2679

Qy       1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db       2680 GGCTGGATGTACGGCGATCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 2739

Qy       1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
              |||||||| ||||| || ||||||||||||||||||||||||||||||||||||||||||
Db       2740 TTCGAGCGTCTCCCGCCCGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 2799

Qy       1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2800 AAGACAATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 2859

Qy       1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
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Db       2860 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 2919

Qy       1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980

Db       2920 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 2979

Qy       1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040

Db       2980 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAAT 3039

Qy       2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100

Db       3040 GAGGACTCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 3099

Qy       2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160

Db       3100 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 3159

Qy       2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 2220

Db       3160 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 3219

Qy       2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280

Db       3220 CAGAAGCAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 3279

Qy       2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340

Db       3280 AAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 3339

Qy       2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400

Db       3340 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCATTTGATGGT 3399

Qy       2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460

Db       3400 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 3459

Qy       2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520

Db       3460 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAC 3519

Qy       2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 2580

Db       3520 GGTGAGTTATTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 3579

Qy       2581 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 2640

Db       3580 AACTTTGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAG 3639

Qy       2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700

Db       3640 GACGTAAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTC 3699

Qy       2701 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 2760

Db       3700 TGTGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAG 3759

Qy       2761 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 2820

Db       3760 AATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGAT 3819

Qy       2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880

Db       3820 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGG 3879

Qy       2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940

Db       3880 GAGTTCTTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAA 3939

Qy       2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTT 3000

Db       3940 AAAGCCAGGCGTTGGGTAGAAATCAAGGACCGCCAACAGATCCTAATGAAAGAGGCAGTT 3999

Qy       3001 G 3001

Db       4000 G 4000
```

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RESULT 5
ADM68899
ID   ADM68899 standard; DNA; 15429 BP.
XX
AC   ADM68899;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:143.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS   Heliothis virescens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15429
FT                   /*tag=  a
FT                   /product= "ryanodine receptor"
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
DR   P-PSDB; ADM68900.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Claim 6; SEQ ID NO 143; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
```

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CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 15429 BP; 4084 A; 3856 C; 4190 G; 3299 T; 0 U; 0 Other;

  Query Match             94.6%;  Score 2839.4;  DB 12;  Length 15429;
  Best Local Similarity   96.6%;  Pred. No. 0;
  Matches 2900;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              |||||||||||||||||||||| || ||||||||||||||||||||||||||||||||||
Db       1015 GTCATAGGCGCGCCCATCATCAAGTACGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 1074

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 1134

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1135 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGACGGCCTCGACTTCTCC 1194

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1195 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGAAAGTGTTCTTCGCTGTTC 1254

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1255 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 1314

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1315 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 1374

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              || |||||||| |||||||||||||||||||| |||||||||||||| || ||||| |||
Db       1375 CAACCCGATGAAGATATGGAACACGAAGAAAAGCAAAACAAATTCCGCGCCCTCCGCAAC 1434

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1435 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGTCAAG 1494

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              |||||||||||||||| |||||||||||| ||||| ||||||||||||||||||||||||
Db       1495 ATCAACGTCATCACGTCTCAGGGGTTCCTGGCTGGTTTCCTGGCGGGAGACGAATCTGGA 1554

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db       1555 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGTTGGCGGCAATAATAAAGGGC 1614

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db       1615 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGGCTGAACTGGCTGTTCTCGCGC 1674

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1675 CTCGGCTCGCAGGCCTCGGGCGAGGGCACTGGCATGCTCGACGTGCTGCACTGCGTGCTC 1734

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
              || |||||||||||||  | ||||||||||||||||||||||||||||||||||||||||
Db       1735 ATCGACTCGCCTGAAGCGTTGAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 1794

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
              |||||||||||||| |||||||||||||||||||||||||||||| ||||||| || ||||||
Db       1795 CTATTAGAAAAGCACGGGCGCGACCCTAAAGTACTAGATGTGTTATGTTCACTCTGCGTC 1854

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
              |||||||||||||||||||||||||||||||||||||||||||||||| || |||||||||

Db       1855 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTATTTGCTGCCCGGC 1914

Qy         901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
               |||||||||||||||||||||||||||||| || ||||||||||||||||||||||||||||
Db        1915 AAGAACCTGTTGCTGCAAACTGCGCTTGTAGATCACGTATCTAGTGTCCGTCCGAACATC 1974

Qy         961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        1975 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAAGTGACTATG 2034

Qy        1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        2035 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCTAACACT 2094

Qy        1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
               ||||| || |||||||||||||| ||||| || || |||||||||||||||||||||||||
Db        2095 ACTGGCTACGTCCCATACCCGGGTGGTGGTGAAAAGTGGGGAGGTAACGGCGTGGGAGAC 2154

Qy        1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
               |||||||||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||
Db        2155 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGCGGGAGGAAAACTCCC 2214

Qy        1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
               |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||| ||
Db        2215 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGGAAAGGTGACGTGATAGGTTGTGCG 2274

Qy        1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
               || |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        2275 TTAGACCTGACGGTACCCATCATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 2334

Qy        1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        2335 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAATTG 2394

Qy        1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
               ||||| |||||||||||||||| ||||| ||| | |||||| ||||||||||||||||||
Db        2395 AGTTGCCGGTTCCTGCTGGGCGGGGAACATGGTAGACTCCGGCACGCGGCTCCAGAAGGC 2454

Qy        1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
               ||||| ||  |||||||||||||||||||||||||||||||||||||||||| ||||||
Db        2455 TACTCCCCGCTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCTTGCTTC 2514

Qy        1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
               |||||||||||||||||||| ||| |||||||||| ||||||||||||||||||||||||
Db        2515 TACTTCGGCAACCTGTCCAAGCGCGCCCTGGCTGGACCCCCGCTAGTACAGGACGATACG 2574

Qy        1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
               || || |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        2575 GCTTTTGTGCCTACACCTGTTGACACTTTACAGATTACTCTGCCTACATATGTGGAACAA 2634

Qy        1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
               || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2635 ATCAGAGACAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 2694

Qy        1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
               |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        2695 GGCTGGATGTACGGCGATCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 2754

Qy        1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
               |||||||| ||||| || ||||||||||||||||||||||||||||||||||||||||||
Db        2755 TTCGAGCGTCTCCCGCCCGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 2814

Qy        1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
               ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2815 AAGACAATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 2874

Qy        1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2875 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 2934

Qy        1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
               |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2935 GACCTGGGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 2994
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Qy       1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       2995 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTACGGACTTAAT 3054

Qy       2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       3055 GAGGACTCGGACATGCATCGATCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 3114

Qy       2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3115 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 3174

Qy       2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 2220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3175 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 3234

Qy       2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3235 CAGAAGCAAGCCGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 3294

Qy       2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340
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Db       3295 AAGTGGTACTTCGAGTTTGAGATCCTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 3354

Qy       2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       3355 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCCTGGGCATTTGATGGT 3414

Qy       2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3415 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 3474

Qy       2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3475 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAC 3534

Qy       2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 2580
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3535 GGTGAGTTATTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 3594

Qy       2581 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 2640
             |||||||||||| |||||||| |||||||| |||||||||||||||||||||| || ||
Db       3595 AACTTTGTACCTGCTTGCACGCTTGGTGTCGGCCAAAAAGCCAGGTTAACATACGGTCAG 3654

Qy       2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700
             || ||||| || |||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3655 GACGTGAACACGCTGAAATACTTCACAACATGTGGTCTGCAGGAGGGATATGAACCATTC 3714

Qy       2701 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 2760
             || ||||||||| ||||||||||||||||||||||||||||| ||||||||||||||||||
Db       3715 TGTGTCAATATGGAGAGAGACGTGACTCACTGGTACACCAAAGACCAGCCGATCTTCGAG 3774

Qy       2761 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 2820
             ||||| |||||||||||||||||| || ||||||||||||||||||||||||||||||||
Db       3775 AATACGGATGAGATGATCGACACCAGAATAGATGTGACCAGGATACCAGCTGGTTCAGAT 3834

Qy       2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880
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Db       3835 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTTGAGACGATGGAGAAAGCTAACTGG 3894

Qy       2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       3895 GAGTTCTTACGTCTCTCACTGCCTGTCATCTGCCATAACGAGTTCATTGACGAGGCAGAA 3954

Qy       2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAGTT 3000
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Db       3955 AAAGCCAGGCGTTGGGTAGAAATCAAGGACCGCCAACAGATCCTAATGAAAGAGGCAGTT 4014

Qy       3001 G 3001
             |
Db       4015 G 4015
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RESULT 6
ABL16881
ID   ABL16881 standard; DNA; 15606 BP.
XX
AC   ABL16881;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 2116.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 2116; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 15606 BP; 3731 A; 4275 C; 4399 G; 3201 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 1620.4;  DB 4;  Length 15606;
  Best Local Similarity   71.5%;  Pred. No. 0;
  Matches 2147;  Conservative    0;  Mismatches  851;  Indels    6;  Gaps    1;

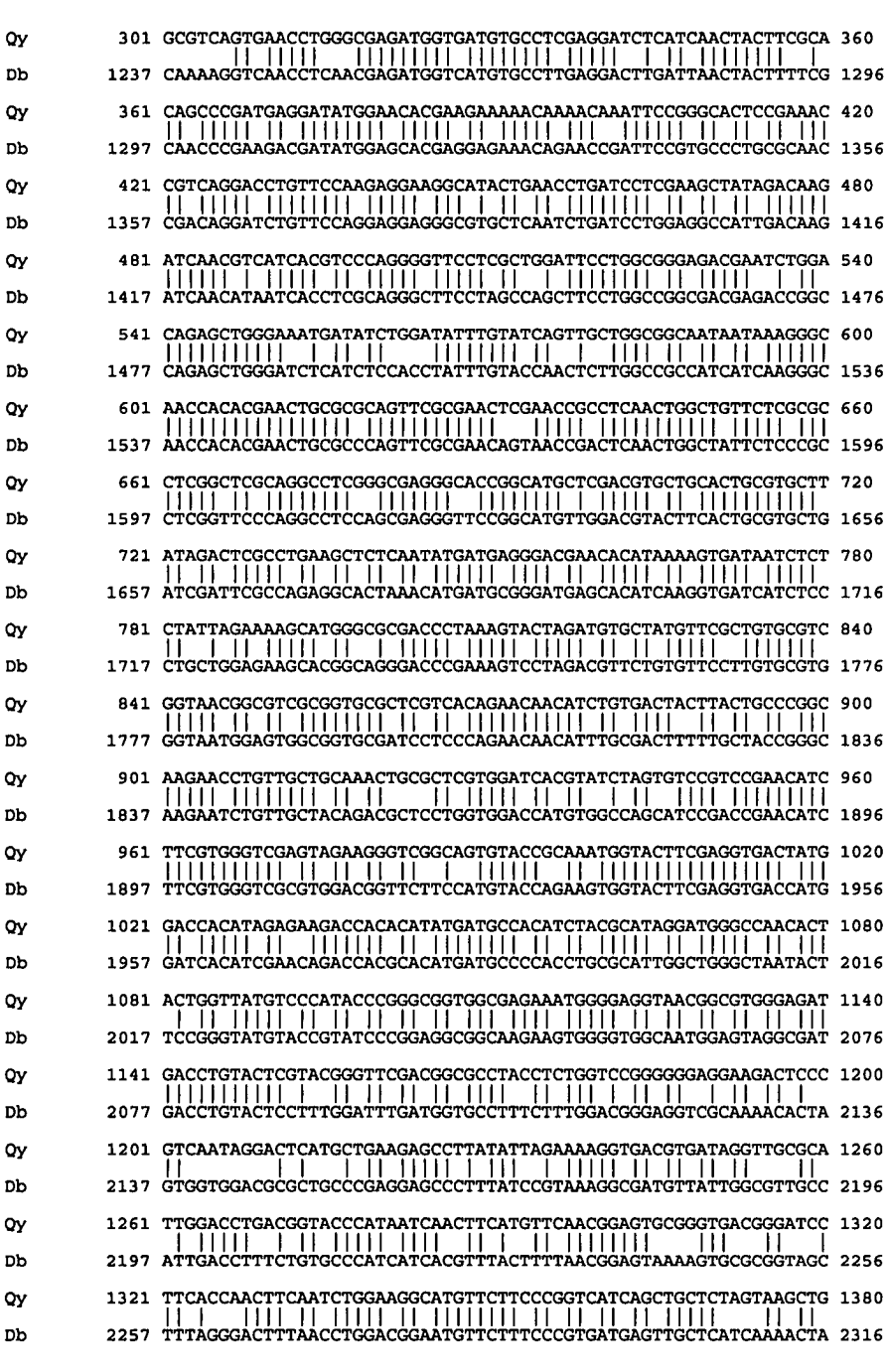
Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              || || ||| |||| |||||||| || || ||| | |||||||| || ||||| | ||||
Db        937 GTGATCGGCTCGCCGATCATCAAGTACGGCGACACTACCGTCATCGTTCAGCACTGCGAG 996

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              ||| ||||||||||     || |||  ||| || ||||| |||||||| || || || ||
Db        997 ACTAGCTTGTGGCTCAGCTACAAGAGTTATGAGACGAAAAAGAAGGGCGTAGGAAAGGTG 1056

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              || |||||||||||||| || |||||||| |||||||||||||| | ||||||||||
Db       1057 GAGGAGAAGCAAGCGATCCTGCACGAGGAGGGCAAGATGGACGATTGTCTCGACTTCTCG 1116

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              | || |||||||| || || | ||| ||||| || ||| | |||||        || |||
Db       1117 CGCTCCCAGGAGGAGGAGTCCAAGACAGCTCGTGTCATCCGCAAGTGCAGCAGCCTCTTC 1176

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              ||  ||||||| |  |   ||||||| || ||     || || || ||||| || ||||||
Db       1177 ACCCAGTTTATTACAGCCTTGGAAACACTGCAGTCAAATCGCCGACACTCCATTTTCTTC 1236
```


Qy 301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
Db 1237 CAAAAGGTCAACCTCAACGAGATGGTCATGTGCCTTGAGGACTTGATTAACTACTTTTCG 1296
Qy 361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
Db 1297 CAACCCGAAGACGATATGGAGCACGAGGAGAAACAGAACCGATTCCGTGCCCTGCGCAAC 1356
Qy 421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
Db 1357 CGACAGGATCTGTTCCAGGAGGAGGGCGTGCTCAATCTGATCCTGGAGGCCATTGACAAG 1416
Qy 481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
Db 1417 ATCAACATAATCACCTCGCAGGGCTTCCTAGCCAGCTTCCTGGCCGGCGACGAGACCGGC 1476
Qy 541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
Db 1477 CAGAGCTGGGATCTCATCTCCACCTATTTGTACCAACTCTTGGCCGCCATCATCAAGGGC 1536
Qy 601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
Db 1537 AACCACACGAACTGCGCCCAGTTCGCGAACAGTAACCGACTCAACTGGCTATTCTCCCGC 1596
Qy 661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
Db 1597 CTCGGTTCCCAGGCCTCCAGCGAGGGTTCCGGCATGTTGGACGTACTTCACTGCGTGCTG 1656
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Qy 1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
Db 1957 GATCACATCGAACAGACCACGCACATGATGCCCCACCTGCGCATTGGCTGGGCTAATACT 2016
Qy 1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
Db 2017 TCCGGGTATGTACCGTATCCCGGAGGCGGCAAGAAGTGGGGTGGCAATGGAGTAGGCGAT 2076
Qy 1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
Db 2077 GACCTGTACTCCTTTGGATTTGATGGTGCCTTTCTTTGGACGGGAGGTCGCAAAACACTA 2136
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Db 2137 GTGGTGGACGCGCTGCCCGAGGAGCCCTTTATCCGTAAAGGCGATGTTATTGGCGTTGCC 2196
Qy 1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
Db 2197 ATTGACCTTTCTGTGCCCATCATCACGTTTACTTTTAACGGAGTAAAAGTGCGCGGTAGC 2256
Qy 1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
Db 2257 TTTAGGGACTTTAACCTGGACGGAATGTTCTTTCCCGTGATGAGTTGCTCATCAAAACTA 2316
Qy 1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
Db 2317 AGCTGTCGCTTCCTTTCGGAGGTGATCATGGTCGTTTAAAGTTTGCCCCGCCCATGGGA 2376
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Qy 1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
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Qy 1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
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Qy 1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
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Qy 1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
Db 2917 AACACTCACAATCTGTGGGCACGGGAGCGCATCCAGCAGGGTTGGACTTATGGTCTGAAC 2976
Qy 2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
Db 2977 GAGGATAGTGAAAACCACAGGAGTCCACACTTGGTGCCATATGCCAAAGTGGACGAGGCT 3036
Qy 2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160
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Qy 2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280
Db 3157 CTCAAGTTCGCCGGATTCCGGACTTACAGGGTGGAGCGCAACTACGCCGTGACATCGGGC 3216
Qy 2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340
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Qy 2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400
Db 3277 GCCGATTGCTATCCGGGAGCGATGCTGGGCAGCGAGGACACCAGTTGGGCCTTCGATGGA 3336
Qy 2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460
Db 3337 CACAATGTGACCAAAATGCACGCCGGATCCATTGAGCACTTCGGAGTGCGGTATGAGGCT 3396
Qy 2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520

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                 || || ||  | ||    ||| | ||| |||  ||  | ||||| || |||||  | ||
Db       3397 GGCGATGTCATTGGTTGTTTCATCGATGTCAAGGAGCAAACGATCAGCTTCTCGTTGAAC 3456

Qy       2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGT------CCAG 2574
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Db       3457 GGAGAACTCCTGATGGACGCGCTGGGCGGCGAGACGACCTTTGCCGACGTAACCGCCGAG 3516

Qy       2575 GGTGACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATAT 2634
                || |    ||| || || || ||||| || || |||||||| || ||   |  | |  ||
Db       3517 GGGGTGGGCTTCGTGCCCGCCTGCACCCTGGGAGTGGGCCAGAAGGCGCGCCTCATCTAC 3576

Qy       2635 GGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAA 2694
                ||||| || ||| |  | || || | |||||| || ||||| || || |||||||| ||
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Qy       2695 CCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATC 2754
                || || ||||| || |||     |     || || ||||||||||||||||||||||| ||
Db       3637 CCGTTCTGCGTGAACATGCGCCGCCCGGTTACCCACTGGTACACCAAGGACCAGCCCATT 3696

Qy       2755 TTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGT 2814
                || ||||| || || ||||||  ||||  | | || ||||| ||| |||| || |  ||
Db       3697 TTTGAGAACACCGAGGAGATGCCCGACTGCCGCATCGATGTCACCCGGATTCCCGGCGGC 3756

Qy       2815 TCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCT 2874
                | || || || ||    | | ||||| || |||||||| |||||||| |||||||| ||
Db       3757 GCCGACACCCCGCCGCACTTAAAGATCTCGCACAACACCTTCGAGACCATGGAGAAGGCC 3816

Qy       2875 AACTGGGAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAG 2934
                ||||||||||| | ||||| || ||||| || | ||||      |||||||    |||
Db       3817 AACTGGGAGTTCCTGCGTCTTTCCCTGCCCGTGACCTGCATGGGTGAGTTTATCAGCGAA 3876

Qy       2935 GCAGAAAAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAG 2994
                || || |||||||| ||||  || || ||| |||| ||  |    || |||   |||
Db       3877 CAGGAGAAGGCCAGACGCTGGGACGAGATTAAGAACCGGCAGTACCGACTGATGCGCGAG 3936

Qy       2995 GCAG 2998
                || |
Db       3937 GCGG 3940
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RESULT 7
ADM68765
ID ADM68765 standard; DNA; 16363 BP.
XX
AC ADM68765;
XX
DT 17-JUN-2004 (first entry)
XX
DE Drosophila melanogaster ryanodine receptor encoding DNA SEQ ID NO:9.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Drosophila melanogaster.
XX
FH Key Location/Qualifiers
FT CDS 1. .15330
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68766.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 9; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 16363 BP; 3940 A; 4448 C; 4559 G; 3414 T; 0 U; 2 Other;

 Query Match 53.9%; Score 1617.2; DB 12; Length 16363;
 Best Local Similarity 71.4%; Pred. No. 0;
 Matches 2145; Conservative 0; Mismatches 853; Indels 6; Gaps 1;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              || || ||| |||| |||||||| || || ||| | |||||||| || ||||| | ||||
Db        997 GTGATCGGCTCGCCGATCATCAAGTACGGCGACACTACCGTCATCGTCCAGCACTGCGAG 1056

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              ||| ||||||||||    || |||  ||| || ||||| |||||||| || || || ||
Db       1057 ACTAGCTTGTGGCTCAGCTACAAGAGTTATGAGACGAAAAAGAAGGGCGTAGGAAAGGTG 1116

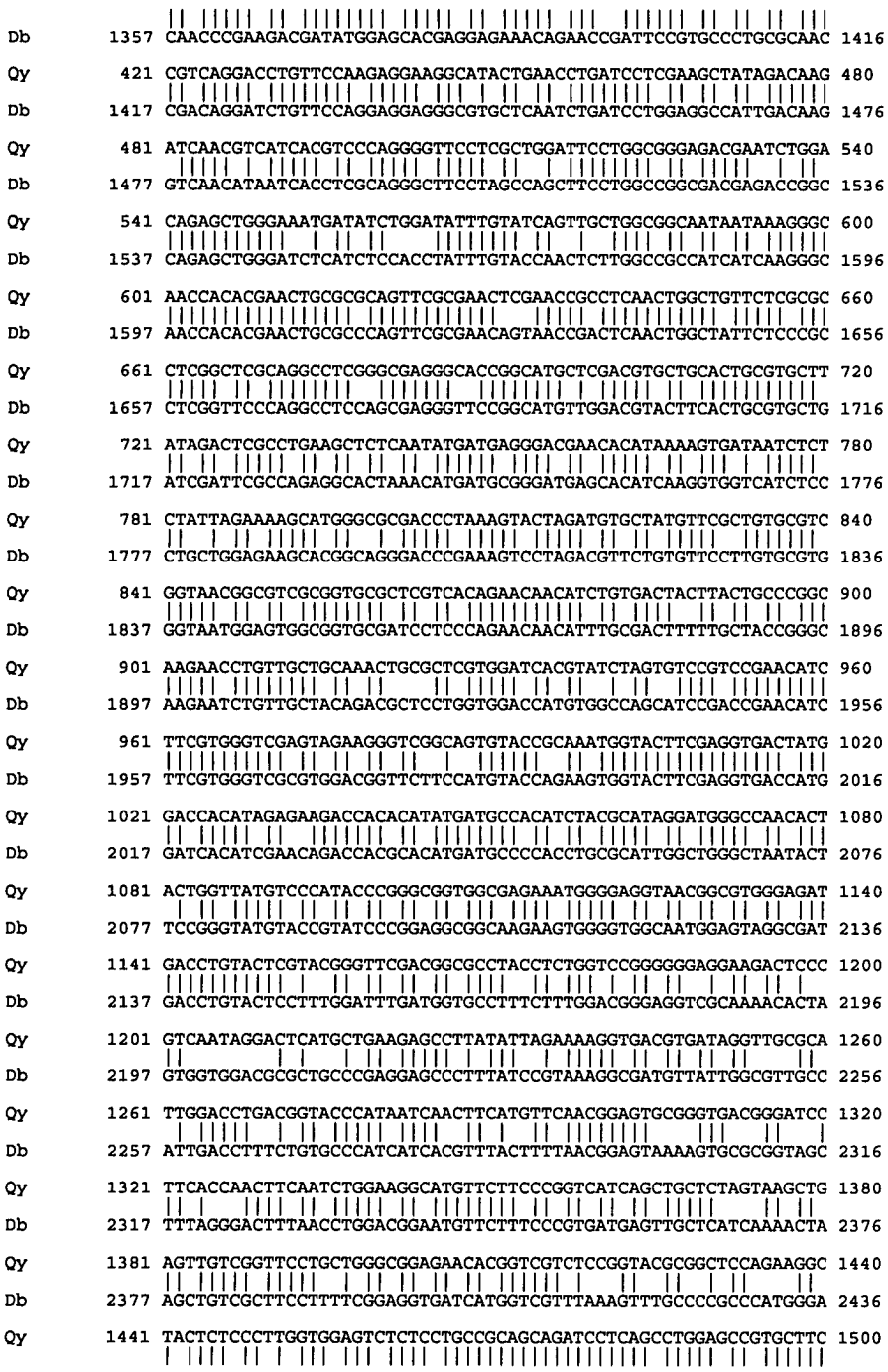
Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              || |||||||||||||| || |||||||| |||||||||||||| | ||||||||||||
Db       1117 GAGGAGAAGCAAGCGATCCTGCACGAGGAGGGCAAGATGGACGATTGTCTCGACTTCTCG 1176

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              | || |||||||| || || | ||| ||||| || ||| | |||||        || |||
Db       1177 CGCTCCCAGGAGGAGGAGTCCAAGACGGCTCGTGTCATCCGCAAGTGCAGCAGCCTCTTC 1236

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              ||  ||||||| |  |    ||||||| || ||      || || || ||||| || ||||||
Db       1237 ACCCAGTTTATTACAGCCTTGGAAACACTGCAGTCAAATCGCCGACACTCCATTTTCTTC 1296

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
                    || |||||   ||||||||| |||||||| |||||  | || ||||||||  |
Db       1297 CAAAAGGTCAACCTCAACGAGATGGTCATGTGCCTTGAGGACTTGATTAACTACTTTTCG 1356

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
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Db 1357 CAACCCGAAGACGATATGGAGCACGAGGAGAAACAGAACCGATTCCGTGCCCTGCGCAAC 1416
Qy 421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
Db 1417 CGACAGGATCTGTTCCAGGAGGAGGGCGTGCTCAATCTGATCCTGGAGGCCATTGACAAG 1476
Qy 481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
Db 1477 GTCAACATAATCACCTCGCAGGGCTTCCTAGCCAGCTTCCTGGCCGGCGACGAGACCGGC 1536
Qy 541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
Db 1537 CAGAGCTGGGATCTCATCTCCACCTATTTGTACCAACTCTTGGCCGCCATCATCAAGGGC 1596
Qy 601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
Db 1597 AACCACACGAACTGCGCCCAGTTCGCGAACAGTAACCGACTCAACTGGCTATTCTCCCGC 1656
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Qy 961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
Db 1957 TTCGTGGGTCGCGTGGACGGTTCTTCCATGTACCAGAAGTGGTACTTCGAGGTGACCATG 2016
Qy 1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
Db 2017 GATCACATCGAACAGACCACGCACATGATGCCCCACCTGCGCATTGGCTGGGCTAATACT 2076
Qy 1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
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Qy 1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
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Db 2617 ATCAAGGAGAAGCTGGCGGAGAATATCCACGAGATGTGGGCTCTAAACAAAATCGAAGCG 2676
Qy 1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
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Db 2917 GACCTAAGCGCCGTGACACTCACCCCCAAGTTGGAGGAGCTTGTGGACCAGCTGGCCGAG 2976
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Db 3397 CACAATGTGACCAAAATGCACGCCGGATCCATTGAGCACTTCGGAGTGCGGTATGAGGCT 3456
Qy 2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520
Db 3457 GGCGATGTCATTGGTTGTTTCATCGATGTCAAGGAGCAAACGATCAGCTTCTCGTTGAAC 3516
Qy 2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGT------CCAG 2574
Db 3517 GGAGAACTCCTGATGGACGCGCTGGGCGGCGAGACGACCTTTGCCGACGTAACCGCCGAG 3576

```
Qy       2575 GGTGACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATAT 2634
Db       3577 GGGGTGGGCTTCGTGCCCGCCTGCACCCTGGGAGTGGGCCAGAAGGCGCGCCTCATCTAC 3636

Qy       2635 GGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAA 2694
Db       3637 GGCCAGGACGTGGACTCACTCAAGTTCTTCACCACTTGTGGCCTGCAAGAGGGATACGAG 3696

Qy       2695 CCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATC 2754
Db       3697 CCGTTCTGCGTGAACATGCGCCGCCCGGTTACCCACTGGTACACCAAGGACCAGCCCATT 3756

Qy       2755 TTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGT 2814
Db       3757 TTTGAGAACACCGAGGAGATGCCCGACTGCCGCATCGATGTCACCCGGATTCCCGGCGGC 3816

Qy       2815 TCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCT 2874
Db       3817 GCCGACACCCCGCCGCACTTAAAGATCTCGCACAACACCTTCGAGACCATGGAGAAGGCC 3876

Qy       2875 AACTGGGAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAG 2934
Db       3877 AACTGGGAGTTCCTGCGTCTTTCCCTGCCCGTGACCTGCATGGGTGAGTTTATCAGCGAA 3936

Qy       2935 GCAGAAAAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAG 2994
Db       3937 CAGGAGAAGGCCAGACGCTGGGACGAGATTAAGAACCGGCAGTACCGACTAATGCGCGAG 3996

Qy       2995 GCAG 2998
Db       3997 GCGG 4000
```

RESULT 8
ADM68763
ID ADM68763 standard; DNA; 15413 BP.
XX
AC ADM68763;
XX
DT 17-JUN-2004 (first entry)
XX
DE Peregrinus maidis ryanodine receptor encoding DNA SEQ ID NO:7.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 17. .15400
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68764.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 7; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15413 BP; 4666 A; 2966 C; 3619 G; 4160 T; 0 U; 2 Other;

 Query Match 51.4%; Score 1542.2; DB 12; Length 15413;
 Best Local Similarity 70.1%; Pred. No. 0;
 Matches 2101; Conservative 1; Mismatches 890; Indels 6; Gaps 2;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
Db       1013 GTAATAGGTGCACCAATTATCAAGTATGGTGACAGTACTGTTCTGGTTCAGCATTCTGAG 1072

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
Db       1073 ACTGGCTTGTGGCTTACATACAAATCATATGAAACTAAAAAGAAAGGAGTTGGAAAAGTT 1132

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
Db       1133 GAAGAGAAACAAGCTGTGCTCCATGAGGAAGGAAAGATGGACGACGGCTTGGATTTCTCC 1192

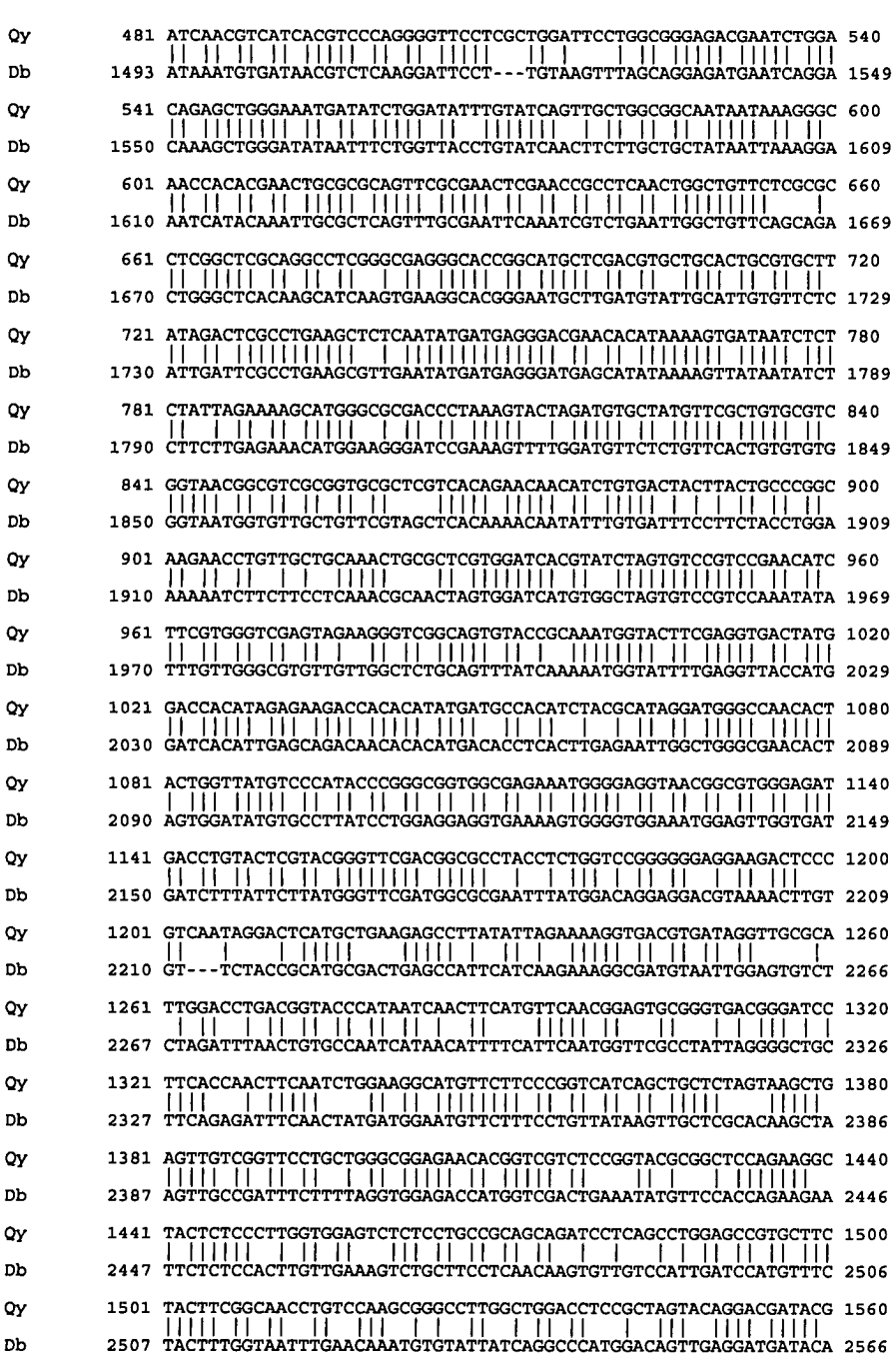
Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
Db       1193 CGCAGTCAAGAAGAAGAATCGCGTACCGCTCGTGTAATTAGGAAGTGTTCATCCTTGTTC 1252

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
Db       1253 ACTCAGTTTATNAGAGGTCTAGAGACCTTGCAGGTGAATAGAAGGCACTCGTTATTTTGT 1312

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
Db       1313 GCAACTGTGAATTTGAATGAAATGGTAATGTGCCTCGAAGATTTGATTAACTATTTTGCG 1372

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
Db       1373 CAGCCAGCAGATGATATGGAACACGAAGAAAAACAAAATAGGTTCCGTGCATTGAGAAAT 1432

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
Db       1433 CGTCAAGATCTGTTTCAAGAAGAAGGCATATTAAATTTAATTCTGGAAGCCATCGATAAA 1492
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Qy 481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
Db 1493 ATAAATGTGATAACGTCTCAAGGATTCCT---TGTAAGTTTAGCAGGAGATGAATCAGGA 1549
Qy 541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
Db 1550 CAAAGCTGGGATATAATTTCTGGTTACCTGTATCAACTTCTTGCTGCTATAATTAAAGGA 1609
Qy 601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
Db 1610 AATCATACAAATTGCGCTCAGTTTGCGAATTCAAATCGTCTGAATTGGCTGTTCAGCAGA 1669
Qy 661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
Db 1670 CTGGGCTCACAAGCATCAAGTGAAGGCACGGGAATGCTTGATGTATTGCATTGTGTTCTC 1729
Qy 721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
Db 1730 ATTGATTCGCCTGAAGCGTTGAATATGATGAGGGATGAGCATATAAAAGTTATAATATCT 1789
Qy 781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
Db 1790 CTTCTTGAGAAACATGGAAGGGATCCGAAAGTTTTGGATGTTCTCTGTTCACTGTGTGTG 1849
Qy 841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
Db 1850 GGTAATGGTGTTGCTGTTCGTAGCTCACAAAACAATATTTGTGATTTCCTTCTACCTGGA 1909
Qy 901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
Db 1910 AAAAATCTTCTTCCTCAAACGCAACTAGTGGATCATGTGGCTAGTGTCCGTCCAAATATA 1969
Qy 961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
Db 1970 TTTGTTGGGCGTGTTGTTGGCTCTGCAGTTTATCAAAAATGGTATTTTGAGGTTACCATG 2029
Qy 1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
Db 2030 GATCACATTGAGCAGACAACACACATGACACCTCACTTGAGAATTGGCTGGGCGAACACT 2089
Qy 1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
Db 2090 AGTGGATATGTGCCTTATCCTGGAGGAGGTGAAAAGTGGGGTGGAAATGGAGTTGGTGAT 2149
Qy 1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
Db 2150 GATCTTTATTCTTATGGGTTCGATGGCGCGAATTTATGGACAGGAGGACGTAAAACTTGT 2209
Qy 1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
Db 2210 GT---TCTACCGCATGCGACTGAGCCATTCATCAAGAAAGGCGATGTAATTGGAGTGTCT 2266
Qy 1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
Db 2267 CTAGATTTAACTGTGCCAATCATAACATTTTCATTCAATGGTTCGCCTATTAGGGGCTGC 2326
Qy 1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
Db 2327 TTCAGAGATTTCAACTATGATGGAATGTTCTTTCCTGTTATAAGTTGCTCGCACAAGCTA 2386
Qy 1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
Db 2387 AGTTGCCGATTTCTTTTAGGTGGAGACCATGGTCGACTGAAATATGTTCCACCAGAAGAA 2446
Qy 1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
Db 2447 TTCTCTCCACTTGTTGAAAGTCTGCTTCCTCAACAAGTGTTGTCCATTGATCCATGTTTC 2506
Qy 1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
Db 2507 TACTTTGGTAATTTGAACAAATGTGTATTATCAGGCCCATGGACAGTTGAGGATGATACA 2566
Qy 1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
Db 2567 GCATTTGTTCCAACACCTGTTGATACAACAAAGGTTTCGCTCCCAAATTATATTGAGAGC 2626
Qy 1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
Db 2627 ATAAGAGATAAGTTGGCAGAAAATATTCATGAAATGTGGGCTATGAACAAGATAGAAGCT 2686
Qy 1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
Db 2687 GGCTGGATGTTTGGGGAGAAGCGAGATGACATACGTAAAGTGCATCCATGCCTTATTCAG 2746
Qy 1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
Db 2747 TTCGACCAACTTCCACCAGCTGAGAAGCGCTATGACTCACAACTCGCAGTTCAAACTCTC 2806
Qy 1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
Db 2807 AAGACAATTCTGGCACTCGGCTACTACATAACGATGGATAAGCCTCCTTCGCGTATAAAA 2866
Qy 1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
Db 2867 ACAATTCGTCTTCCAAATGAGCCTTTCATGCAATCAAATGGCTACAAGCCAGCACCACTT 2926
Qy 1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
Db 2927 GATCTCACGGCCATATCATTAACACCGAAAATGGAGGAATTAGTTGATCAACTAGCCGAG 2986
Qy 1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
Db 2987 AATACACATAATCTATGGGCCAAAGAACGAATCCAACAAGGGTGGACGTATGGACTCAAT 3046
Qy 2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
Db 3047 GAGGACTCTGATATGTTGAGAAGTCCGCATCTGGTGCCTTACTGCAAAGTTGACGAAGCT 3106
Qy 2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160
Db 3107 ATAAAAAAAGCTAACAGGGATACTGCAAGTGAAACGGTCAGAACTCTATTGGTGTATGGC 3166
Qy 2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAAGCGTCAAAA 2220
Db 3167 TACAATCTAGATCCCCCCACCGGCGAAGCACATGAAGCTCTTCTTGCAGAGGCTAGTCGT 3226
Qy 2221 CAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGG 2280
Db 3227 TTAAGACAGACTCACTTCAGAACGTACCGAGCAGAAAAGAACTATGCCGTGACAACGGGA 3286
Qy 2281 AAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCAC 2340
Db 3287 AAGTGGTATTTTGAATTTGAAATCCTTACTGCTGGACCAATGAGAGTAGGTTGGGCACGG 3346
Qy 2341 GCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGT 2400
Db 3347 TCAGATTGTCCGCCAGGATCACAATTGGGAAATGACGAATATTCGTGGGCATTTGATGGC 3406
Qy 2401 TACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCTGTT 2460
Db 3407 TTCAACGAGGAAAAAGTGTACTTGGGAACAGGCGAGTCGTTTGGTCGCCAGTGGCAGGTT 3466
Qy 2461 GGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTCAAT 2520
Db 3467 GGAGATGTGGTTGGAGTATTTCTTGATCTATTGGACCATACCATGAGTTTCTCTTTGAAT 3526
Qy 2521 GGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGTGAC 2580
Db 3527 GGAGAACTGCTTATGGATGCCCTTGGAGGGGAGACTTCATTCGCTGACGTTCAAGGGGAA 3586
Qy 2581 AACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAA 2640
Db 3587 AGCTTTGTTCCTGCTTTCACCCTTGGCGTAGGCCAGAAAGCTAAACTGACTTTTGGGCAA 3646
Qy 2641 GATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTT 2700

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                |||||  | |    | || |  || ||||| || |||||||| || ||||||||||||||:
Db       3647 GATGTTACTGTATTAAAGTTTTTTACAACTTGCGGTCTTCAAGAAGGATATGAACCATTY 3706

Qy       2701 TGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTCGAG 2760
                || ||||||||||| ||||  || ||  | |||||||||||||||||| || ||  || |||
Db       3707 TGTGTCAATATGAACAGAGCGGTAACGTATTGGTACACCAAGGACCACCCAATTTTTGAG 3766

Qy       2761 AATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCAGAT 2820
                |||||||| ||       |||| |  | |||||||| || || ||  |||||||||| |||
Db       3767 AATACTGAAGATTATGCCGACTCACGAATTGATGTTACAAGAATTCCAGCTGGTTCGGAT 3826

Qy       2821 ACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAACTGG 2880
                || || || |||||||| ||    ||||||   |||||| | ||||| ||||| || |||
Db       3827 ACTCCACCTTGCCTCAAAATAAGTCACAACCTATTCGAGTCAATGGAAAAAGCCAATTGG 3886

Qy       2881 GAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCAGAA 2940
                || ||| |  | |||||||| || ||||| |||||        || || || |||   |||
Db       3887 GAATTCCTCAGACTCTCACTCCCAGTTATTTGCCACTCATCATTTATCGAAGAGAGTGAA 3946

Qy       2941 AAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCAG 2998
                |||   | |||||||   || || |    |||||| || |  ||  |    |||||
Db       3947 AAATTGAAACGTTGGCAGGAGATAAGAATCCGTCAGCATAGACTGTTAGTCGAGGCTG 4004
```

RESULT 9
ADM68761
ID ADM68761 standard; DNA; 15315 BP.
XX
AC ADM68761;
XX
DT 17-JUN-2004 (first entry)
XX
DE Periplaneta americana ryanodine receptor encoding DNA SEQ ID NO:5.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Periplaneta americana.
XX
FH Key Location/Qualifiers
FT CDS 1. .15315
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68762.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 5; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15315 BP; 5206 A; 2494 C; 3141 G; 4474 T; 0 U; 0 Other;

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  Query Match             44.5%;  Score 1335.4;  DB 12;  Length 15315;
  Best Local Similarity   66.2%;  Pred. No. 0;
  Matches 1988;  Conservative    0;  Mismatches 1001;  Indels   12;  Gaps    4;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              || || || || || || || || |||||||||    || ||  | || || ||||| ||
Db       1000 GTAATTGGAGCACCTATTATTAAGTATGGTGACAGTACGGTATTAGTACAACATTCTGAT 1059

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              || || || ||| |  | || |||||||| ||||| || || || || || |||||||||
Db       1060 ACAGGTTTATGGTTAACATACAAGTCTTATGAAACAAAAAAAAAAGGCGTCGGTAAAGTA 1119

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              ||||| || |||||  |  | || || ||||| || ||||||||||  | |||||
Db       1120 GAAGAAAAACAAGCAGTATTACATGAAGAAGGTAAAATGGACGATGGGTTAGACTTTAGT 1179

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              |||   || || ||||| ||||| |||||| |||| ||  | || || || ||  | |||
Db       1180 AGGAGTCAAGAAGAAGAGTCTAGAACTGCTAGAGTGATACGTAAATGCTCCTCATTATTC 1239

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              ||  |||||||    || |||||||| | |||||   ||| | |||   ||  | || |
Db       1240 ACACAGTTTATTTCCGGACTGGAAAATTTACAAAGTAACAGACGTTCGTCATTATTTTGT 1299

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              | |  || || ||     || ||||| ||||| || || ||| | || || || || || ||
Db       1300 TCATTCGTTAATCTAAATGAAATGGTCATGTGTCTAGAAGATTTAATAAATTATTTTGCT 1359

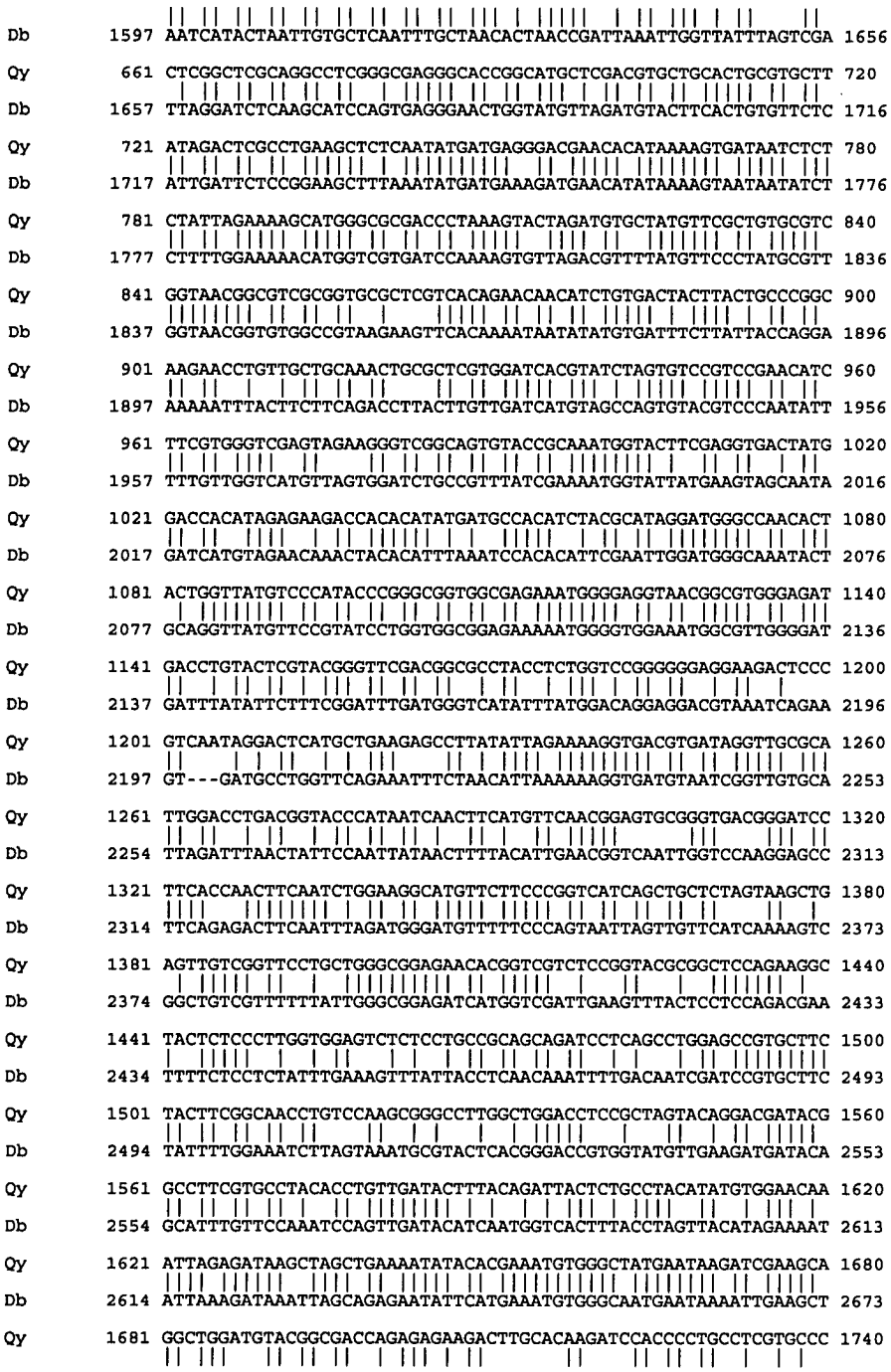
Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              || || || || ||||||||||||||||||||||||||   ||| | ||| |  ||||
Db       1360 CAACCTGAAGAAGATATGGAACACGAAGAAAAACAAAATCGATTTAGAGCATTAAGAAAT 1419

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              | || ||  | || ||||| ||||||||| | || ||||| || |||||||| || ||
Db       1420 AGACAAGATTTATTTCAAGAAGAAGGCATATTAAATCTGATTCTAGAAGCTATTGATAAA 1479

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              | ||  | || ||||| || || ||  | |  | |   | || || || || ||||||
Db       1480 GTTAATATTATTACGTCACAAGGATTTATGGTCAGTT---TAGCTGGTGATGAGTCTGGA 1536

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              || || |||||  |||| ||||| ||||| || |||||||| || ||||| ||||||||
Db       1537 CAAAGTTGGGATGTGATTTCTGGTTATTTATACCAGTTGCTAGCTGCAATTATAAAGGGA 1596

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
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Db 1597 AATCATACTAATTGTGCTCAATTTGCTAACACTAACCGATTAAATTGGTTATTTAGTCGA 1656
Qy 661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
Db 1657 TTAGGATCTCAAGCATCCAGTGAGGGAACTGGTATGTTAGATGTACTTCACTGTGTTCTC 1716
Qy 721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
Db 1717 ATTGATTCTCCGGAAGCTTTAAATATGATGAAAGATGAACATATAAAAGTAATAATATCT 1776
Qy 781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
Db 1777 CTTTTGGAAAAACATGGTCGTGATCCAAAAGTGTTAGACGTTTTATGTTCCCTATGCGTT 1836
Qy 841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
Db 1837 GGTAACGGTGTGGCCGTAAGAAGTTCACAAAATAATATATGTGATTTCTTATTACCAGGA 1896
Qy 901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
Db 1897 AAAAATTTACTTCTTCAGACCTTACTTGTTGATCATGTAGCCAGTGTACGTCCCAATATT 1956
Qy 961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
Db 1957 TTTGTTGGTCATGTTAGTGGATCTGCCGTTTATCGAAAATGGTATTATGAAGTAGCAATA 2016
Qy 1021 GACCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACT 1080
Db 2017 GATCATGTAGAACAAACTACACATTTAAATCCACACATTCGAATTGGATGGGCAAATACT 2076
Qy 1081 ACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGAT 1140
Db 2077 GCAGGTTATGTTCCGTATCCTGGTGGCGGAGAAAAATGGGGTGGAAATGGCGTTGGGGAT 2136
Qy 1141 GACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCC 1200
Db 2137 GATTTATATTCTTTCGGATTTGATGGGTCATATTTATGGACAGGAGGACGTAAATCAGAA 2196
Qy 1201 GTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGCGCA 1260
Db 2197 GT---GATGCCTGGTTCAGAAATTTCTAACATTAAAAAAGGTGATGTAATCGGTTGTGCA 2253
Qy 1261 TTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGATCC 1320
Db 2254 TTAGATTTAACTATTCCAATTATAACTTTTACATTGAACGGTCAATTGGTCCAAGGAGCC 2313
Qy 1321 TTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAGCTG 1380
Db 2314 TTCAGAGACTTCAATTTAGATGGGATGTTTTTCCCAGTAATTAGTTGTTCATCAAAAGTC 2373
Qy 1381 AGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAAGGC 1440
Db 2374 GGCTGTCGTTTTTTATTGGGCGGAGATCATGGTCGATTGAAGTTTACTCCTCCAGACGAA 2433
Qy 1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
Db 2434 TTTTCTCCTCTATTTGAAAGTTTATTACCTCAACAAATTTGACAATCGATCCGTGCTTC 2493
Qy 1501 TACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAGGACGATACG 1560
Db 2494 TATTTTGGAAATCTTAGTAAATGCGTACTCACGGGACCGTGGTATGTTGAAGATGATACA 2553
Qy 1561 GCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTGGAACAA 1620
Db 2554 GCATTTGTTCCAAATCCAGTTGATACATCAATGGTCACTTTACCTAGTTACATAGAAAAT 2613
Qy 1621 ATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATCGAAGCA 1680
Db 2614 ATTAAAGATAAATTAGCAGAGAATATTCATGAAATGTGGGCAATGAATAAAATTGAAGCT 2673
Qy 1681 GGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTCGTGCCC 1740
Db 2674 GGTTGGCAATATGGTGATAAAAGAAATGATACTAGGAAATATCATCCATGTTTAATACAG 2733
Qy 1741 TTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAGACACTC 1800
Db 2734 TTTGACAAGTTGCCTCCAGCCGAGAAGCGTTATGATTCTCAATTAGCTGTGCAAACGCTT 2793
Qy 1801 AAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGCACGCATCCGC 1860
Db 2794 AAAACGGTTATTGCGTTGGGATATCACATATCCATCGATAATCCACCGTCCCGCATTAAA 2853
Qy 1861 AACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCAGCACCACTC 1920
Db 2854 ACGGTACGGTTGCCCAACGAACCATTTATGCAATCCAATGGTTACAAACCAGCACCACTA 2913
Qy 1921 GACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAGCTGGCTGAG 1980
Db 2914 GATTTATCTGCAATAAATTTGTCAGGGAAAATGGAAGAATTAATTGACCAGTTAGCTGAG 2973
Qy 1981 AACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTATGGACTTAAT 2040
Db 2974 AATACACATAATTTATGGGCAAAAGAAAGAATACAACAAGGATGGACGTATGGTTTAAAT 3033
Qy 2041 GAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTTGACGATGCC 2100
Db 3034 GAAGAATTACAAATGTTACGCAGTCCTCATTTAGTACCGTACAGCAAAGTAGATGACGCT 3093
Qy 2101 ATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTGGTCTACGGG 2160
Db 3094 ATTAAAAAAGCTAATAGAGATACAGCAAGTGAAACAGTCCGCACTTTATTAGTATATGGT 3153
Qy 2161 TATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAG---CACTCTTGTTGGAAGCGTCA 2217
Db 3154 TACAACTTAGACCCACCGACTGGAGAAACAAACGAAGCGACACTCCTAACAGACGAAAAC 3213
Qy 2218 AAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCT 2277
Db 3214 ACTAATAGATACTTGACGTTCAGAACATATCGTGCTGAAAAAACATATGCTGTTGCAAGT 3273
Qy 2278 GGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCT 2337
Db 3274 GGAAAATGGTATTTCGAGTTTGAGATATTGACAAACGGGCCCATGCGAGTTGGATGGGCC 3333
Qy 2338 CACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGAT 2397
Db 3334 AGGTTTACATGTTCTCCGGGTTATCAAATCGGTAGTGACGAAAATTCTTGGGCATTTGAT 3393
Qy 2398 GGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAATGGGCT 2457
Db 3394 GGTTATAACGAAGAAAAAATTTATATGGGCACAGCCGAATCATTTGGGAGGCAGTGGCAA 3453
Qy 2458 GTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTCTCACTC 2517
Db 3454 GTTGGAGATGTCGTGGGAGTGTTTTTAGACCTAATGGATCATACAATAAGTTTTTCGTTG 3513
Qy 2518 AATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTCCAGGGT 2577
Db 3514 AATGGAGAATTACTAATGGATACATTGGGAGGAGAAACTACGTTTTCTGAAGTTCAAGGA 3573
Qy 2578 GACAACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGC 2637
Db 3574 GAAGGATTTGTACCTGCATTTACTCTGGGACTAGGACAAAAAGCAAAATTAACTTTTGGT 3633
Qy 2638 CAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCA 2697
Db 3634 CAAGACGTAAACTCATTGAAATACTTCACGACTTGTGGTCTTCAAGAAGGATATGAACCA 3693
Qy 2698 TTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCCGATCTTC 2757
Db 3694 TTTTGCGTAAACATGAAGAGACCAGTAACATATTGGTATACTAAGGATCAACCAATATTT 3753
Qy 2758 GAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATACCAGCTGGTTCA 2817
Db 3754 GAAAATACTGATGA---CTTTTCGTCTGTAATTGATGTTACAAGAATTCCAGCTGGTTCA 3810

```
Qy       2818 GATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCGAGACGATGGAGAAAGCTAAC 2877
             ||||||||  ||  ||  ||  ||  ||     ||  ||  ||  ||  ||  ||  |||||  |  ||||||
Db       3811 GATACACCACCGTGTCTAAAAATAAGTCATAATACATTTGAAACCATGGAAAGAGCTAAT 3870

Qy       2878 TGGGAGTTCTTACGTCTCTCACTGCCTGTTATCTGCCATAACGAGTTCATTGACGAGGCA 2937
             |||||  ||  |||||  ||  ||  |||||||  ||  ||  |       |  ||  |||||  ||    |
Db       3871 TGGGAATTTTTACGGCTATCTTTGCCTGTCATATGTCTACCAAATTTTATTGATGAACAA 3930

Qy       2938 GAAAAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATGAAAGAGGCA 2997
             ||||||    ||  |  |||  ||||||||       |  ||  ||  |    ||  ||  |  |  |
Db       3931 GAAAAACAAAGGAGATGGCAAGAAATCAGAATTAGGCAGCACAGGTTATTGTCACAATCT 3990

Qy       2998 G 2998
              |
Db       3991 G 3991
```

RESULT 10
ADM68759
ID ADM68759 standard; DNA; 15845 BP.
XX
AC ADM68759;
XX
DT 17-JUN-2004 (first entry)
XX
DE Myzus persicae ryanodine receptor encoding DNA SEQ ID NO:3.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Myzus persicae.
XX
FH Key Location/Qualifiers
FT CDS 277. .15582
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68760.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 3; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15845 BP; 5273 A; 2716 C; 3325 G; 4528 T; 0 U; 3 Other;

Query Match 44.0%; Score 1319; DB 12; Length 15845;
Best Local Similarity 66.0%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 1005; Indels 12; Gaps 4;

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Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              ||  ||  ||  ||  ||  ||  ||  ||  |||||||||   |||  ||   |  |||||  |||||  ||
Db       1276 GTAATTGGTGCACCTATAATTAAGTATGGTGACAGCACAGTGTTAGTGCAACATTCTGAT 1335

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              ||  ||  ||  |||  |   |  ||||||||||||  |||||  ||  ||  ||  ||  ||  ||||||||||
Db       1336 ACAGGTTTATGGTTAACATATAAGTCTTATGAAACAAAAAAAAAAAGGTGTCGGTAAAGTA 1395

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              |||||  ||  |||||   |   |  |||||  |||||  ||||||||||||||   |  |||||
Db       1396 GAAGAAAAACAAGCAGTATTACACGAAGAAGGTAAGATGGACGATGGGTTAGACTTTAGT 1455

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              |||   ||  ||  |||||  ||  ||  ||||||  ||||  ||   |  ||  ||  |||||   |  |||
Db       1456 AGGAGTCAAGAAGAAGAGTCAAGAACTGCTAGAGTAATACGCAAATGCTCTTCATTATTC 1515

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              ||   |||||||   |||  ||||  |   |||||   |||  |  |||   ||   |  ||  |
Db       1516 ACACAGTTTATTTCTGGATTGGAGAACTTACAAAGTAACAGGCGTTCGTCATTATTTTGT 1575

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              |  |   ||  ||  ||     ||  |||||  |||||  ||  ||  |||  |  ||  ||  |||||  ||
Db       1576 TCATTCGTTAATCTAAATGAAATGGTCATGTGTCTAGAAGATTTAATAAATTACTTTGCT 1635

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              ||  ||  ||  ||||||||||||  ||||||||||||||||||  |||  |  |||  |  ||||
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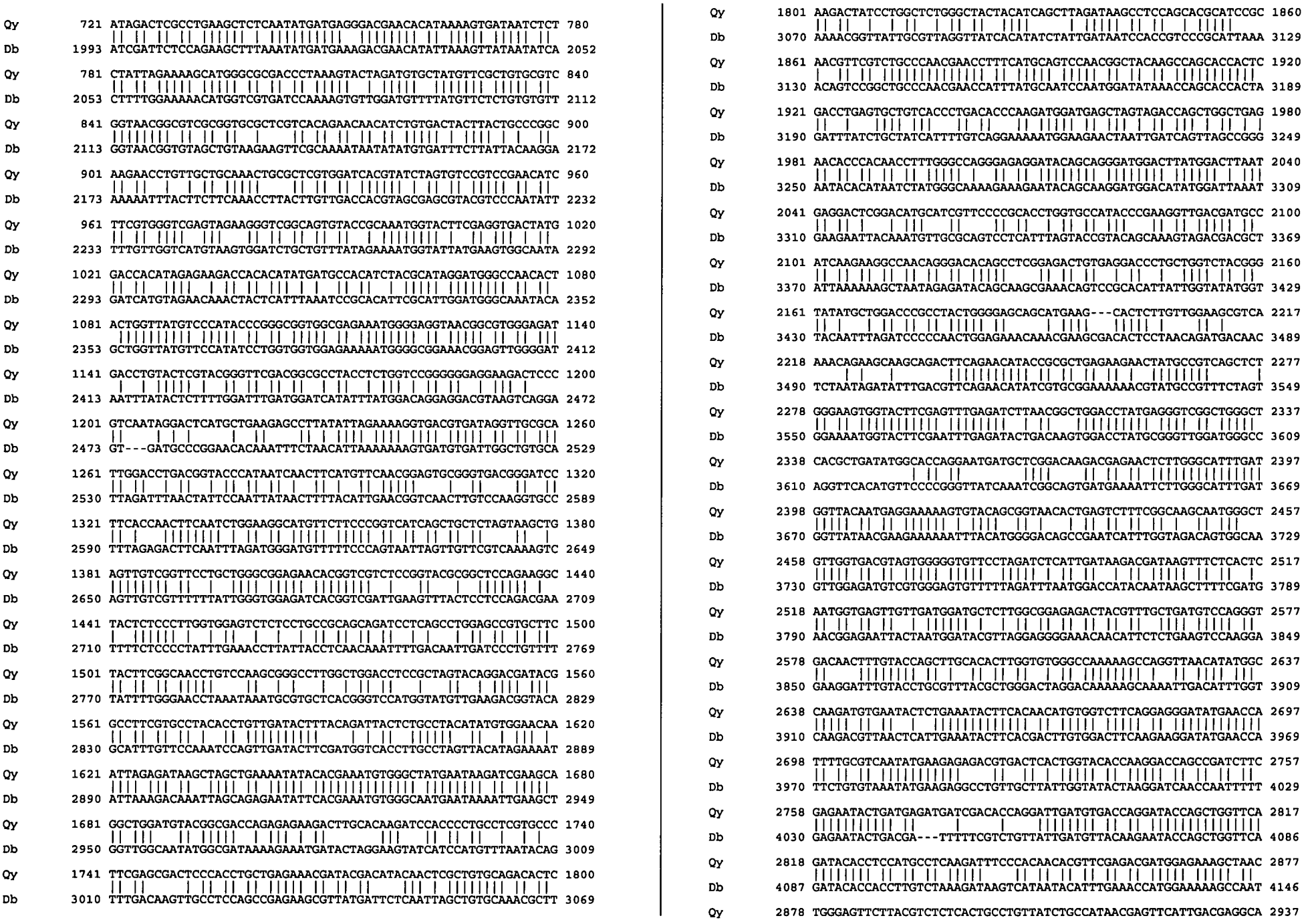
Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              |  ||  ||  |  ||  |||||  |||||  |||  |  ||  |  |||  |  |||||  ||  ||  ||
Db       1696 AGACAAGATTTATTTCAAGAAGAAGGAATATTAAATTTAATCTTAGAAGCCATTGATAAA 1755

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              |  |||  |  |||||  ||  |||||  |||  |  |  |  |  ||  ||  ||  ||  ||||||
Db       1756 GTTAACATTATCACATCTCAGGGATTCATGGTCAGTT---TAGCCGGTGATGAGTCTGGA 1812

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              ||  ||  |||||  ||||  |||||  |||||  ||  ||||||  |  ||  |||||  ||  ||  ||
Db       1813 CAAAGTTGGGATGTGATTTCTGGTTATTTATACCAGTTGTTAGCTGCAATTATTAAAGGA 1872

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              ||  ||  ||  |||||  ||  ||  ||  ||  ||  |  |||||  |  ||  |||  |  |||  ||
Db       1873 AATCATACCAACTGTGCTCAATTTGCTAATACTAACCGATTAAATTGGTTATTCAGCCGT 1932

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
              |  ||  ||  ||  ||  ||  |  ||  ||  ||  ||  |||  |  ||  |||||  ||  ||  ||  ||
Db       1933 TTAGGATCTCAAGCATCCAGTGAAGGAACTGGTATGTTAGATGTGCTTCATTGTGTTCTC 1992
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Db       4147 TGGGAATTTTTACGGCTATCATTACCTGTCATATGTCTACCAAGTTTTATTGGCGATCAA 4206

Qy       2938 GAAAAAGCCAGACGTTGGGTAGAAATCAAGGACCGTCAACAGATCCTAATG 2988
Db       4207 GAAAAACAAAGGGGATGGCAAGAAATAAGAATTAGGCAACACAGGTTATTG 4257


RESULT 11
ABL16880/c
ID   ABL16880 standard; DNA; 24236 BP.
XX
AC   ABL16880;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 2113.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 2113; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 24236 BP; 5975 A; 5769 C; 6109 G; 6383 T; 0 U; 0 Other;

  Query Match           38.3%;  Score 1150;  DB 4;  Length 24236;
  Best Local Similarity   67.7%;  Pred. No. 0;
  Matches 1749;  Conservative    0;  Mismatches  660;  Indels  173;  Gaps    3;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
Db      21229 GTGATCGGCTCGCCGATCATCAAGTACGGCGACACTACCGTCATCGTTCAGCACTGCGAG 21170

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
Db      21169 ACTAGCTTGTGGCTCAGCTACAAGAGTTATGAGACGAAAAAGAAGGGCGTAGGAAAGGTG 21110

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
Db      21109 GAGGAGAAGCAAGCGATCCTGCACGAGGAGGGCAAGATGGACGATTGTCTCGACTTCTCG 21050

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
Db      21049 CGCTCCCAGGAGGAGGAGTCCAAGACAGCTCGTGTCATCCGCAAGTGCAGCAGCCTCTTC 20990

Qy        241 ACTAAGTTTA---------------------------------------------------- 250
Db      20989 ACCCAGTTTATTACGTAGGTGACTTGGAAGTCCTTTACGAGTGATTTTCTTATCGTATTC 20930

Qy        251 ---------TCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTCG 301
Db      20929 ACACTCATTTCAGAGCCTTGGAAACACTGCAGTCAAATCGCCGACACTCCATTTTCTTCC 20870

Qy        302 CGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCAC 361
Db      20869 AAAAGGTCAACCTCAACGAGATGGTCATGTGCCTTGAGGACTTGATTAACTACTTTTCGC 20810

Qy        362 AGCCCGATGAGGATATG---------------------------------------------- 378
Db      20809 AACCCGAAGACGATATGGGTAAGGTCATTCAAAATATGACCCTAAGATGTTCAATAAAAT 20750

Qy        379 ----------------GAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAACCG 422
Db      20749 CTATAACTAATTTTCAGAGCACGAGGAGAAACAGAACCGATTCCGTGCCCTGCGCAACCG 20690

Qy        423 TCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGAT 482
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Qy        483 CAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGACA 542
Db      20629 CAACATAATCACCTCGCAGGGCTTCCTAGCCAGCTTCCTGGCCGGCGACGAGACCGGCCA 20570

Qy        543 GAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGCAA 602
Db      20569 GAGCTGGGATCTCATCTCCACCTATTTGTACCAACTCTTGGCCGCCATCATCAAGGGCAA 20510

Qy        603 CCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGCCT 662
Db      20509 CCACACGAACTGCGCCCAGTTCGCGAACAGTAACCGACTCAACTGGCTATTCTCCCGCCT 20450

Qy        663 CGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTTAT 722
Db      20449 CGGTTCCCAGGCCTCCAGCGAGGGTTCCGGCATGTTGGACGTACTTCACTGCGTGCTGAT 20390

Qy        723 AGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCT 782
Db      20389 CGATTCGCCAGAGGCACTAAACATGATGCGGGATGAGCACATCAAGGTGATCATCTCCCT 20330

Qy        783 ATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTCGG 842
Db      20329 GCTGGAGAAGCACGGCAGGGACCCGAAAGTCCTAGACGTTCTGTGTTCCTTGTGCGTGGG 20270

Qy        843 TAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGCAA 902
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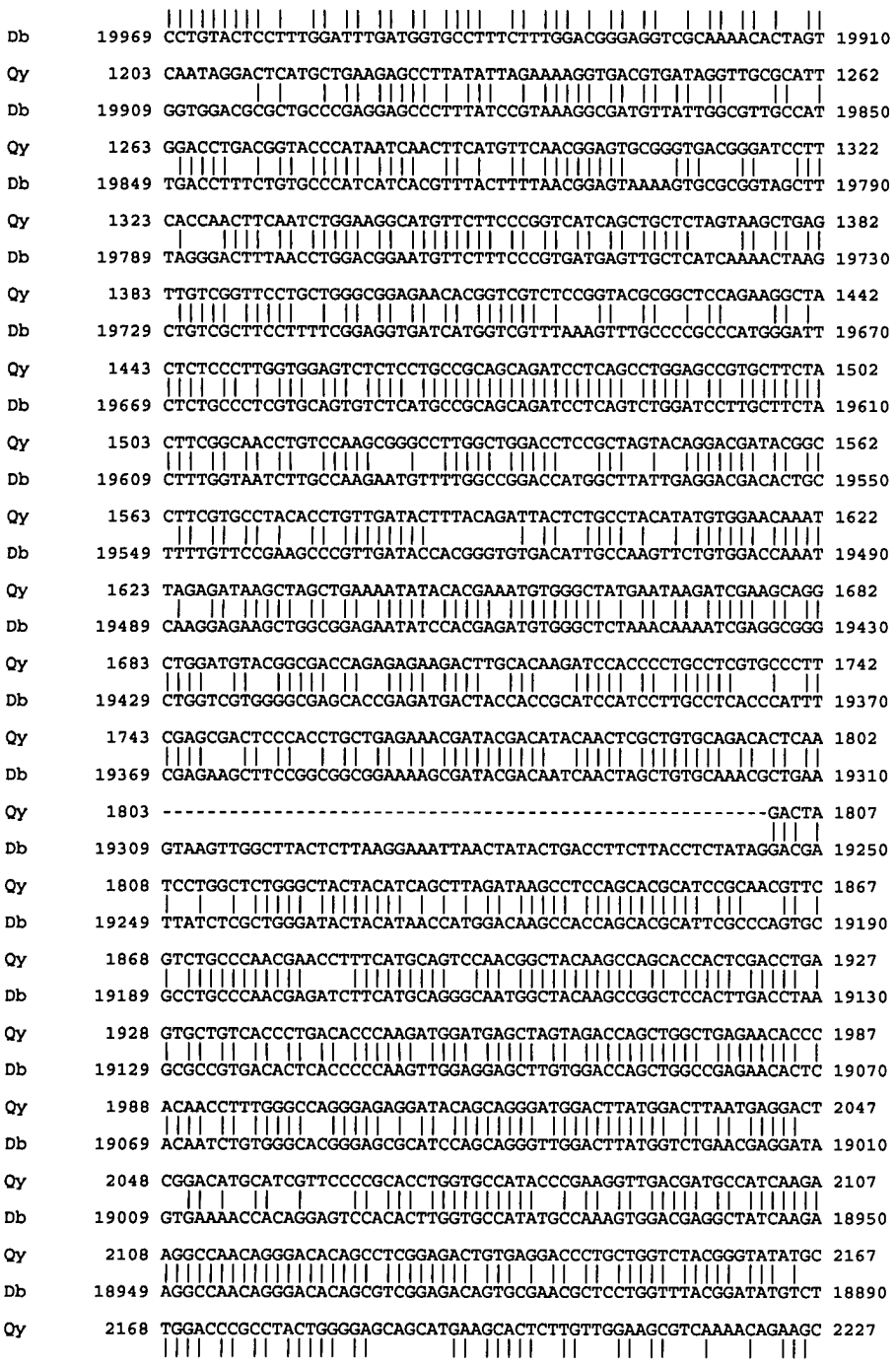
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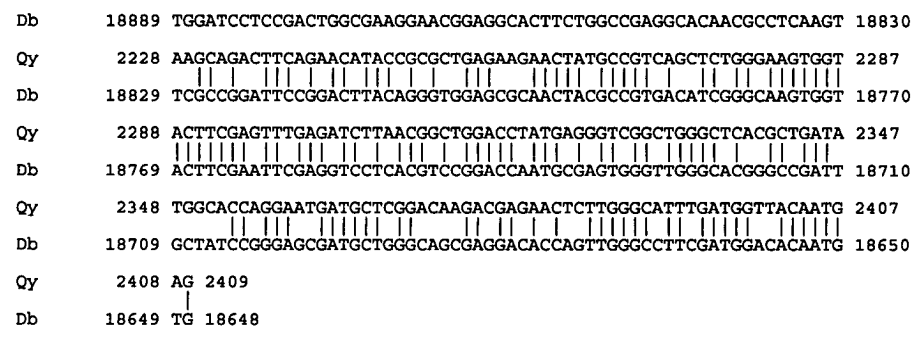
Qy        963 CGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATGGA 1022
Db      20149 CGTGGGTCGCGTGGACGGTTCTTCCATGTACCAGAAGTGGTACTTCGAGGTGACCATGGA 20090

Qy       1023 CCACATAGAGAAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAACACTAC 1082
Db      20089 TCACATCGAACAGACCACGCACATGATGCCCCACCTGCGCATTGGCTGGGCTAATACTTC 20030

Qy       1083 TGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGAGATGA 1142
Db      20029 CGGGTATGTACCGTATCCCGGAGGCGGCAAGAAGTGGGGTGGCAATGGAGTAGGCGATGA 19970

Qy       1143 CCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACTCCCGT 1202
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RESULT 12
AAQ25975
ID AAQ25975 standard; DNA; 15377 BP.
XX
AC AAQ25975;
XX
DT 25-MAR-2003 (revised)
DT 08-JAN-1993 (first entry)
XX
DE MH mutant porcine ryanodine receptor cDNA.
XX
KW MH; RYR1; calcium release channel; sarcoplasmic reticulum;
KW transverse tubule; Pietrain; Yorkshire; polymorphism; beta strand; ss.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
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FT	variation	207
FT		/*tag= b
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FT	variation	405
FT		/*tag= c
FT		/label= Polymorphic_site
FT	variation	438
FT		/*tag= d
FT		/label= Polymorphic_site
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FT	variation	2007
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FT   variation       8940
FT                   /*tag= o
FT                   /label= Polymorphic_site
FT   variation       9192
FT                   /*tag= p
FT                   /label= Polymorphic_site
FT   variation       9585
FT                   /*tag= q
FT                   /label= Polymorphic_site
FT   variation       9600
FT                   /*tag= r
FT                   /label= Polymorphic_site
FT   variation       9951
FT                   /*tag= s
FT                   /label= Polymorphic_site
FT   variation       10111
FT                   /*tag= t
FT                   /label= Polymorphic_site
FT   variation       11250
FT                   /*tag= u
FT                   /label= Polymorphic_site
FT   variation       12300
FT                   /*tag= v
FT                   /label= Polymorphic_site
FT   variation       14007
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FT   polyA_signal    15355. .15360
FT                   /*tag= x
XX
PN   WO9211387-A1.
XX
PD   09-JUL-1992.
XX
PF   20-DEC-1991;   91WO-CA000457.
XX
PR   21-DEC-1990;   90GB-00027869.
PR   20-MAY-1991;   91GB-00010865.
PR   09-SEP-1991;   91GB-00019250.
XX
PA   (UTOR ) UNIV TORONTO INNOVATIONS FOUND.
PA   (UYGU-) UNIV GUELPH.
XX
PI   Maclennan DH,  Obrien PJ;
XX
DR   WPI; 1992-250106/30.
DR   P-PSDB; AAR25450.
XX
PT   Purified DNA mol. for diagnosis of porcine malignant hyperthermia -
PT   comprises DNA sequence encoding normal or mutant ryanodine receptor with
PT   specified endonuclease restriction map.
XX
PS   Disclosure; Fig 2; 96pp; English.
XX
CC   The sequence given is the mutant pig ryanodine receptor (RYR1) gene from
CC   swine cDNA. The polymorphic sites were observed in comparisons of
CC   Pietrain and Yorkshire breeds. There are 17 polymorphisms between the two
CC   breeds. The polymorphism at position 1972 causes a mutation from Arg to
CC   Cys and this is thought to be the molecular basis of porcine malignant
CC   hyperthermia (MH). This mutation lies within the region of RYR1 that is
CC   concerned with the binding of regulators of Ca2+ release channel gating.
CC   Analysis of surrounding sequences suggests that this mutation lies within
CC   a beta strand domain comprising roughly of amino acids 520 to 830. RYR1
CC   is the calcium release channel of the sarcoplasmic reticulum and is a
CC   large protein which spans the gap between the transverse tubule and the
CC   sarcoplasmic reticulum. The cannel is activated by ATP, calcium, caffine,
CC   and micro-molar ryanodine. It is inhibited by ruthenium red, tetracaine,
CC   calmodulin, high Mg2+ and ryanodine. (Updated on 25-MAR-2003 to correct
CC   PN field.)
XX
SQ   Sequence 15377 BP; 3197 A; 4630 C; 4755 G; 2773 T; 0 U; 22 Other;

  Query Match            22.4%;  Score 673.4;  DB 2;  Length 15377;
  Best Local Similarity  55.6%;  Pred. No. 1.5e-188;
  Matches 1546;  Conservative    2;  Mismatches 1173;  Indels   60;  Gaps   11;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              | ||| ||| | ||     ||||| ||||| || ||       | | |||||||||   |
Db       1126 GGCATGGGCCCCCCTGAGATCAAGTATGGGGAGTCACTGTGCTTCGTGCAGCATGTGGCC 1185

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
             | ||| |||||||  | |||    |   ||  | |||     | |  | ||   ||
Db       1186 TCGGGCCTGTGGCTTACCTATGCTGCCCCAGACCCCAAGGCCCTGCGGCTCGGC---GTG 1242

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
              |||||  | || ||||| ||| |||||||| | ||||||||||   ||      |  ||
Db       1243 CTCAAGAAGAAGGCCATTCTGCACCAGGAAGGCCACATGGACGATGCACTGTCACTGACC 1302

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              | |  ||| |||| || ||    | | || ||  | |||    |    | ||   || | |
Db       1303 CGCTGTCAGCAGGAGGAGTCCCAGGCRGCCCGCATGATCTATAGCACTGCTGGCCTCTAC 1362

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTC--- 297
              |   | || ||||| || ||||| |   |   |  || |  ||  |||  | |
Db       1363 AACCACTTCATCAAGGGCCTGGACAGCTTCAGCGGAAAGCCACGGGGCTCTGGGGCCCCG 1422

Qy        298 ---TTCGCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTAC 354
                 | |  |  |  ||| |  |   |  | || ||||  |||| |||||  ||||
Db       1423 GCTGGCACAGCGCTACCCCTCGAGGGCGTCATCCTGAGCCTGCAGGACCTCATCGGCTAC 1482

Qy        355 TTCGCACAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTC 414
              || |  | ||||   || ||  || | ||||| || || || | |||  | ||    ||
Db       1483 TTTGAGCCGCCCTCGGAAGAGCTGCAGCACGAGGAGAAGCAGAGCAAGCTGCGCAGCCTG 1542

Qy        415 CGAAACCGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATA 474
              || ||||| |||  ||| ||||| ||||| || || ||   |||| |||| |   ||
Db       1543 CGCAACCGCCAGAGCCTCTTCCAGGAGGAGGGGATGCTCTCCCTGGTCCTGAATTGCATT 1602

Qy        475 GACAAGATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAA 534
              |||   | || |||  |||  |    |   | | ||||  |   | ||| ||||| ||
Db       1603 GACCGCCTAAATGTCTACACCACTGCTGCCCACTTTGCTGAGT---TTGCAGGAGAGGAG 1659

Qy        535 TCTGGACAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATA 594
              | |   ||  |||| ||  |||          ||||| || | |||||  |  | ||
Db       1660 GCAGCCGAGTCCTGGAAAGAGATTGTGAACCTGCTGTATGAGATCCTGGCCTCTCTGATC 1719

Qy        595 AAGGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTC 654
              |||||  |   | |||||  || |  ||| | ||            |||||  |   |
Db       1720 CGTGGCAATCGTGCCAACTGTGCCCTTTTCTCCAA-----------CAACTTGGATTGG 1767

Qy        655 TCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGC 714
              |  |  |      |  |       ||  |    | || || || || |||||| ||||
Db       1768 CTGGTCAGCAAGCTGGATCGACTGGAGGCCTCCTCAGGGATCCTGGAGGTGCTGTACTGT 1827

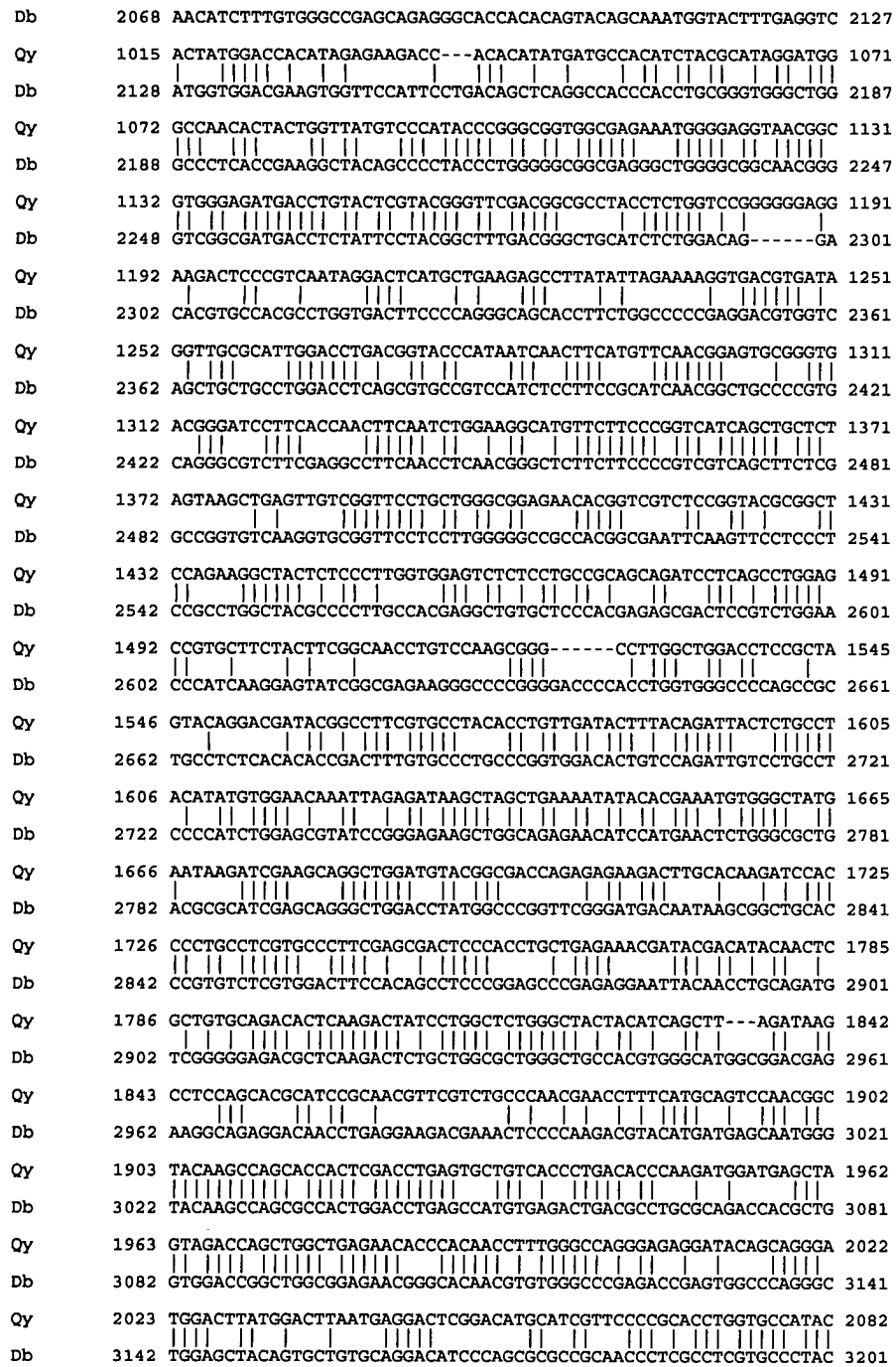
Qy        715 GTGCTTATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATA 774
              || || || ||   |||||  |  || || || ||    |||  | |||||  ||    ||
Db       1828 GTCCTGATTGAGAGTCCTGAGGTCCTGAACATCATCCAGGAGAACCACATCAAGTCCATC 1887

Qy        775 ATCTCTCTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTG 834
              |||||  |  | || |||||||||  |  |||  || || || ||||| || ||||| |||
Db       1888 ATCTCCCTTCTGGACAAGCATGGGAGGAACCACAAGGTGCTGGATGTCCTGTGTTCCCTG 1947

Qy        835 TGCGTCGGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTG 894
              || ||  | || || || || |||:||||    || |   |||   ||| |||| ||:
Db       1948 TGTGTGTGCAATGGTGTGGCCGTGYGCTCCAACCAAGATCTCATTACTGAGAACTTGCTS 2007

Qy        895 CCCGGCAAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCG 954
              || |||    | ||  ||||||| ||     ||| |  |  | ||  | ||  |||| ||
Db       2008 CCTGGCCGCGAGCTTCTGCTGCAGACAAACCTCATCAACTATGTCACCAGCATCCGCCCC 2067

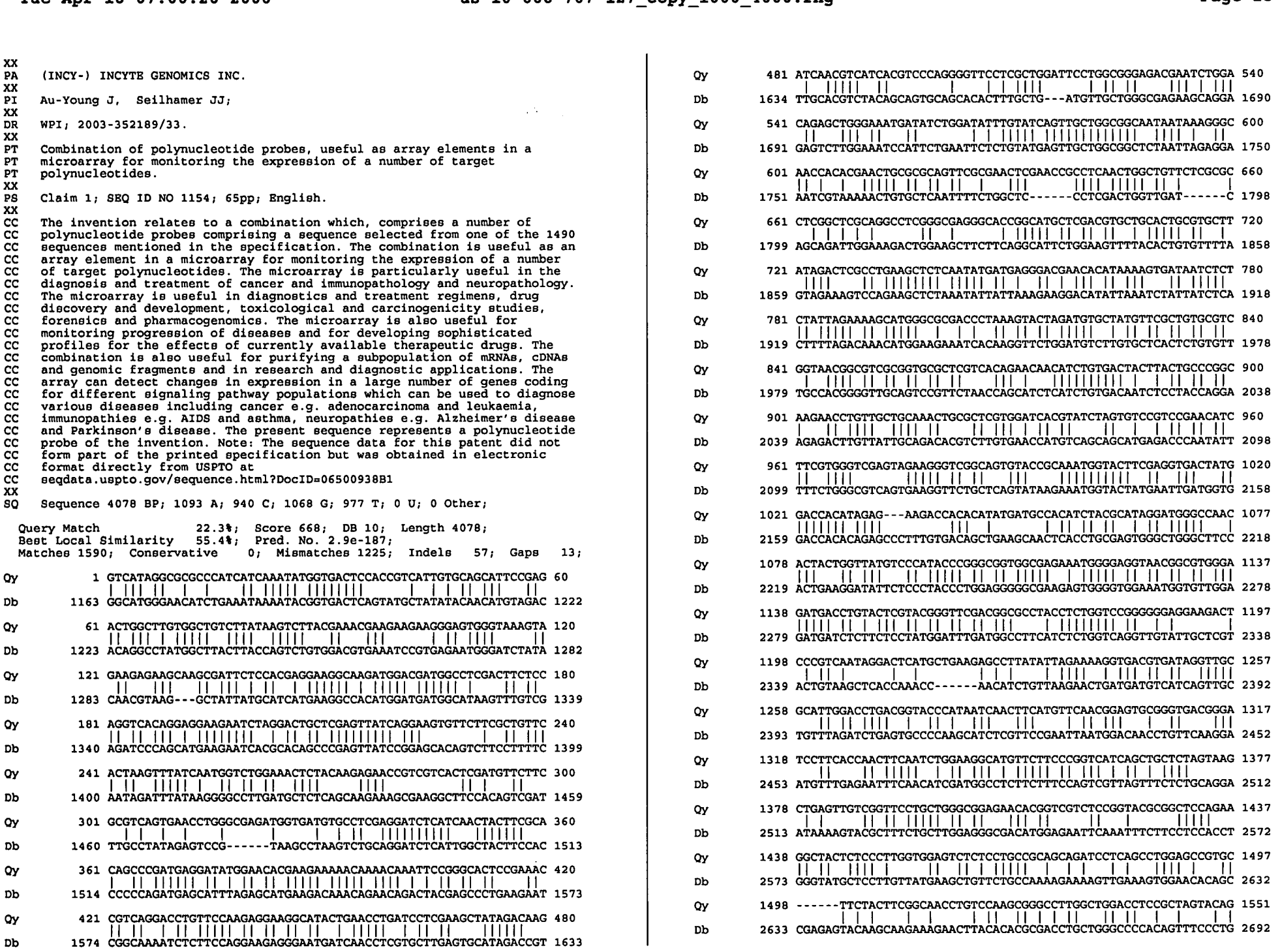
Qy        955 AACATCTTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTG 1014
              |||||||| |||| |||| ||| ||  |  ||  |||| |||||||||||||| |||||
```



RESULT 13
ACA56556
ID ACA56556 standard; cDNA; 4078 BP.
XX
AC ACA56556;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1154.
XX
KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.

XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
PS Claim 1; SEQ ID NO 1154; 65pp; English.
XX
CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ Sequence 4078 BP; 1093 A; 940 C; 1068 G; 977 T; 0 U; 0 Other;

Query Match 22.3%; Score 668; DB 10; Length 4078;
Best Local Similarity 55.4%; Pred. No. 2.9e-187;
Matches 1590; Conservative 0; Mismatches 1225; Indels 57; Gaps 13;



```
Qy       1552 GACGATACGGCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATAT 1611
Db       2693 ACGCAAGCTGCCTTCACACCCATCCCTGTGGATACCAGCCAGATCGTGTTGCCTCCTCAT 2752

Qy       1612 GTGGAACAAATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAG 1671
Db       2753 CTAGAAAGAATAAGAGAAAAACTGGCAGAGAATATCCATGAACTCTGGGTTATGAATAAA 2812

Qy       1672 ATCGAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGC 1731
Db       2813 ATTGAGCTTGGCTGGCAGTATGGTCCGGTTAGAGATGACAACAAGAGACAACACCCATGC 2872

Qy       1732 CTCGTGCCCTTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTG 1791
Db       2873 CTGGTGGAGTTCTCCAAGCTGCCTGAACAGGAGCGCAATTACAACTTACAAATGTCGCTT 2932

Qy       1792 CAGACACTCAAGACTATCCTGGCTCTGGGCTACTACAT---CAGCTTAGATAAGCCTCCA 1848
Db       2933 GAGACCCTGAAGACTTTGTTGGCATTAGGATGTCATGTGGGTATATCAGATGAACATGCT 2992

Qy       1849 GCACGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAG 1908
Db       2993 GAAGACAAGGTGAAAAAAATGAAGCTACCCAAGAATTACCAGCTGACAAGTGGATACAAG 3052

Qy       1909 CCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGAC 1968
Db       3053 CCTGCCCCTATGGACCTGAGCTTTATCAAACTCACCCCATCGCAAGAAGCAATGGTGGAC 3112

Qy       1969 CAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACT 2028
Db       3113 AAGTTGGCAGAAAATGCACATAATGTGTGGGCGCGGGATCGAATCCGGCAGGGCTGGACT 3172

Qy       2029 TATGGACTTAATGAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAG 2088
Db       3173 TATGGCATCCAACAGGACGTAAAGAACAGAAGAAATCCTCGCCTTGTTCCCTACACTCCT 3232

Qy       2089 GTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTG 2148
Db       3233 CTGGATGACCGAACCAAGAAATCCAACAAGGACAGCCTCCGCGAGGCTGTGCGCACGCTG 3292

Qy       2149 CTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTG 2208
Db       3293 CTGGGGTACGGCTACAACTTGGAAGCACC------AGATCAAGATCATGCAGCCAGAGCC 3346

Qy       2209 GAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCC 2268
Db       3347 GAAGTGTGCAGCGGCACCGGGGAAAGGTTCCGAATCTTCCGTGCCGAGAAGACCTATGCA 3406

Qy       2269 GTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTC 2328
Db       3407 GTGAAGGCCGGACGGTGGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGGTT 3466

Qy       2329 GGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGG 2388
Db       3467 GGTTGGAGTCGTCCTGGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTGCCTTT 3526

Qy       2389 GCATTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAG 2448
Db       3527 GCCTTTGATGGCTTCAAGGCCCAGCGGTGGCATCAGGG---CAATGAACACTATGGGCGC 3583

Qy       2449 CAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGT 2508
Db       3584 TCTTGGCAAGCAGGCGATGTCGTGGGGTGTATGGTTGACATGAACGAACACACCATGATG 3643

Qy       2509 TTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGAT 2568
Db       3644 TTCACACTGAATGGTGAAATCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTCAAGGAC 3703

Qy       2569 GTCCAGGGTGACAA---CTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGG 2625
Db       3704 TTTGATGTTGGCGATGGATTCATACCTGTGTGTAGCCTTGGAGTGGCTCAAGTGGGTAGG 3763

Qy       2626 TTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAG 2685
Db       3764 ATGAACTTTGGAAAGGATGTCAGCACCTTGAAATATTTCACCATCTGTGGCTTACAAGAG 3823

Qy       2686 GGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGAC 2745
Db       3824 GGCTATGAACCATTTGCCGTTAATACAAACAGGGATATTACCATGTGGCTGAGCAAGAGG 3883

Qy       2746 CAGCCGATCTTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATA 2805
Db       3884 CTTCCTCAGTT---TCTTCAAGTTCCATCAAACCATGAACATATAGAGGTGACCAGAATA 3940

Qy       2806 CCAGCTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCG 2857
Db       3941 GACGGCACCATAGACAGTTCCCCATGTTTAAAGGTCACTCAGAAGTCTTTTG 3992
```

RESULT 14
ADI56352
ID ADI56352 standard; DNA; 4078 BP.
XX
AC ADI56352;
XX
DT 22-APR-2004 (first entry)
XX
DE Human polynucleotide probe #1154.
XX
KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
KW effector-like polypeptide; cancer; immunopathology; neuropathology;
KW drug development; toxicology; carcinogenicity;
KW signalling pathway polypeptide; adrenal gland; bladder; bone;
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
OS Homo sapiens.
XX
PN US2004010136-A1.
XX
PD 15-JAN-2004.
XX
PF 26-NOV-2002; 2002US-00305720.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2004-090520/09.
XX
PT New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
XX
PS Claim 6; SEQ ID NO 1154; 73pp; English.
XX
CC The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the
CC diagnosis and treatment of cancer, an immunopathology or a
CC neuropathology. It can also be used for drug discovery and development,
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for monitoring the progression of diseases
CC that may be associated with the altered expression of signalling pathway
CC polypeptides. The composition can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of

CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC human polynucleotide probe of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 4078 BP; 1093 A; 940 C; 1068 G; 977 T; 0 U; 0 Other;

Query Match 22.3%; Score 668; DB 12; Length 4078;
Best Local Similarity 55.4%; Pred. No. 2.9e-187;
Matches 1590; Conservative 0; Mismatches 1225; Indels 57; Gaps 13;

```
Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              | ||| ||  |  |    || ||||| ||||||||      |  | | || |||  ||
Db       1163 GGCATGGGAACATCTGAAATAAAATACGGTGACTCAGTATGCTATATACAACATGTAGAC 1222

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              || ||| | |||||  ||||  |||||   ||  |||       | || ||||     ||
Db       1223 ACAGGCCTATGGCTTACTTACCAGTCTGTGGACGTGAAATCCGTGAGAATGGGATCTATA 1282

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
               ||   |||   || ||| | ||  | |||||| | ||||| |||||| |   || ||
Db       1283 CAACGTAAG---GCTATTATGCATCATGAAGGCCACATGGATGATGGCATAAGTTTGTCG 1339

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              || || ||| | |||||||| | || || ||||||||| ||| |      |  || |||
Db       1340 AGATCCCAGCATGAAGAATCACGCACAGCCCGAGTTATCCGGAGCACAGTCTTCCTTTTC 1399

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              | ||  ||||| |  || || ||  ||||      |||          || |   ||
Db       1400 AATAGATTTATAAGGGGCCTTGATGCTCTCAGCAAGAAAGCGAAGGCTTCCACAGTCGAT 1459

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              | |  |  |  |     |  | | ||  ||||||||||   |||||||
Db       1460 TTGCCTATAGAGTCCG------TAAGCCTAAGTCTGCAGGATCTCATTGGCTACTTCCAC 1513

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              |  || ||||||  || | || || ||||| ||||| ||| | | || || ||    ||
Db       1514 CCCCCAGATGAGCATTTAGAGCATGAAGACAAACAGAACAGACTACGAGCCCTGAAGAAT 1573

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              || ||  | || ||||| || || || ||  | |||||  | || ||     ||||||
Db       1574 CGGCAAAATCTCTTCCAGGAAGAGGGAATGATCAACCTCGTGCTTGAGTGCATAGACCGT 1633

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              |  |||||  ||        |  | | ||||     | || ||    ||| | |||
Db       1634 TTGCACGTCTACAGCAGTGCAGCACACTTTGCTG---ATGTTGCTGGGCGAGAAGCAGGA 1690

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              ||   ||| ||   ||       | | ||||| ||||||||||||  |||| | ||
Db       1691 GAGTCTTGGAAATCCATTCTGAATTCTCTGTATGAGTTGCTGGCGGCTCTAATTAGAGGA 1750

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              || |  | ||||| || || ||  |  |||       |||| ||||| || |      |
Db       1751 AATCGTAAAAACTGTGCTCAATTTTCTGGCTC------CCTCGACTGGTTGAT------C 1798

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
              | | | | |      ||  |      | |||||| || || ||  | ||||| ||  |
Db       1799 AGCAGATTGGAAAGACTGGAAGCTTCTTCAGGCATTCTGGAAGTTTTACACTGTGTTTTA 1858

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
              ||||     || ||||||| ||||| || |  || | ||| || |||   || |||||
Db       1859 GTAGAAAGTCCAGAAGCTCTAAATATTATTAAAGAAGGACATATTAAATCTATTATCTCA 1918

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
              || ||||| || |||||  |  | |  || || || |||||  | || || || || ||
Db       1919 CTTTTAGACAAACATGGAAGAAATCACAAGGTTCTGGATGTCTTGTGCTCACTCTGTGTT 1978

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
                |  |||| || || || || ||    ||| |  ||||||||||  |  | || || ||
```

```
Db       1979 TGCCACGGGGTTGCAGTCCGTTCTAACCAGCATCTCATCTGTGACAATCTCCTACCAGGA 2038

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
              |  || ||||  |||| ||    || ||| | || ||    ||  |  | || || ||
Db       2039 AGAGACTTGTTATTGCAGACACGTCTTGTGAACCATGTCAGCAGCATGAGACCCAATATT 2098

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
              ||  ||||        ||||| || ||   |||     ||||||||||  ||  |||  ||
Db       2099 TTTCTGGGCGTCAGTGAAGGTTCTGCTCAGTATAAGAAATGGTACTATGAATTGATGGTG 2158

Qy       1021 GACCACATAGAG---AAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAAC 1077
              ||||||| ||||         |||  |        | || || ||  | || |||||   |
Db       2159 GACCACACAGAGCCCTTTGTGACAGCTGAAGCAACTCACCTGCGAGTGGGCTGGGCTTCC 2218

Qy       1078 ACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGA 1137
              |||   || |||   || ||||| || || |||||  | |||||  || || || |||
Db       2219 ACTGAAGGATATTCTCCCTACCCTGGAGGGGGCGAAGAGTGGGGTGGAAATGGTGTTGGA 2278

Qy       1138 GATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACT 1197
              ||||| || | ||| || || || || |||    | ||||||| ||  | |       |
Db       2279 GATGATCTCTTCTCCTATGGATTTGATGGCCTTCATCTCTGGTCAGGTTGTATTGCTCGT 2338

Qy       1198 CCCGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGC 1257
              | || |     | |       | | |    | |||  | ||| || ||  |||||
Db       2339 ACTGTAAGCTCACCAAACC------AACATCTGTTAAGAACTGATGATGTCATCAGTTGC 2392

Qy       1258 GCATTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGA 1317
              || || |||| | || |  |||  |||    | ||| |||   |  ||  |||
Db       2393 TGTTTAGATCTGAGTGCCCCAAGCATCTCGTTCCGAATTAATGGACAACCTGTTCAAGGA 2452

Qy       1318 TCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAG 1377
              ||  || ||||| | || ||| | ||||| || ||| | || |  ||||
Db       2453 ATGTTTGAGAATTTCAACATCGATGGCCTCTTCTTTCCAGTCGTTAGTTTCTCTGCAGGA 2512

Qy       1378 CTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAA 1437
              | |    || || ||||| || ||   ||| ||      ||   |      |||||
Db       2513 ATAAAAGTACGCTTTCTGCTTGGAGGGCGACATGGAGAATTCAAATTTCTTCCTCCACCT 2572

Qy       1438 GGCTACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGC 1497
              || ||  |||| |     ||  || | |||||  |  | |  |  | |||| |   ||
Db       2573 GGGTATGCTCCTTGTTATGAAGCTGTTCTGCCAAAAGAAAAGTTGAAAGTGGAACACAGC 2632

Qy       1498 ------TTCTACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAG 1551
                   | |  |      |  || || | |||  | | |  || ||  | |  | | |
Db       2633 CGAGAGTACAAGCAAGAAAGAACTTACACACGCGACCTGCTGGGCCCCACAGTTTCCCTG 2692

Qy       1552 GACGATACGGCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATAT 1611
              |  | ||||||   || |  |||| ||||     ||||      ||||| |  ||
Db       2693 ACGCAAGCTGCCTTCACACCCATCCCTGTGGATACCAGCCAGATCGTGTTGCCTCCTCAT 2752

Qy       1612 GTGGAACAAATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAG 1671
              | |||  ||| ||||| || || || || ||||| || ||| | |||| |||||||||
Db       2753 CTAGAAAGAATAAGAGAAAAACTGGCAGAGAATATCCATGAACTCTGGGTTATGAATAAA 2812

Qy       1672 ATCGAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGC 1731
              || ||    ||||| ||| ||      ||||| |||    | |    ||||| |||
Db       2813 ATTGAGCTTGGCTGGCAGTATGGTCCGGTTAGAGATGACAACAAGAGACAACACCCATGC 2872

Qy       1732 CTCGTGCCCTTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTG 1791
              || |||   |||       || ||       |||      ||| || ||||| |  | |
Db       2873 CTGGTGGAGTTCTCCAAGCTGCCTGAACAGGAGCGCAATTACAACTTACAAATGTCGCTT 2932

Qy       1792 CAGACACTCAAGACTATCCTGGCTCTGGGCTACTACAT---CAGCTTAGATAAGCCTCCA 1848
              ||||  || |||||| |  ||||  | || |  |  |   |  | ||||  | | | |
Db       2933 GAGACCCTGAAGACTTTGTTGGCATTAGGATGTCATGTGGGTATATCAGATGAACATGCT 2992

Qy       1849 GCACGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAG 1908
              | |  ||      ||      | |   || | | || | | | || ||||||
Db       2993 GAAGACAAGGTGAAAAAAATGAAGCTACCCAAGAATTACCAGCTGACAAGTGGATACAAG 3052

Qy       1909 CCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGAC 1968
              || || ||  | |||||||   | ||| || || ||  |  || |  | || |||
Db       3053 CCTGCCCCTATGGACCTGAGCTTTATCAAACTCACCCCATCGCAAGAAGCAATGGTGGAC 3112
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Qy       1969 CAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACT 2028
Db       3113 AAGTTGGCAGAAAATGCACATAATGTGTGGGCGCGGGATCGAATCCGGCAGGGCTGGACT 3172

Qy       2029 TATGGACTTAATGAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAG 2088
Db       3173 TATGGCATCCAACAGGACGTAAAGAACAGAAGAAATCCTCGCCTTGTTCCCTACACTCCT 3232

Qy       2089 GTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTG 2148
Db       3233 CTGGATGACCGAACCAAGAAATCCAACAAGGACAGCCTCCGCGAGGCTGTGCGCACGCTG 3292

Qy       2149 CTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTG 2208
Db       3293 CTGGGGTACGGCTACAACTTGGAAGCACC------AGATCAAGATCATGCAGCCAGAGCC 3346

Qy       2209 GAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCC 2268
Db       3347 GAAGTGTGCAGCGGCACCGGGGAAAGGTTCCGAATCTTCCGTGCCGAGAAGACCTATGCA 3406

Qy       2269 GTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTC 2328
Db       3407 GTGAAGGCCGGACGGTGGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGGTT 3466

Qy       2329 GGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGG 2388
Db       3467 GGTTGGAGTCGTCCTGGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTGCCTTT 3526

Qy       2389 GCATTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAG 2448
Db       3527 GCCTTTGATGGCTTCAAGGCCCAGCGGTGGCATCAGGG---CAATGAACACTATGGGCGC 3583

Qy       2449 CAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGT 2508
Db       3584 TCTTGGCAAGCAGGCGATGTCGTGGGGTGTATGGTTGACATGAACGAACACACCATGATG 3643

Qy       2509 TTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGAT 2568
Db       3644 TTCACACTGAATGGTGAAATCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTCAAGGAC 3703

Qy       2569 GTCCAGGGTGACAA---CTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGG 2625
Db       3704 TTTGATGTTGGCGATGGATTCATACCTGTGTGTGTAGCCTTGGAGTGGCTCAAGTGGGTAGG 3763

Qy       2626 TTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAG 2685
Db       3764 ATGAACTTTGGAAAGGATGTCAGCACCTTGAAATATTTCACCATCTGTGGCTTACAAGAG 3823

Qy       2686 GGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGAC 2745
Db       3824 GGCTATGAACCATTTGCCGTTAATACAAACAGGGATATTACCATGTGGCTGAGCAAGAGG 3883

Qy       2746 CAGCCGATCTTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATA 2805
Db       3884 CTTCCTCAGTT---TCTTCAAGTTCCATCAAACCATGAACATATAGAGGTGACCAGAATA 3940

Qy       2806 CCAGCTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCG 2857
Db       3941 GACGGCACCATAGACAGTTCCCCATGTTTAAAGGTCACTCAGAAGTCTTTTG 3992
```

RESULT 15
ABA08776
ID ABA08776 standard; cDNA; 14302 BP.
XX
AC ABA08776;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human ryanodine receptor homologue-encoding cDNA, SEQ ID NO:552.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB11532.
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 1; Page 571-574; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a

```
CC   novel human polypeptide of the invention
XX
SQ   Sequence 14302 BP; 4077 A; 3115 C; 3591 G; 3519 T; 0 U; 0 Other;

  Query Match             22.3%;  Score 668;  DB 4;  Length 14302;
  Best Local Similarity   55.4%;  Pred. No. 6e-187;
  Matches 1590;  Conservative    0;  Mismatches 1225;  Indels   57;  Gaps   13;

Qy          1 GTCATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAG 60
              |  |||  |   |    || ||||| |||||||     |  | | || |||   ||
Db       1163 GGCATGGGAACATCTGAAATAAAATACGGTGACTCAGTATGCTATATACAACATGTAGAC 1222

Qy         61 ACTGGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTA 120
              || ||| | |||||  ||||  |||||   ||  |||      | || ||||     ||
Db       1223 ACAGGCCTATGGCTTACTTACCAGTCTGTGGACGTGAAATCCGTGAGAATGGGATCTATA 1282

Qy        121 GAAGAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCC 180
               ||   |||   || ||| | ||  | |||||| | ||||| ||||||  |    || ||
Db       1283 CAACGTAAG---GCTATTATGCATCATGAAGGCCACATGGATGATGGCATAAGTTTGTCG 1339

Qy        181 AGGTCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTC 240
              || || ||| | |||||||  | || || |||||||| |||      |  || |||
Db       1340 AGATCCCAGCATGAAGAATCACGCACAGCCCGAGTTATCCGGAGCACAGTCTTCCTTTTC 1399

Qy        241 ACTAAGTTTATCAATGGTCTGGAAACTCTACAAGAGAACCGTCGTCACTCGATGTTCTTC 300
              | ||  ||||| |  || || ||  ||||      ||||                || |  ||
Db       1400 AATAGATTTATAAGGGGCCTTGATGCTCTCAGCAAGAAAGCGAAGGCTTCCACAGTCGAT 1459

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360
              | |  |  |   |      |      | | ||  |||||||||    |||||||
Db       1460 TTGCCTATAGAGTCCG------TAAGCCTAAGTCTGCAGGATCTCATTGGCTACTTCCAC 1513

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420
              |  || |||||| || | || || ||||| ||||| |||| | | || || ||    ||
Db       1514 CCCCCAGATGAGCATTTAGAGCATGAAGACAAACAGAACAGACTACGAGCCCTGAAGAAT 1573

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480
              || ||  | || ||||| || || || ||  | |||||  | || ||     ||||||
Db       1574 CGGCAAAATCTCTTCCAGGAAGAGGGAATGATCAACCTCGTGCTTGAGTGCATAGACCGT 1633

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540
              |  |||||  ||       |  | |||||      |||| ||    ||| | |||
Db       1634 TTGCACGTCTACAGCAGTGCAGCACACTTTGCTG---ATGTTGCTGGGCGAGAAGCAGGA 1690

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600
              ||   ||| ||   ||       | | ||||| ||||||||||||  |||| |  ||
Db       1691 GAGTCTTGGAAATCCATTCTGAATTCTCTGTATGAGTTGCTGGCGGCTCTAATTAGAGGA 1750

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660
              || |  |  ||||| || || ||  |||      |||| ||||| || |       |
Db       1751 AATCGTAAAAACTGTGCTCAATTTTCTGGCTC------CCTCGACTGGTTGAT------C 1798

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720
               | | | |    ||  |     | ||||| || || ||  | ||||| ||  |
Db       1799 AGCAGATTGGAAAGACTGGAAGCTTCTTCAGGCATTCTGGAAGTTTTACACTGTGTTTTA 1858

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780
              ||||    || |||||||| ||||| || |  || | ||| || |||    || ||||||
Db       1859 GTAGAAAGTCCAGAAGCTCTAAATATTATTAAAGAAGGACATATTAAATCTATTATCTCA 1918

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840
              || ||||| || ||||| |  | |  || || || ||||  | || || || || ||
Db       1919 CTTTTAGACAAACATGGAAGAAATCACAAGGTTCTGGATGTCTTGTGCTCACTCTGTGTT 1978

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900
              |  |||| || || || || ||  |||  |  ||||||||||  |  | || || ||
Db       1979 TGCCACGGGGTTGCAGTCCGTTCTAACCAGCATCTCATCTGTGACAATCTCCTACCAGGA 2038

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960
              |  || ||||  |||| ||    || ||| | || ||    ||  |  | || || ||
Db       2039 AGAGACTTGTTATTGCAGACACGTCTTGTGAACCATGTCAGCAGCATGAGACCCAATATT 2098

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020
              || |||  |||       ||||| || ||   |||     |||||||||  ||  |||  ||
Db       2099 TTTCTGGGCGTCAGTGAAGGTTCTGCTCAGTATAAGAAATGGTACTATGAATTGATGGTG 2158

Qy       1021 GACCACATAGAG---AAGACCACACATATGATGCCACATCTACGCATAGGATGGGCCAAC 1077
              ||||||| ||||      |||  |      | || || ||  | || |||||     |
Db       2159 GACCACACAGAGCCCTTTGTGACAGCTGAAGCAACTCACCTGCGAGTGGGCTGGGCTTCC 2218

Qy       1078 ACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGA 1137
              |||   || |||   || ||||| || || |||||  | ||||| || || || || |||
Db       2219 ACTGAAGGATATTCTCCCTACCCTGGAGGGGGCGAAGAGTGGGGTGGAAATGGTGTTGGA 2278

Qy       1138 GATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACT 1197
              ||||| || | ||| || || || || ||| | |||||||| || | |       |
Db       2279 GATGATCTCTTCTCCTATGGATTTGATGGCCTTCATCTCTGGTCAGGTTGTATTGCTCGT 2338

Qy       1198 CCCGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGC 1257
              | || |      | |      | | |  | |||  | ||| || ||  |||||
Db       2339 ACTGTAAGCTCACCAAACC------AACATCTGTTAAGAACTGATGATGTCATCAGTTGC 2392

Qy       1258 GCATTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGA 1317
              || || |||| |  || |  |||   |||     | || |||   | ||      |||
Db       2393 TGTTTAGATCTGAGTGCCCCAAGCATCTCGTTCCGAATTAATGGACAACCTGTTCAAGGA 2452

Qy       1318 TCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAG 1377
              ||   || |||||  | || ||| | |||| || ||| | || | ||||
Db       2453 ATGTTTGAGAATTTCAACATCGATGGCCTCTTCTTTCCAGTCGTTAGTTTCTCTGCAGGA 2512

Qy       1378 CTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAA 1437
              | |     || || |||| || ||  ||| ||  ||  |  |||||
Db       2513 ATAAAAGTACGCTTTCTGCTTGGAGGGCGACATGGAGAATTCAAATTTCTTCCTCCACCT 2572

Qy       1438 GGCTACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGC 1497
              || ||  |||| |      ||  || | |||||  | | |  | |  |||| |   ||
Db       2573 GGGTATGCTCCTTGTTATGAAGCTGTTCTGCCAAAAGAAAAGTTGAAAGTGGAACACAGC 2632

Qy       1498 ------TTCTACTTCGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAG 1551
                    | | |  |  |  | || || | ||  || ||  |  |    | |
Db       2633 CGAGAGTACAAGCAAGAAAGAACTTACACACGCGACCTGCTGGGCCCCACAGTTTCCCTG 2692

Qy       1552 GACGATACGGCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATAT 1611
                |  | ||||||    || |  ||||| |||||    |||||  |  ||
Db       2693 ACGCAAGCTGCCTTCACACCCATCCCTGTGGATACCAGCCAGATCGTGTTGCCTCCTCAT 2752

Qy       1612 GTGGAACAAATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAG 1671
              | |||  ||| ||||| || || || || |||||  || ||| | |||| |||||||||
Db       2753 CTAGAAAGAATAAGAGAAAAACTGGCAGAGAATATCCATGAACTCTGGGTTATGAATAAA 2812

Qy       1672 ATCGAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGC 1731
              || ||   |||||  ||| ||       ||||| |||    | |     ||||| |||
Db       2813 ATTGAGCTTGGCTGGCAGTATGGTCCGGTTAGAGATGACAACAAGAGACAACACCCATGC 2872

Qy       1732 CTCGTGCCCTTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTG 1791
              || |||   |||       || ||      |||      ||| || ||||| |  |  |
Db       2873 CTGGTGGAGTTCTCCAAGCTGCCTGAACAGGAGCGCAATTACAACTTACAAATGTCGCTT 2932

Qy       1792 CAGACACTCAAGACTATCCTGGCTCTGGGCTACTACAT---CAGCTTAGATAAGCCTCCA 1848
              |||| || |||||| |  ||||  | || |   |  |    | | |||| | | | |
Db       2933 GAGACCCTGAAGACTTTGTTGGCATTAGGATGTCATGTGGGTATATCAGATGAACATGCT 2992

Qy       1849 GCACGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAG 1908
              | |  ||     ||          ||   | |   || |  || | | |  || ||||||
Db       2993 GAAGACAAGGTGAAAAAAATGAAGCTACCCAAGAATTACCAGCTGACAAGTGGATACAAG 3052

Qy       1909 CCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGAC 1968
              || || ||  | |||||||||  | ||| || || ||  |    ||| |  || |||
Db       3053 CCTGCCCCTATGGACCTGAGCTTTATCAAACTCACCCCATCGCAAGAAGCAATGGTGGAC 3112

Qy       1969 CAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACT 2028
              || |||| || ||  | || ||  | |||||  |||| | || | |||||| ||||||
Db       3113 AAGTTGGCAGAAAATGCACATAATGTGTGGGCGCGGGATCGAATCCGGCAGGGCTGGACT 3172

Qy       2029 TATGGACTTAATGAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAG 2088
              |||||  |  | |||||    | |      |  || | ||| || || ||| |
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Db       3173 TATGGCATCCAACAGGACGTAAAGAACAGAAGAAATCCTCGCCTTGTTCCCTACACTCCT 3232

Qy       2089 GTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTG 2148

Db       3233 CTGGATGACCGAACCAAGAAATCCAACAAGGACAGCCTCCGCGAGGCTGTGCGCACGCTG 3292

Qy       2149 CTGGTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTG 2208

Db       3293 CTGGGGTACGGCTACAACTTGGAAGCACC------AGATCAAGATCATGCAGCCAGAGCC 3346

Qy       2209 GAAGCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCC 2268

Db       3347 GAAGTGTGCAGCGGCACCGGGGAAAGGTTCCGAATCTTCCGTGCCGAGAAGACCTATGCA 3406

Qy       2269 GTCAGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTC 2328

Db       3407 GTGAAGGCCGGACGGTGGTATTTTGAATTTGAGACGGTCACTGCTGGAGACATGAGGGTT 3466

Qy       2329 GGCTGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGG 2388

Db       3467 GGTTGGAGTCGTCCTGGTTGTCAACCGGATCAGGAGCTTGGCTCAGATGAACGTGCCTTT 3526

Qy       2389 GCATTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAG 2448

Db       3527 GCCTTTGATGGCTTCAAGGCCCAGCGGTGGCATCAGGG---CAATGAACACTATGGGCGC 3583

Qy       2449 CAATGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGT 2508

Db       3584 TCTTGGCAAGCAGGCGATGTCGTGGGGTGTATGGTTGACATGAACGAACACACCATGATG 3643

Qy       2509 TTCTCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGAT 2568

Db       3644 TTCACACTGAATGGTGAAATCCTTCTTGATGATTCAGGCTCAGAACTGGCTTTCAAGGAC 3703

Qy       2569 GTCCAGGGTGACAA---CTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGG 2625

Db       3704 TTTGATGTTGGCGATGGATTCATACCTGTGTGTAGCCTTGGAGTGGCTCAAGTGGGTAGG 3763

Qy       2626 TTAACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAG 2685

Db       3764 ATGAACTTTGGAAAGGATGTCAGCACCTTGAAATATTTCACCATCTGTGGCTTACAAGAG 3823

Qy       2686 GGATATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGAC 2745

Db       3824 GGCTATGAACCATTTGCCGTTAATACAAACAGGGATATTACCATGTGGCTGAGCAAGAGG 3883

Qy       2746 CAGCCGATCTTCGAGAATACTGATGAGATGATCGACACCAGGATTGATGTGACCAGGATA 2805

Db       3884 CTTCCTCAGTT---TCTTCAAGTTCCATCAAACCATGAACATATAGAGGTGACCAGAATA 3940

Qy       2806 CCAGCTGGTTCAGATACACCTCCATGCCTCAAGATTTCCCACAACACGTTCG 2857

Db       3941 GACGGCACCATAGACAGTTCCCCATGTTTAAAGGTCACTCAGAAGTCTTTTG 3992

Search completed: April 14, 2006, 14:57:28
Job time : 1691.5 secs
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 14:57:45 ; Search time 1272.5 Seconds
(without alignments)
9499.034 Million cell updates/sec

Title: US-10-668-767-127_COPY_1000_4000
Perfect score: 3001
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	616.8	20.6	15564	14	US-11-000-688-1500	Sequence 1500, Ap
	2	539.8	18.0	14620	14	US-11-044-111-17	Sequence 17, Appl
	3	521.2	17.4	3168	14	US-11-044-111-8	Sequence 8, Appli
	4	155.8	5.2	717	14	US-11-044-111-18	Sequence 18, Appl
	5	138.6	4.6	636	14	US-11-044-111-19	Sequence 19, Appl
	6	96.6	3.2	524	14	US-11-044-111-20	Sequence 20, Appl
	7	81.6	2.7	479	9	US-10-301-480-3997	Sequence 3997, Ap
	8	81.6	2.7	479	10	US-10-301-480-617406	Sequence 617406,
	9	70	2.3	595	10	US-10-301-480-261241	Sequence 261241,
	10	70	2.3	595	10	US-10-301-480-261242	Sequence 261242,
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	22	54.6	1.8	646	10	US-10-301-480-1041059	Sequence 1041059,
	23	44.6	1.5	864	8	US-10-750-185-41204	Sequence 41204, A
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	44	36.6	1.2	4376	14	US-11-121-438-15	Sequence 15, Appl
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ALIGNMENTS

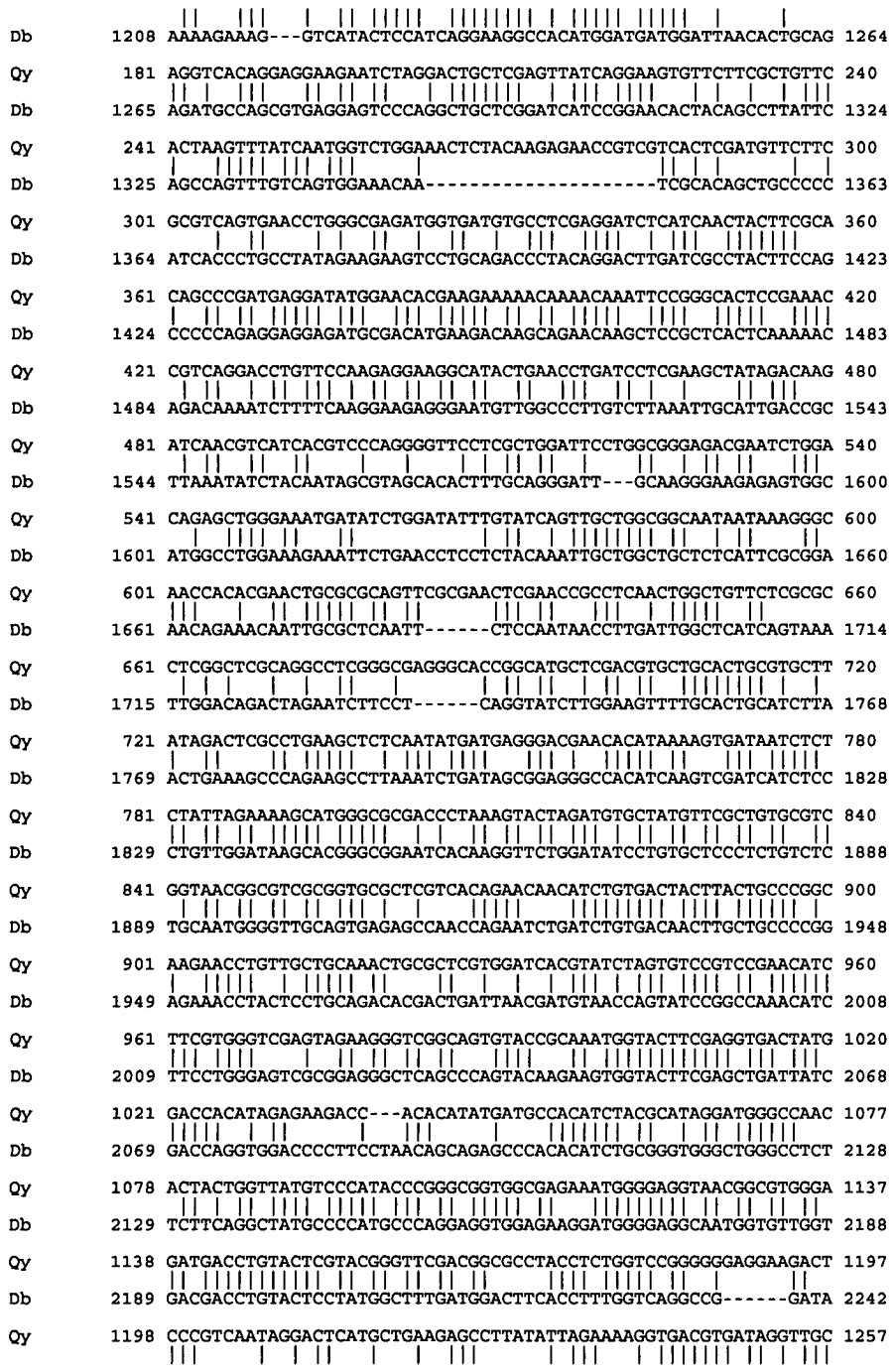
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US-11-000-688-1500
; Sequence 1500, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1500
; LENGTH: 15564
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15564)
; OTHER INFORMATION: ryanodine receptor 3(RYR3) gene.
US-11-000-688-1500

Query Match 20.6%; Score 616.8; DB 14; Length 15564;
Best Local Similarity 54.3%; Pred. No. 6.9e-184;
Matches 1567; Conservative 0; Mismatches 1242; Indels 75; Gaps 13;

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; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 14620
; TYPE: DNA
; ORGANISM: Meleagris gallopavo
US-11-044-111-17

Query Match 18.0%; Score 539.8; DB 14; Length 14620;
Best Local Similarity 53.0%; Pred. No. 1.9e-159;
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Qy       1441 TACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGCTTC 1500
Db       2413 TATGCTCCCTGTTATGAAGCCTTGCTTCCAAAAGAAAAGATGAAATTGGAACCAGTGAAA 2472

Qy       1501 TACTTCGGCAACCTGTCCAA------GCGGGCCTTGGCTGGACCTCCGCTAGTACAGGAC 1554
Db       2473 GAATATAAGAGAGATTCTGATGGAGTGAGAGATTTGCTGGGTACGACACAATTCCTCTCC 2532

Qy       1555 GATACGGCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATATGTG 1614
Db       2533 CAAGCTTCATTTATACCTTGTCCTATAGACACCAGTCAGATTGCTCTTCCTTTTCATCTT 2592

Qy       1615 GAACAAATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAGATC 1674
Db       2593 GAAAAGATCAGGGATAAACTAGCAGAAAATATCCATGAACTGTGGGGAATGAATAAAATA 2652

Qy       1675 GAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGCCTC 1734
Db       2653 GAGCTGGGCTGGACATATGGCAAGATACGGGATGATAATAAAAGGCATCATCCTTGTCTT 2712

Qy       1735 GTGCCCTTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTGCAG 1794
Db       2713 GTGGAATTCTCAAAGTTACCTGAGACAGAGAAGAATTATAATCTACAAATGTCAACAGAA 2772

Qy       1795 ACACTCAAGACTATCCTGGCTCTGGGCTACTACATCAGCTTAGATAAGCCTCCAGC---A 1851
Db       2773 ACCCTCAAAACGCTTTTGGCCCTTGGATGTCACATTGTTCATGCTAATCCAGCAGCTGAG 2832

Qy       1852 CGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAGCCA 1911
Db       2833 GAAGATCTTAAAAAAGTCAAGCTTCCTAAAAATTATATCATGTCAAATGGTTATAAACCT 2892

Qy       1912 GCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGACCAG 1971
Db       2893 GCCCCTCTTGATCTTTCTGAAGTGAAATTGTTACCTTCTCAAGAATTTCTAGTTGACAAA 2952

Qy       1972 CTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACTTAT 2031
Db       2953 CTAGCAGAAAATGCACATAATGTCTGGGCAAAAGACAGAATAAAGCAAGGATGGACCTAT 3012

Qy       2032 GGACTTAATGAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAGGTT 2091
Db       3013 GGCATTCAGCAGGATCTTAAGAACAAACGTAATCCTCGGCTAGTGCCATATGCATTACTA 3072

Qy       2092 GACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTGCTG 2151
Db       3073 GATGAACGTACTAAAAAATCAAACAGAGATAGCCTCCGTGAAGCTGTTAGGACATTTGCA 3132

Qy       2152 GTCTACGGGTATATGCTGGACCCGCCTACTGGGGAGCAGCATGAAGCACTCTTGTTGGAA 2211
Db       3133 GGCTATGGTTATAATATTGAGCCACCTGACCAAGAAATAGCTGACCAAACATTGGAAAAA 3192

Qy       2212 GCGTCAAAACAGAAGCAAGCAGACTTCAGAACATACCGCGCTGAGAAGAACTATGCCGTC 2271
Db       3193 GTCAGCATTGACAAGATACGTTTTTTCAGA---------GTAGAACAGTCTTATGCAGTG 3243

Qy       2272 AGCTCTGGGAAGTGGTACTTCGAGTTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGC 2331
Db       3244 AAGTCTGGAAAGTGGTATTTTGAATTTGAAGCTGTAACAGGTGGAGATATGCGTGTTGGC 3303

Qy       2332 TGGGCTCACGCTGATATGGCACCAGGAATGATGCTCGGACAAGACGAGAACTCTTGGGCA 2391
Db       3304 TGGGCCAGGCCAGGCTGTCGACCTGACATTGAACTGGGAGCTGATGACCAAGCATTTGTT 3363

Qy       2392 TTTGATGGTTACAATGAGGAAAAAGTGTACAGCGGTAACACTGAGTCTTTCGGCAAGCAA 2451
Db       3364 TTTGAAGGAAGCAAAGGCCAGCGTTGGCATCAAGG---CAGTGGGTTTTTTGGACGAAGT 3420

Qy       2452 TGGGCTGTTGGTGACGTAGTGGGGGTGTTCCTAGATCTCATTGATAAGACGATAAGTTTC 2511
Db       3421 TGGCAACCGGGAGATGTGGTTGGATGCATGATAAACTTGGATGACAAATCAATTATCTTT 3480

Qy       2512 TCACTCAATGGTGAGTTGTTGATGGATGCTCTTGGCGGAGAGACTACGTTTGCTGATGTC 2571
Db       3481 ACTCTGAATGGAGAGTTGCTTATAACCAGTAAAGGTTCAGAACTTGCATTTGCTGACTTT 3540

Qy       2572 CAGGGTGACA---ACTTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTA 2628
Db       3541 GGAATAGAAAGTGGTTTTGTTCCAATTTGCTCACTGGGTCTAGCTCAGATTGGACGTATG 3600

Qy       2629 ACATATGGCCAAGATGTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGA 2688
Db       3601 AACCTTGGAATGGATGCCAGTACATTCAAGTATTATACCATGTGTGGTCTTCAAGAAGGT 3660

Qy       2689 TATGAACCATTTTGCGTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAG 2748
Db       3661 TTTGAACCTTTTGCAGTGAACATGAACCGAGATGTCGCTATGTGGTTTAGTAAACGCTTA 3720

Qy       2749 CCGATCTTCGAGAAT 2763
Db       3721 CCAACATTTGTTAAT 3735
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RESULT 3
US-11-044-111-8
; Sequence 8, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 3168
; TYPE: DNA
; ORGANISM: Meleagris gallopavo
US-11-044-111-8

Query Match 17.4%; Score 521.2; DB 14; Length 3168;
Best Local Similarity 55.4%; Pred. No. 6.5e-154;
Matches 1213; Conservative 0; Mismatches 938; Indels 39; Gaps 9;

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Qy          4 ATAGGCGCGCCCATCATCAAATATGGTGACTCCACCGTCATTGTGCAGCATTCCGAGACT 63
Db        997 ATGGGACCCCCGGAGATCAAATATGGGGAGTCGCTGTGCTTCGTGCAGCACGCGGCCTCG 1056

Qy         64 GGCTTGTGGCTGTCTTATAAGTCTTACGAAACGAAGAAGAAGGGAGTGGGTAAAGTAGAA 123
Db       1057 GGGCTGTGGCTCACCTACGCTGCTGCTGACACCAAAGCGCTGCGCCTGGGGCTGATGAAA 1116

Qy        124 GAGAAGCAAGCGATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCCAGG 183
Db       1117 CGGAGGC---CCATCCTGCACCAGGAGGGCCACATGGACGACGCGCTGTCGCTCAGCCGC 1173

Qy        184 TCACAGGAGGAAGAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACT 243
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Db       1174 TCGCAGGGCGAGGAGTCGCAGGCGGCGCGGATGATTTACAGCACGGCGGGGCTCTACGGG 1233

Qy        244 AAGTTTATCAATGGTCTGGAAACTCT---ACAAGAGAACCGTCGTCACTCGATGTTCTTC 300

Db       1234 AGCTTCATCCGGAGCCTGGACGCGCTGAGCTCTCGTGGCCGTGGCGGCGGTGCGGGGAAC 1293

Qy        301 GCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCA 360

Db       1294 GCGGCTCTGCCCATCGCCGCCGTCATCCTCAGCCTGCGGGATCTGATCGCTTATTTCCGC 1353

Qy        361 CAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAAC 420

Db       1354 GCCCCGCACACCGAGCTGCAGCACGAGCAGCGCCAGAACCGCCTGCGCTCCCTGCGGCGC 1413

Qy        421 CGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAG 480

Db       1414 CGCCAGGACCTCTTCCAGCAGGAGGGGATGATCTCCCTGGTGCTGAACTGCATCGACCGG 1473

Qy        481 ATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGA 540

Db       1474 CTGAACGTGTACAGCACGGCCGCGCACTTCGCCGAGTTC---GCCGGGGAGGAGGCGGCG 1530

Qy        541 CAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGC 600

Db       1531 GCCGCCTGGAAGGAGATCGTCAACCTCCTCTATGAGCTGCTGGCGTCGCTGATCCGGGGG 1590

Qy        601 AACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGC 660

Db       1591 AACCGAACCAACTGCGCCCTGTT------CTCCACCAACCTGGACTGGCTGGTCAGCAAA 1644

Qy        661 CTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTT 720

Db       1645 CTGGACCGGC------TGGAGGCGTCGTCAGGGATCCTGGAGGTGCTTTACTGCGTCCTG 1698

Qy        721 ATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCT 780

Db       1699 ATCGAGAGCCCCGAGGTTCTGAACATCATCCAGGAGAACCACATCAAGTCCATCATCTCC 1758

Qy        781 CTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTC 840

Db       1759 CTGCTGGACAAACACGGCCGCAACCATAAGGTCCTGAACGTGCTCTGCTCTCTGTGTGTC 1818

Qy        841 GGTAACGGCGTCGCGGTGCGCTCGTCACAGAACAACATCTGTGACTACTTACTGCCCGGC 900

Db       1819 TGCAATGCTGTGGCCGTTCGTTCCAACCAAAATCTCATCACCGAAAATCTGCTCCCGCGA 1878

Qy        901 AAGAACCTGTTGCTGCAAACTGCGCTCGTGGATCACGTATCTAGTGTCCGTCCGAACATC 960

Db       1879 CGCGACCTCCTGCTGCAGACCGGGCCGGTCAGCTACGTCAGCAGCATCCGGCCCAACATC 1938

Qy        961 TTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCAAATGGTACTTCGAGGTGACTATG 1020

Db       1939 CTCCTGGGGACCCACGAGGGCTCCACGCAGTACCCACGCTGGTACTTCGAGGTGGCCGTG 1998

Qy       1021 GACCACATAGAGAAGACC---ACACATATGATGCCACATCTACGCATAGGATGGGCCAAC 1077

Db       1999 GATCACGTGGAGCCCTTCGTGACGGCGCAGCCCACCCACCTGCGCGTGGGGTGGGCGATG 2058

Qy       1078 ACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGAAATGGGGAGGTAACGGCGTGGGA 1137

Db       2059 GCGGAGGGTTACAGCCCCTACCCGGGGGGGGGAGAGGGCTGGGGGGCCTACGGAGCCGGA 2118

Qy       1138 GATGACCTGTACTCGTACGGGTTCGACGGCGCCTACCTCTGGTCCGGGGGGAGGAAGACT 1197

Db       2119 GACGACCTTTATTCCTTCGCCTTTGATGGGCTGCACCTCTGGGCCGGCGGGGTTCCGCGG 2178

Qy       1198 CCCGTCAATAGGACTCATGCTGAAGAGCCTTATATTAGAAAAGGTGACGTGATAGGTTGC 1257

Db       2179 GCCGCCCCCTCCCCCCAGC------AGCACATCCTGGCCCCCGGGGACGTGGTGAGCTGC 2232

Qy       1258 GCATTGGACCTGACGGTACCCATAATCAACTTCATGTTCAACGGAGTGCGGGTGACGGGA 1317

Db       2233 TGCCTGGACCTCTCTGTTCCCACCATCTCCTCCCGCCTCAACGGCAGCCCGGTGCTGGGG 2292

Qy       1318 TCCTTCACCAACTTCAATCTGGAAGGCATGTTCTTCCCGGTCATCAGCTGCTCTAGTAAG 1377

Db       2293 ATGTTCGAGAAGTTCAATCGCGACGCGCTCTTCTCCCCCGTCGTCAGCTTCTCCGCCGGC 2352

Qy       1378 CTGAGTTGTCGGTTCCTGCTGGGCGGAGAACACGGTCGTCTCCGGTACGCGGCTCCAGAA 1437

Db       2353 GTGCGGCTGCGCTTCCTGCTGGGGGGCCGCCACGGGGATTTCCAGTTCCTGCCCCCCCCC 2412

Qy       1438 GGCTACTCTCCCTTGGTGGAGTCTCTCCTGCCGCAGCAGATCCTCAGCCTGGAGCCGTGC 1497

Db       2413 GGTTACTCCCCCTGTGCCGAGGCGCTGCTGCCCCGCGAGCGGCTGCGCCTGGAACCCATC 2472

Qy       1498 TTCTACTT------CGGCAACCTGTCCAAGCGGGCCTTGGCTGGACCTCCGCTAGTACAG 1551

Db       2473 AAAGCTTATAGGGGCGACGGCCCCCCGCCCCACTGCCTGCTCGGCCCCACAAAGGCGCTG 2532

Qy       1552 GACGATACGGCCTTCGTGCCTACACCTGTTGATACTTTACAGATTACTCTGCCTACATAT 1611

Db       2533 CCCCACACCGCCTTCACCCCCTGCCCCGTGGACACCGCGCAGATCGTTCTGCCCCCCCAC 2592

Qy       1612 GTGGAACAAATTAGAGATAAGCTAGCTGAAAATATACACGAAATGTGGGCTATGAATAAG 1671

Db       2593 CTGGAGCGCATCCGGGAGAAGCTGGCGGAGAACATCCATGAGCTGTGGGCGCTGACCCGC 2652

Qy       1672 ATCGAAGCAGGCTGGATGTACGGCGACCAGAGAGAAGACTTGCACAAGATCCACCCCTGC 1731

Db       2653 ATCGAGCAGGGATGGACCTACGGCCCCATCCATGACGATGCTGAGCAGCTCCATCCCTGC 2712

Qy       1732 CTCGTGCCCTTCGAGCGACTCCCACCTGCTGAGAAACGATACGACATACAACTCGCTGTG 1791

Db       2713 CTGCTGGATTTCCACAGCCTCCCCGAGCCGGAGCGCAACTACAACCTGCAGATGTCGGGG 2772

Qy       1792 CAGACACTCAAGACTATCCTGGCTCTGGGCTACTACATCAGCTT---AGATAAGCCTCCA 1848

Db       2773 GAGACGCTCAAGACGCTGCTGGCGCTGGGCTGCCACGTGGGGATGGCGGACGAGAAGGCG 2832

Qy       1849 GCACGCATCCGCAACGTTCGTCTGCCCAACGAACCTTTCATGCAGTCCAACGGCTACAAG 1908

Db       2833 GAGGAGAACCTGAGGAAAATCAAACTGCCCAAAACGTACACGATGCGCAACGGTTACAAA 2892

Qy       1909 CCAGCACCACTCGACCTGAGTGCTGTCACCCTGACACCCAAGATGGATGAGCTAGTAGAC 1968

Db       2893 CCGGCCCCGCTGGACCTGGCCCACGTGCGCCTGACGCCGGCGCAGCTGACGCTGGTGGAT 2952

Qy       1969 CAGCTGGCTGAGAACACCCACAACCTTTGGGCCAGGGAGAGGATACAGCAGGGATGGACT 2028

Db       2953 CGGCTGGCGGAGAACGCGCACAACGTCTGGGCGCGGGACCGCGTGCAGCAGGGCCGGACC 3012

Qy       2029 TATGGACTTAATGAGGACTCGGACATGCATCGTTCCCCGCACCTGGTGCCATACCCGAAG 2088

Db       3013 TACAGCATCGTGCAGGACATTAAGAACAAGCGCAACCCCCGCCTGGTGCCCTACAACCTG 3072

Qy       2089 GTTGACGATGCCATCAAGAAGGCCAACAGGGACACAGCCTCGGAGACTGTGAGGACCCTG 2148

Db       3073 CTGGACGAGCGCACCAAGAAGACCAACAGGGACAGCCTGTGCGAGGCGGTGCGGACCCTC 3132

Qy       2149 CTGGTCTACGGGTATATGCTGGACCCGCCT 2178

Db       3133 ATCGGCTACGGCTACAACATCGAGCCACCT 3162
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RESULT 4
US-11-044-111-18
; Sequence 18, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308

```
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Meleagris gallopavo
US-11-044-111-18

  Query Match             5.2%;  Score 155.8;  DB 14;  Length 717;
  Best Local Similarity   54.9%;  Pred. No. 3.3e-38;
  Matches  401;  Conservative    0;  Mismatches  312;  Indels   18;  Gaps    4;

Qy        136 ATTCTCCACGAGGAAGGCAAGATGGACGATGGCCTCGACTTCTCCAGGTCACAGGAGGAA 195
              ||||| ||| |||| ||| | |||||||| |  ||     ||  | | || ||||  ||
Db          1 ATTCTGCACCAGGAGGGCCACATGGACGACGCGCTGTCGCTCAGCCGCTCGCAGGGCGAG 60

Qy        196 GAATCTAGGACTGCTCGAGTTATCAGGAAGTGTTCTTCGCTGTTCACTAAGTTTATCAAT 255
              || ||   | | || ||  | ||    |      |   ||| | |   |  || |||
Db         61 GAGTCGCAGGCGGCGCGGATGATTTACAGCACGGCGGGGCTCTACGGGAGCTTCATCCGG 120

Qy        256 GGTCTGGAAACTCTACAAGA---GAACCGTCGTCACTCGATGTTCTTCGCGTCAGTGAAC 312
              | |||||  | ||         |  |||  |   |      |    |||| | ||  |
Db        121 AGCCTGGACGCGCTGAGCTCTCGGGGCCGCGGCGGCGGTGCGGGGAACGCGGCTCTGCCC 180

Qy        313 CTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAACTACTTCGCACAGCCCGATGAG 372
              | | ||   | | |  ||||   |||||| |||   || |||     ||  |
Db        181 ATCGCCGCCGTCATCCTCAGCCTGCGGGATCTGATCGCTTATTTCCGCGCCCCGCACACC 240

Qy        373 GATATGGAACACGAAGAAAAACAAAACAAATTCCGGGCACTCCGAAACCGTCAGGACCTG 432
              ||  || | |||||  |    || |||   | ||  | || ||   ||| ||||||||
Db        241 GAGCTGCAGCACGAGCAGCGCCAGAACCGCCTGCGCTCCCTGCGGCGCCGCCAGGACCTC 300

Qy        433 TTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAACGTCATC 492
              |||||  |||| || ||  |  |||| | ||  |   || |||  | | |||||   |
Db        301 TTCCAGCAGGAGGGGATGATCTCCCTGGTGCTGAACTGCATCGACCGGCTGAACGTGTAC 360

Qy        493 ACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGCTGGGAA 552
              |   |    | |  | |||| |  |||   || || || ||  | |        |||| |
Db        361 AGCACGGCCGCGCACTTCGCCGAGTTC---GCCGGGGAGGAGGCGGCGGCCGCCTGGAAG 417

Qy        553 ATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGCAACCACACGAAC 612
                |||       | ||| || |||||||| |  | ||   ||| ||||  || |||
Db        418 GAGATCGTCAACCTCCTCTATGAGCTGCTGGCGTCGCTGATCCGGGGGAACCGAACCAAC 477

Qy        613 TGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGCCTCGGCTCGCAG 672
              |||||  | |||       ||| | |  |||  |||||||| ||       || | |  ||
Db        478 TGCGCCCTGTT------CTCCACCAACCTGGACTGGCTGGTCAGCAAACTGGACCGGC-- 529

Qy        673 GCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTTATAGACTCGCCT 732
                ||  | |     | || || || || |||||  |||||||  || || ||    ||
Db        530 ----TGGAGGCGTCGTCAGGGATCCTGGAGGTGCTTTACTGCGTCCTGATCGAGAGCCCC 585

Qy        733 GAAGCTCTCAATATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTAGAAAAG 792
              || | ||| || || ||   |||  | ||||| ||     || ||||| ||  | || ||
Db        586 GAGGTTCTGAACATCATCCAGGAGAACCACATCAAGTCCATCATCTCCCTGCTGGACAAA 645

Qy        793 CATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTCGGTAACGGCGTC 852
              || || ||| ||| ||| || || || ||||| || || ||||| ||| | || |  ||
Db        646 CACGGCCGCAACCATAAGGTCCTGGACGTGCTCTGCTCTCTGTGTGTCTGCAATGCTGTG 705

Qy        853 GCGGTGCGCTC 863
              || || || ||
Db        706 GCCGTTCGTTC 716


RESULT 5
US-11-044-111-19
; Sequence 19, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 636
;   TYPE: DNA
;   ORGANISM: Meleagris gallopavo
US-11-044-111-19

  Query Match             4.6%;  Score 138.6;  DB 14;  Length 636;
  Best Local Similarity   56.5%;  Pred. No. 9.1e-33;
  Matches  324;  Conservative    0;  Mismatches  234;  Indels   15;  Gaps    3;

Qy        291 GATGTTCTTCGCGTCAGTGAACCTGGGCGAGATGGTGATGTGCCTCGAGGATCTCATCAA 350
              |||| | | |    | | |   ||   || ||   | ||  ||||   |||||| |||
Db         78 GATGATTTACAGCACGGCGGGGCTCTACGGGAGCTTCATCCGCCTGCGGGATCTGATCGC 137

Qy        351 CTACTTCGCACAGCCCGATGAGGATATGGAACACGAAGAAAAACAAAACAAATTCCGGGC 410
              || |||       ||  |   ||  || | |||||  |    || |||     | ||  |
Db        138 TTATTTCCGCGCCCCGCACACCGAGCTGCAGCACGAGCAGCGCCAGAACCGCCTGCGCTC 197

Qy        411 ACTCCGAAACCGTCAGGACCTGTTCCAAGAGGAAGGCATACTGAACCTGATCCTCGAAGC 470
              || ||   ||| |||||||| |||||  |||| || ||   |   |||| | ||  |
Db        198 CCTGCGGCGCCGCCAGGACCTCTTCCAGCAGGAGGGGATGATCTCCCTGGTGCTGAACTG 257

Qy        471 TATAGACAAGATCAACGTCATCACGTCCCAGGGGTTCCTCGCTGGATTCCTGGCGGGAGA 530
              || |||  | | |||||   ||   |   | |  | |||| |  |||   || || ||
Db        258 CATCGACCGGCTGAACGTGTACAGCACGGCCGCGCACTTCGCCGAGTTC---GCCGGGGA 314

Qy        531 CGAATCTGGACAGAGCTGGGAAATGATATCTGGATATTTGTATCAGTTGCTGGCGGCAAT 590
              ||  | |        |||| |   |||           | ||| || ||||||| |  |
Db        315 GGAGGCGGCGGCCGCCTGGAAGGAGATCGTCAACCTCCTCTATGAGCTGCTGGCGTCGCT 374

Qy        591 AATAAAGGGCAACCACACGAACTGCGCGCAGTTCGCGAACTCGAACCGCCTCAACTGGCT 650
              ||   ||| ||||  || |||||||| | |||       ||| | |  |||  |||||||
Db        375 GATCCGGGGGAACCGAACCAACTGCGCCCTGTT------CTCCACCAACCTGGACTGGCT 428

Qy        651 GTTCTCGCGCCTCGGCTCGCAGGCCTCGGGCGAGGGCACCGGCATGCTCGACGTGCTGCA 710
              | ||     || | |  ||      || | |  | || || || || |||||  |
Db        429 GGTCAGCAAACTGGACCGGC------TGGAGGCGTCGTCAGGGATCCTGGAGGTGCTTTA 482

Qy        711 CTGCGTGCTTATAGACTCGCCTGAAGCTCTCAATATGATGAGGGACGAACACATAAAAGT 770
              |||||| || || ||    || || | ||| || || ||   |||  | |||||  ||
Db        483 CTGCGTCCTGATCGAGAGCCCCGAGGTTCTGAACATCATCCAGGAGAACCACATCAAGTC 542

Qy        771 GATAATCTCTCTATTAGAAAAGCATGGGCGCGACCCTAAAGTACTAGATGTGCTATGTTC 830
              || ||||| ||  | || || || || ||| ||| ||| || || || ||||| || ||
Db        543 CATCATCTCCCTGCTGGACAAACACGGCCGCAACCATAAGGTCCTGGACGTGCTCTGCTC 602

Qy        831 GCTGTGCGTCGGTAACGGCGTCGCGGTGCGCTC 863
              ||||| ||| | || |  || || || || ||
Db        603 TCTGTGTGTCTGCAATGCTGTGGCCGTTCGTTC 635


RESULT 6
US-11-044-111-20
; Sequence 20, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
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```
; SEQ ID NO 20
;   LENGTH: 524
;   TYPE: DNA
;   ORGANISM: Meleagris gallopavo
US-11-044-111-20

  Query Match             3.2%;  Score 96.6;  DB 14;  Length 524;
  Best Local Similarity   57.3%;  Pred. No. 1.8e-19;
  Matches  240;  Conservative    0;  Mismatches  164;  Indels   15;  Gaps    3;

Qy        445 GGCATACTGAACCTGATCCTCGAAGCTATAGACAAGATCAACGTCATCACGTCCCAGGGG 504
              || ||  |   |||| | ||  |    || ||| | | |||||   ||   |    | |
Db        120 GGGATGATCTCCCTGGTGCTGAACTGCATCGACCGGCTGAACGTGTACAGCACGGCCGCG 179

Qy        505 TTCCTCGCTGGATTCCTGGCGGGAGACGAATCTGGACAGAGCTGGGAAATGATATCTGGA 564
                | |||| |  |||   || || || ||  | |      |||| |   |||
Db        180 CACTTCGCCGAGTTC---GCCGGGGAGGAGGCGGCGGCCGCCTGGAAGGAGATCGTCAAC 236

Qy        565 TATTTGTATCAGTTGCTGGCGGCAATAATAAAGGGCAACCACACGAACTGCGCGCAGTTC 624
                | ||| || |||||||| |  | ||   ||| |||| || |||||||| | |||
Db        237 CTCCTCTATGAGCTGCTGGCGTCGCTGATCCGGGGGAACCGAACCAACTGCGCCCTGTT- 295

Qy        625 GCGAACTCGAACCGCCTCAACTGGCTGTTCTCGCGCCTCGGCTCGCAGGCCTCGGGCGAG 684
                |||  |  |  |||  |||||||| ||      || | |  || ||   ||
Db        296 -----CTCCACCAACCTGGACTGGCTGGTCAGCAAACTGGACCGGCTGGAGGCGTCG--- 347

Qy        685 GGCACCGGCATGCTCGACGTGCTGCACTGCGTGCTTATAGACTCGCCTGAAGCTCTCAAT 744
                | || || || || ||||| ||||||| || || ||    || || | ||| ||
Db        348 ---TCAGGGATCCTGGAGGTGCTTTACTGCGTCCTGATCGAGAGCCCCGAGGTTCTGAAC 404

Qy        745 ATGATGAGGGACGAACACATAAAAGTGATAATCTCTCTATTAGAAAAGCATGGGCGCGAC 804
              || ||   |||  | ||||| ||    || ||||| ||  | || || || || ||| ||
Db        405 ATCATCCAGGAGAACCACATCAAGTCCATCATCTCCCTGCTGGACAAACACGGCCGCAAC 464

Qy        805 CCTAAAGTACTAGATGTGCTATGTTCGCTGTGCGTCGGTAACGGCGTCGCGGTGCGCTC 863
              | ||| || || || ||||| || || ||||| ||| | || |  || || || || ||
Db        465 CATAAGGTCCTGGACGTGCTCTGCTCTCTGTGTGTCTGCAATGCTGTGGCCGTTCGTTC 523


RESULT 7
US-10-301-480-3997
; Sequence 3997, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3997
;   LENGTH: 479
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-3997

  Query Match             2.7%;  Score 81.6;  DB 9;  Length 479;
  Best Local Similarity   60.4%;  Pred. No. 9.9e-15;
  Matches  151;  Conservative    1;  Mismatches   95;  Indels    3;  Gaps    1;

Qy        938 TATCTAGTGTCCGTCCGAACATCTTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCA 997
              | |  ||  |  | || |: || ||  ||||      ||||| || ||   |||    |
Db        219 TTTAAAGCATGAGACCCARTATTTTTCTGGGCGTCAGTGAAGGTTCTGCTCAGTATAAGA 278

Qy        998 AATGGTACTTCGAGGTGACTATGGACCACATAGAGAAGAC---CACACATATGATGCCAC 1054
              |||||||||  ||  |||   ||||||||| ||||          ||| |       | |
Db        279 AATGGTACTATGAATTGATGGTGGACCACACAGAGCCCTTTGTGACAGCTGAAGCAACTC 338

Qy       1055 ATCTACGCATAGGATGGGCCAACACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGA 1114
              | || ||  | || |||||   ||||   || |||   || ||||| || || |||||
Db        339 ACCTGCGAGTGGGCTGGGCTTCCACTGAAGGATATTCTCCCTACCCTGGAGGGGGCGAAG 398

Qy       1115 AATGGGGAGGTAACGGCGTGGGAGATGACCTGTACTCGTACGGGTTCGACGGCGCCTACC 1174
              | ||||| || || || || |||||||| || | ||| || || || || |||    | |
Db        399 AGTGGGGTGGAAATGGTGTTGGAGATGATCTCTTCTCCTATGGATTTGATGGCCTTCATC 458

Qy       1175 TCTGGTCCGG 1184
              |||||||  ||
Db        459 TCTGGTCAGG 468


RESULT 8
US-10-301-480-617406
; Sequence 617406, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 617406
;   LENGTH: 479
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-617406

  Query Match             2.7%;  Score 81.6;  DB 10;  Length 479;
  Best Local Similarity   60.4%;  Pred. No. 9.9e-15;
  Matches  151;  Conservative    1;  Mismatches   95;  Indels    3;  Gaps    1;

Qy        938 TATCTAGTGTCCGTCCGAACATCTTCGTGGGTCGAGTAGAAGGGTCGGCAGTGTACCGCA 997
              | |  ||  |  | || |: || ||  ||||      ||||| || ||   |||    |
Db        219 TTTAAAGCATGAGACCCARTATTTTTCTGGGCGTCAGTGAAGGTTCTGCTCAGTATAAGA 278

Qy        998 AATGGTACTTCGAGGTGACTATGGACCACATAGAGAAGAC---CACACATATGATGCCAC 1054
              |||||||||  ||  |||   ||||||||| ||||          ||| |       | |
Db        279 AATGGTACTATGAATTGATGGTGGACCACACAGAGCCCTTTGTGACAGCTGAAGCAACTC 338

Qy       1055 ATCTACGCATAGGATGGGCCAACACTACTGGTTATGTCCCATACCCGGGCGGTGGCGAGA 1114
              | || ||  | || |||||   ||||   || |||   || ||||| || || |||||
Db        339 ACCTGCGAGTGGGCTGGGCTTCCACTGAAGGATATTCTCCCTACCCTGGAGGGGGCGAAG 398

Qy       1115 AATGGGGAGGTAACGGCGTGGGAGATGACCTGTACTCGTACGGGTTCGACGGCGCCTACC 1174
              | ||||| || || || || |||||||| || | ||| || || || || |||    | |
Db        399 AGTGGGGTGGAAATGGTGTTGGAGATGATCTCTTCTCCTATGGATTTGATGGCCTTCATC 458

Qy       1175 TCTGGTCCGG 1184
              |||||||  ||
Db        459 TCTGGTCAGG 468


RESULT 9
US-10-301-480-261241
; Sequence 261241, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
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;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261241
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-261241

  Query Match             2.3%;  Score 70;  DB 10;  Length 595;
  Best Local Similarity   62.6%;  Pred. No. 5.4e-11;
  Matches  109;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       2236 TTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGGTACTTCGAG 2295
             ||| |||  | ||| || ||||||| |||||| || |   | ||   |||||| || ||
Db         27 TTCCGAATCTTCCGTGCCGAGAAGACCTATGCAGTGAAGGCCGGACGGTGGTATTTTGAA 86

Qy       2296 TTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATATGGCACCA 2355
             |||||||   | || ||||||   |||||||| || |||  ||   ||| |     |||
Db         87 TTTGAGACGGTCACTGCTGGAGACATGAGGGTTGGTTGGAGTCGTCCTGGTTGTCAACCG 146

Qy       2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGTTACAATGAG 2409
             |    |  ||| ||   ||| ||     | |  || |||||||| | ||| | |
Db        147 GATCAGGAGCTTGGCTCAGATGAACGTGCCTTTGCCTTTGATGGCTTCAAGGTG 200


RESULT 10
US-10-301-480-261242
; Sequence 261242, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 261242
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-261242

  Query Match             2.3%;  Score 70;  DB 10;  Length 595;
  Best Local Similarity   62.6%;  Pred. No. 5.4e-11;
  Matches  109;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       2236 TTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGGTACTTCGAG 2295
             ||| |||  | ||| || ||||||| |||||| || |   | ||   |||||| || ||
Db         27 TTCCGAATCTTCCGTGCCGAGAAGACCTATGCAGTGAAGGCCGGACGGTGGTATTTTGAA 86

Qy       2296 TTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATATGGCACCA 2355
             |||||||   | || ||||||   |||||||| || |||  ||   ||| |     |||
Db         87 TTTGAGACGGTCACTGCTGGAGACATGAGGGTTGGTTGGAGTCGTCCTGGTTGTCAACCG 146

Qy       2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGTTACAATGAG 2409
             |    |  ||| ||   ||| ||     | |  || |||||||| | ||| | |
Db        147 GATCAGGAGCTTGGCTCAGATGAACGTGCCTTTGCCTTTGATGGCTTCAAGGTG 200


RESULT 11
US-10-301-480-874650
; Sequence 874650, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 874650
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-874650

  Query Match             2.3%;  Score 70;  DB 10;  Length 595;
  Best Local Similarity   62.6%;  Pred. No. 5.4e-11;
  Matches  109;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       2236 TTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGGTACTTCGAG 2295
             ||| |||  | ||| || ||||||| |||||| || |   | ||   |||||| || ||
Db         27 TTCCGAATCTTCCGTGCCGAGAAGACCTATGCAGTGAAGGCCGGACGGTGGTATTTTGAA 86

Qy       2296 TTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATATGGCACCA 2355
             |||||||   | || ||||||   |||||||| || |||  ||   ||| |     |||
Db         87 TTTGAGACGGTCACTGCTGGAGACATGAGGGTTGGTTGGAGTCGTCCTGGTTGTCAACCG 146

Qy       2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGTTACAATGAG 2409
             |    |  ||| ||   ||| ||     | |  || |||||||| | ||| | |
Db        147 GATCAGGAGCTTGGCTCAGATGAACGTGCCTTTGCCTTTGATGGCTTCAAGGTG 200


RESULT 12
US-10-301-480-874651
; Sequence 874651, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 874651
;   LENGTH: 595
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-874651

  Query Match             2.3%;  Score 70;  DB 10;  Length 595;
  Best Local Similarity   62.6%;  Pred. No. 5.4e-11;
  Matches  109;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       2236 TTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGGTACTTCGAG 2295
             ||| |||  | ||| || ||||||| |||||| || |   | ||   |||||| || ||
Db         27 TTCCGAATCTTCCGTGCCGAGAAGACCTATGCAGTGAAGGCCGGACGGTGGTATTTTGAA 86

Qy       2296 TTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATATGGCACCA 2355
             |||||||   | || ||||||   |||||||| || |||  ||   ||| |     |||
Db         87 TTTGAGACGGTCACTGCTGGAGACATGAGGGTTGGTTGGAGTCGTCCTGGTTGTCAACCG 146

Qy       2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGTTACAATGAG 2409
             |    |  ||| ||   ||| ||     | |  || |||||||| | ||| | |
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Db        147 GATCAGGAGCTTGGCTCAGATGAACGTGCCTTTGCCTTTGATGGCTTCAAGGTG 200


RESULT 13
US-09-925-065A-169264/c
; Sequence 169264, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 169264
;   LENGTH: 608
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-169264

  Query Match             2.3%;  Score 70;  DB 6;  Length 608;
  Best Local Similarity   62.6%;  Pred. No. 5.5e-11;
  Matches  109;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       2236 TTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGGTACTTCGAG 2295
             ||| |||  | ||| || ||||||| |||||| || |   | ||   |||||| || ||
Db        582 TTCCGAATCTTCCGTGCCGAGAAGACCTATGCAGTGAAGGCCGGACGGTGGTATTTTGAA 523

Qy       2296 TTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATATGGCACCA 2355
             |||||||   | || ||||||   |||||||| || |||  ||   ||| |     |||
Db        522 TTTGAGACGGTCACTGCTGGAGACATGAGGGTTGGTTGGAGTCGTCCTGGTTGTCAACCG 463

Qy       2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGTTACAATGAG 2409
             |    |  ||| ||   ||| ||     | |  || ||||||||| | ||| | |
Db        462 GATCAGGAGCTTGGCTCAGATGAACGTGCCTTTGCCTTTGATGGCTTCAAGGTG 409


RESULT 14
US-09-925-065A-169265/c
; Sequence 169265, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 169265
;   LENGTH: 608
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-169265

  Query Match             2.3%;  Score 70;  DB 6;  Length 608;
  Best Local Similarity   62.6%;  Pred. No. 5.5e-11;
  Matches  109;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       2236 TTCAGAACATACCGCGCTGAGAAGAACTATGCCGTCAGCTCTGGGAAGTGGTACTTCGAG 2295
             ||| |||  | ||| || ||||||| |||||| || |   | ||   |||||| || ||
Db        582 TTCCGAATCTTCCGTGCCGAGAAGACCTATGCAGTGAAGGCCGGACGGTGGTATTTTGAA 523

Qy       2296 TTTGAGATCTTAACGGCTGGACCTATGAGGGTCGGCTGGGCTCACGCTGATATGGCACCA 2355
             |||||||   | || ||||||   |||||||| || |||  ||   ||| |     |||
Db        522 TTTGAGACGGTCACTGCTGGAGACATGAGGGTTGGTTGGAGTCGTCCTGGTTGTCAACCG 463

Qy       2356 GGAATGATGCTCGGACAAGACGAGAACTCTTGGGCATTTGATGGTTACAATGAG 2409
             |    |  ||| ||   ||| ||     | |  || ||||||||| | ||| | |
Db        462 GATCAGGAGCTTGGCTCAGATGAACGTGCCTTTGCCTTTGATGGCTTCAAGGTG 409


RESULT 15
US-10-750-185-28284
; Sequence 28284, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 28284
;   LENGTH: 1761
;   TYPE: DNA
;   ORGANISM: Bovine  19866880569427
US-10-750-185-28284

  Query Match             2.3%;  Score 67.8;  DB 8;  Length 1761;
  Best Local Similarity   62.9%;  Pred. No. 5e-10;
  Matches  105;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy       2584 TTTGTACCAGCTTGCACACTTGGTGTGGGCCAAAAAGCCAGGTTAACATATGGCCAAGAT 2643
             ||  |||| |  || |  || || ||||  |||   | |||| | |  | |||  | |||
Db        740 TTCATACCTGTGTGTAGCCTGGGAGTGGCTCAAGTGGGCAGGCTGAACTTTGGAAAGGAT 799

Qy       2644 GTGAATACTCTGAAATACTTCACAACATGTGGTCTTCAGGAGGGATATGAACCATTTTGC 2703
             || |  ||  ||||||| ||||| |  |||||  | || ||||| ||||||||||||  |
Db        800 GTCAGCACCTTGAAATATTTCACCATCTGTGGCTTACAAGAGGGCTATGAACCATTTGCC 859

Qy       2704 GTCAATATGAAGAGAGACGTGACTCACTGGTACACCAAGGACCAGCC 2750
             || || |  || || ||  | ||     |||   | ||||   |  ||
Db        860 GTTAACACAAATAGGGATATTACCATGTGGCTGAGCAAGAGGCTTCC 906


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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 14:38:23 ; Search time 2288 Seconds
(without alignments)
10846.330 Million cell updates/sec

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Perfect score: 3001
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	3001	100.0	15387	7	US-10-668-767-127	Sequence 127, App
	2	2996.2	99.8	15303	7	US-10-668-767-145	Sequence 145, App
	3	2917.4	97.2	15679	7	US-10-668-767-1	Sequence 1, Appli
	4	2846.4	94.8	15405	7	US-10-668-767-129	Sequence 129, App
	5	2844.8	94.8	15429	7	US-10-668-767-143	Sequence 143, App
	6	1718.2	57.3	15606	10	US-11-097-143-22562	Sequence 22562, A
	7	1718.2	57.3	16363	7	US-10-668-767-9	Sequence 9, Appli
	8	1578.6	52.6	15413	7	US-10-668-767-7	Sequence 7, Appli
	9	1489.6	49.6	15315	7	US-10-668-767-5	Sequence 5, Appli
	10	1456	48.5	15845	7	US-10-668-767-3	Sequence 3, Appli
	11	771.8	25.7	15359	9	US-10-887-553A-489	Sequence 489, App
	12	771.8	25.7	15359	9	US-10-450-763-4960	Sequence 4960, Ap
	13	770.2	25.7	15359	7	US-10-276-774-500	Sequence 500, App
	14	740	24.7	14302	7	US-10-276-774-552	Sequence 552, App
	15	740	24.7	15731	9	US-10-887-553A-490	Sequence 490, App
	16	738.4	24.6	6807	7	US-10-276-774-445	Sequence 445, App
	17	732.2	24.4	15563	7	US-10-764-425-48	Sequence 48, Appl
	18	732.2	24.4	15563	9	US-10-887-553A-491	Sequence 491, App
	19	732.2	24.4	15583	9	US-10-450-763-12305	Sequence 12305, A
	20	731.8	24.4	15820	9	US-10-450-763-23337	Sequence 23337, A
	21	723.4	24.1	15453	8	US-10-723-860-5796	Sequence 5796, Ap
c	22	632.2	21.1	24236	10	US-11-097-143-22561	Sequence 22561, A
	23	211.6	7.1	4278	9	US-10-450-763-23335	Sequence 23335, A
	24	137.4	4.6	323	3	US-09-864-761-20596	Sequence 20596, A
	25	132	4.4	3695	9	US-10-450-763-3692	Sequence 3692, Ap
	26	107.2	3.6	393	3	US-09-864-761-3830	Sequence 3830, Ap
	27	98.2	3.3	427	7	US-10-276-774-38	Sequence 38, Appl
	28	65.2	2.2	354	6	US-10-029-386-16110	Sequence 16110, A
	29	65.2	2.2	581	6	US-10-029-386-2410	Sequence 2410, Ap
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c	33	54.4	1.8	42360	7	US-10-367-094-148	Sequence 148, App
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	35	52.8	1.8	80077	5	US-10-087-192-1789	Sequence 1789, Ap
c	36	52.4	1.7	530	5	US-10-101-487-73	Sequence 73, Appl
c	37	52.4	1.7	530	9	US-10-939-988-73	Sequence 73, Appl
	38	52.4	1.7	554	5	US-10-101-487-69	Sequence 69, Appl
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	40	52.4	1.7	554	9	US-10-939-988-69	Sequence 69, Appl
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	42	52.4	1.7	591	9	US-10-450-763-6325	Sequence 6325, Ap
	43	52.4	1.7	591	9	US-10-450-763-6510	Sequence 6510, Ap
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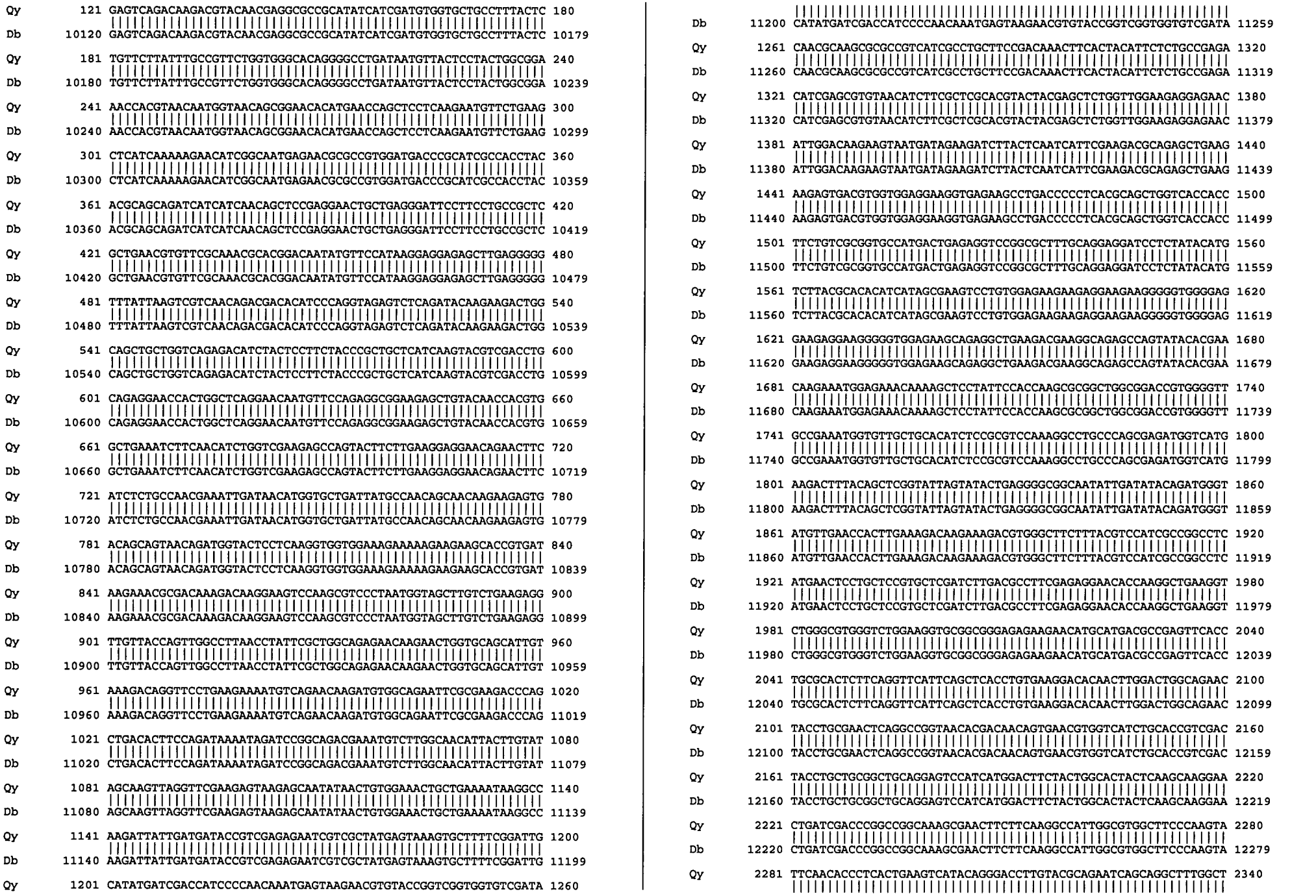
ALIGNMENTS

RESULT 1
US-10-668-767-127
; Sequence 127, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 15387
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15384)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-Hv7
US-10-668-767-127

Query Match 100.0%; Score 3001; DB 7; Length 15387;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
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Qy 121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
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Db 10480 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 10539
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Db 10540 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 10599
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Db 10600 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 10659
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Db 10660 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 10719
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Db 10720 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 10779
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Qy 961 AAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACCCAG 1020
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Db 11440 AAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACCACC 11499
Qy 1501 TTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGATCCTCTATACATG 1560
Db 11500 TTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGATCCTCTATACATG 11559
Qy 1561 TCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAG 1620
Db 11560 TCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAG 11619
Qy 1621 GAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAA 1680
Db 11620 GAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAA 11679
Qy 1681 CAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGTGGGGTT 1740
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Qy       2461 GACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGC 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12640 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 12699

Qy       2701 AGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGC 2760
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US-10-668-767-145
; Sequence 145, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
;   LENGTH: 15303
;   TYPE: DNA
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(15300)
;   OTHER INFORMATION:
;   FEATURE:
;   OTHER INFORMATION: pXL-Hv6
US-10-668-767-145

  Query Match             99.8%;  Score 2996.2;  DB 7;  Length 15303;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2998;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Db       9976 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 10035

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
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Db      10036 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 10095

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Db      10456 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 10515

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Db      10576 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 10635

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10636 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 10695

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Db      10696 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 10755

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Qy       1561 TCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAG 1620

Db      11476 TCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAG 11535

Qy       1621 GAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAA 1680

Db      11536 GAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAA 11595

Qy       1681 CAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGTGGGGTT 1740

Db      11596 CAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGTGGGGTT 11655

Qy       1741 GCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAGATGGTCATG 1800

Db      11656 GCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAGATGGTCATG 11715

Qy       1801 AAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAGATGGGT 1860

Db      11716 AAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAGATGGGT 11775

Qy       1861 ATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTC 1920

Db      11776 ATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTC 11835

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Db      11836 ATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGT 11895

Qy       1981 CTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACC 2040

Db      11896 CTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACC 11955

Qy       2041 TGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAAC 2100

Db      11956 TGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAAC 12015

Qy       2101 TACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGAC 2160

Db      12016 TACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGAC 12075

Qy       2161 TACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAA 2220

Db      12076 TACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAA 12135

Qy       2221 CTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTA 2280

Db      12136 CTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTA 12195

Qy       2281 TTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCT 2340

Db      12196 TTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCT 12255

Qy       2341 CACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGAC 2400

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Qy       2401 AAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAG 2460

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Qy       2461 GACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGC 2520

Db      12376 GACATGATCACCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGC 12435

Qy       2521 AAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATAC 2580

Db      12436 AAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATAC 12495

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Db      12496 TTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGAT 12555

Qy       2641 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 2700

Db      12556 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 12615

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Db      12616 AGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGC 12675

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Db      12856 GAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAAT 12915

Qy       3001 A 3001

Db      12916 A 12916
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RESULT 3
US-10-668-767-1
; Sequence 1, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 15679
;   TYPE: DNA
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (251)..(15676)
;   OTHER INFORMATION:
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5515)
;   OTHER INFORMATION: n = c or g
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (13000)
;   OTHER INFORMATION: n = a or t
US-10-668-767-1

  Query Match             97.2%;  Score 2917.4;  DB 7;  Length 15679;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches 2964;  Conservative    0;  Mismatches   37;  Indels   15;  Gaps    1;

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Db      10277 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 10336

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      10337 AAAATGGAACAATGCATGCCGACGTTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 10396

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db      10397 GAGTCAGACAAGACGTACAACGAAGCGCCGCATATCATCGATGTGGTGTTGCCTTTACTC 10456

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
              |||||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db      10457 TGTTCTTACTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTCACTCCTACTGGCGGA 10516

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10517 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 10576

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      10577 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATAGCCACCTAC 10636

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
              || |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db      10637 ACCCAGCAGATCATCATCAACAGCTCCGAGGAGTTGCTGAGGGATTCCTTCCTGCCGCTC 10696

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||| |||
Db      10697 GCTGAACGTGTTCGCAAGCGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGAGGG 10756

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
              |||||||||||||||||||||||||||||| || |||||||| ||||||||||||||||||
Db      10757 TTTATTAAGTCGTCAACAGACGACACATCTCAAGTAGAGTCACAGATACAAGAAGACTGG 10816

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db      10817 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTACTCATCAAGTACGTCGACCTG 10876

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10877 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 10936

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
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Db      10937 GCCGAAATCTTCAACATATGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 10996

Qy        721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      10997 ATCTCTGCCAACGAGATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 11056

Qy        781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 840
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      11057 ACAGCAGTAACAGATGGTACTCCTCAAGGCGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 11116

Qy        841 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 900
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Db      11117 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 11176

Qy        901 TTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 960
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Db      11177 TTGCTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 11236

Qy        961 AAAGACAGGTTCCTG----------------AAGAAAATGTCAGAACAAGATGTGGCAGAA 1005
              |||||||||||||||                ||||||||||||||||||||||||||||||
Db      11237 AAAGACAGGTTCCTGAAGGTAGGGACCCTCAAGAAAATGTCAGAACAAGATGTGGCAGAA 11296

Qy       1006 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11297 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 11356

Qy       1066 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 1125
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Db      11357 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 11416

Qy       1126 GCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAA 1185
              |||||||||| |||||||||||||||||||| || || || ||||||||||||||||||
Db      11417 GCTGAAAATAAAGCCAAGATTATTGATGATACTGTTGAAAGGATCGTCGCTATGAGTAAA 11476

Qy       1186 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11477 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 11536

Qy       1246 TCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTA 1305
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Db      11537 TCGGTGGTGTCCATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTA 11596

Qy       1306 CATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 1365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11597 CATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 11656

Qy       1366 TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAA 1425
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      11657 TTGGAAGAGGAGAACATTAGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAA 11716

Qy       1426 GACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACG 1485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11717 GACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACG 11776
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Qy       1486 CAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAG 1545
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db      11777 CAGCTGGTCACCACCTCCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAG 11836

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Db      11837 GATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAA 11896

Qy       1606 GAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGA 1665
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Db      11897 GAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGA 11956

Qy       1666 GCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTG 1725
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Qy       1726 GCGGACCGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCC 1785
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Db      12017 GCGGACCGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCC 12076

Qy       1786 AGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATT 1845
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Db      12077 AGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATT 12136

Qy       1846 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACG 1905
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12137 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACG 12196

Qy       1906 TCCATCGCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAAC 1965
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Db      12197 TCCATCGCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAAC 12256

Qy       1966 ACCAAGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCAT 2025
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Db      12257 ACCAAGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCAT 12316

Qy       2026 GACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 2085
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Db      12317 GACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 12376

Qy       2086 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTC 2145
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Db      12377 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTC 12436

Qy       2146 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 2205
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Qy       2206 TACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGC 2265
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Qy       2326 CAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTC 2385
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Qy       2566 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGC 2625
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Db      12857 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGC 12916

Qy       2626 TTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAA 2685
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Db      12917 TTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAA 12976

Qy       2686 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAG 2745
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Db      12977 ATGGAACAACAGAAGAGTTATACNCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAG 13036

Qy       2746 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 2805
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Db      13037 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 13096

Qy       2806 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 2865
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Db      13097 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 13156

Qy       2866 GAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCA 2925
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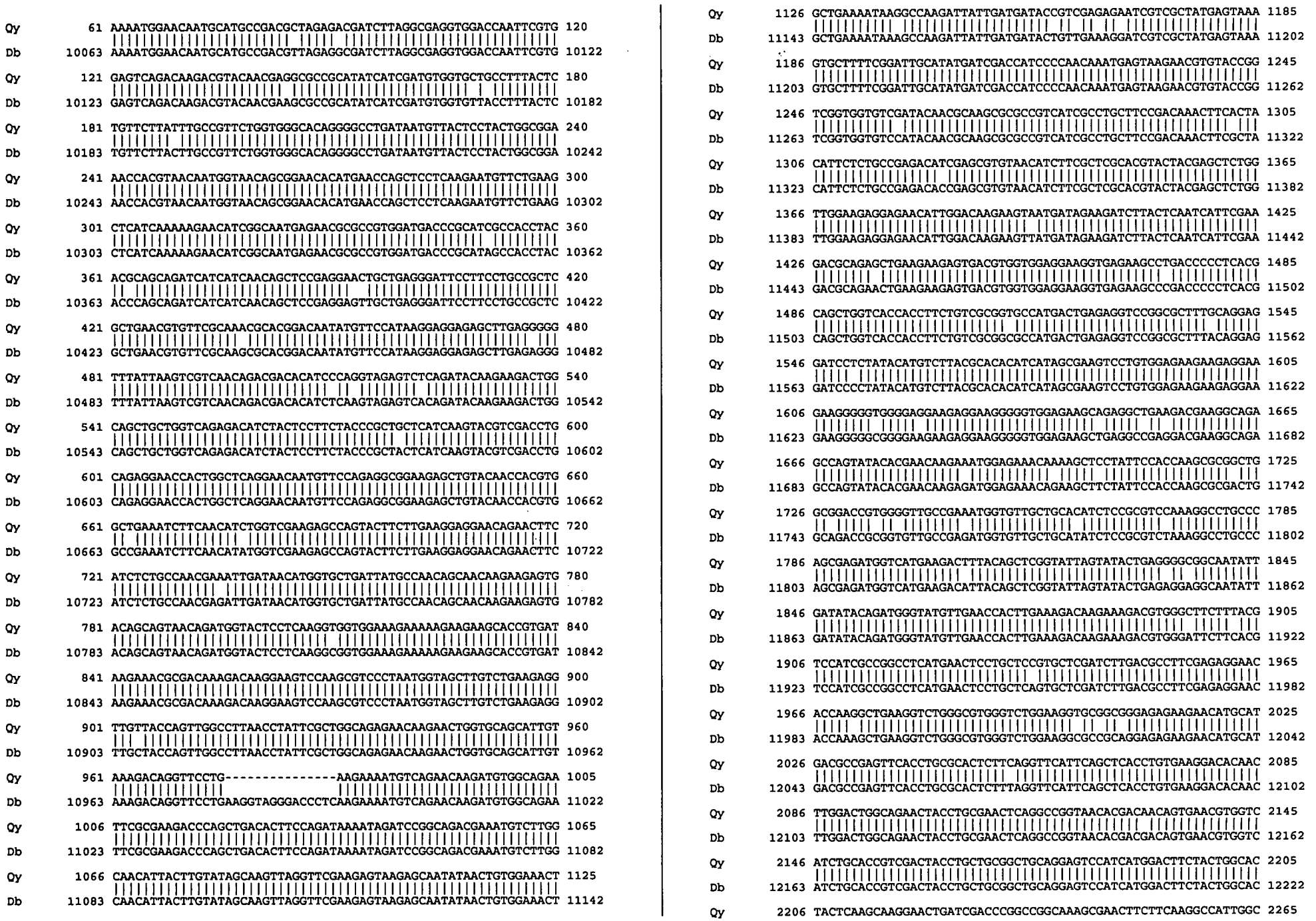
Qy       2926 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAG 2985
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Db      13217 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAG 13276

Qy       2986 ATCAAGGAGTCTAATA 3001
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Db      13277 ATCAAGGAGTCTAATA 13292
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RESULT 4
US-10-668-767-129
; Sequence 129, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 15405
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15402)
; OTHER INFORMATION:
; FEATURE:
; OTHER INFORMATION: pXL-Hv2
US-10-668-767-129

Query Match 94.8%; Score 2846.4; DB 7; Length 15405;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2920; Conservative 0; Mismatches 81; Indels 15; Gaps 1;

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Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10003 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 10062
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Db      12223 TACTCTAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAATTTCTTCAAGGCCATTGGC 12282

Qy       2266 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAAT 2325

Db      12283 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACTCAGAAC 12342

Qy       2326 CAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTC 2385

Db      12343 CAGCAGGCTTTAGCTCACTCTAGGTTATGGGACGCTGTCGGTGGTTTCTTGTTCCTATTC 12402

Qy       2386 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 2445

Db      12403 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 12462

Qy       2446 CTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 2505

Db      12463 CTCAATCTGCAGAAGGACATGATCACCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 12522

Qy       2506 AATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAA 2565

Db      12523 AATGGTACAATCGGCAAGCAAATGGTGGACACTCTAGTAGAATCGGCCTCCAACGTGGAA 12582

Qy       2566 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGC 2625

Db      12583 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACTTCCAGCGCCAGC 12642

Qy       2626 TTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAA 2685

Db      12643 TTCCAAGAGATAGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAG 12702

Qy       2686 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAG 2745

Db      12703 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCTTAGCTTGCTGCGAG 12762

Qy       2746 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 2805

Db      12763 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 12822

Qy       2806 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 2865

Db      12823 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 12882

Qy       2866 GAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCA 2925

Db      12883 GAGCCTAGATTGGCTCGTTTCCTGGAGACGGCGGGTTCAGTCCTGAACTACTTCGAACCA 12942

Qy       2926 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAG 2985

Db      12943 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCTAAGCGCATCGAGCGAGTCTACTTCGAG 13002

Qy       2986 ATCAAGGAGTCTAATA 3001

Db      13003 ATCAAGGAGTCTAATA 13018
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RESULT 5
US-10-668-767-143
; Sequence 143, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
;   LENGTH: 15429
;   TYPE: DNA
;   ORGANISM: Heliothis virescens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(15429)
;   OTHER INFORMATION:
;   FEATURE:
;   OTHER INFORMATION: pXL-Hv3
US-10-668-767-143

  Query Match           94.8%;  Score 2844.8;  DB 7;  Length 15429;
  Best Local Similarity  96.8%;  Pred. No. 0;
  Matches 2919;  Conservative    0;  Mismatches   82;  Indels   15;  Gaps    1;

Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60

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Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120

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Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180

Db      10147 GAGTCAGACAAGACGTACAACGAAGCGCCGCATATCATCGATGTGGTGTTGCCTTTACTC 10206

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240

Db      10207 TGTTCTTACTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 10266

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300

Db      10267 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 10326

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360

Db      10327 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATAGCCACCTAC 10386

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420

Db      10387 ACCCAGCAGATCATCATCAACAGCTCCGAGGAGTTGCTGAGGGATTCCTTCCTGCCGCTC 10446

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480

Db      10447 GCTGAACGTGTTCGCAAGCGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGAGGG 10506

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540

Db      10507 TTTATTAAGTCGTCAACAGACGACACATCTCAAGTAGAGTCACAGATACAAGAAGACTGG 10566

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600

Db      10567 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTACTCATCAAGTACGTCGACCTG 10626

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660

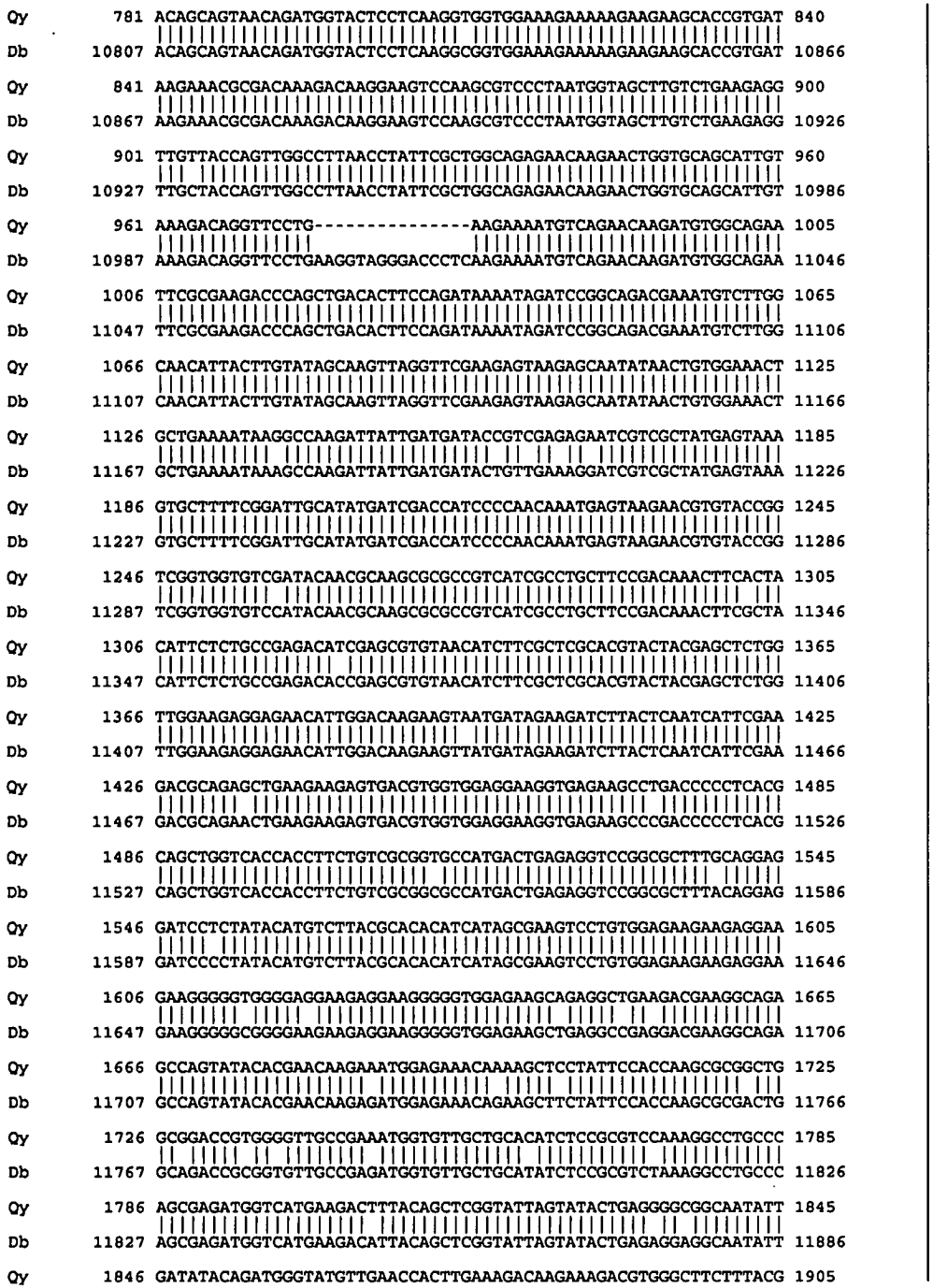
Db      10627 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 10686

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720

Db      10687 GCCGAAATCTTCAACATATGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 10746

Qy        721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780

Db      10747 ATCTCTGCCAACGAGATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 10806
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Qy 781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 840
Db 10807 ACAGCAGTAACAGATGGTACTCCTCAAGGCGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 10866
Qy 841 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 900
Db 10867 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 10926
Qy 901 TTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 960
Db 10927 TTGCTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 10986
Qy 961 AAAGACAGGTTCCTG----------AAGAAAATGTCAGAACAAGATGTGGCAGAA 1005
Db 10987 AAAGACAGGTTCCTGAAGGTAGGGACCCTCAAGAAAATGTCAGAACAAGATGTGGCAGAA 11046
Qy 1006 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 1065
Db 11047 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 11106
Qy 1066 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 1125
Db 11107 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 11166
Qy 1126 GCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAA 1185
Db 11167 GCTGAAAATAAAGCCAAGATTATTGATGATACTGTTGAAAGGATCGTCGCTATGAGTAAA 11226
Qy 1186 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 1245
Db 11227 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 11286
Qy 1246 TCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTA 1305
Db 11287 TCGGTGGTGTCCATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCGCTA 11346
Qy 1306 CATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 1365
Db 11347 CATTCTCTGCCGAGACACCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 11406
Qy 1366 TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAA 1425
Db 11407 TTGGAAGAGGAGAACATTGGACAAGAAGTTATGATAGAAGATCTTACTCAATCATTCGAA 11466
Qy 1426 GACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACG 1485
Db 11467 GACGCAGAACTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCCGACCCCCTCACG 11526
Qy 1486 CAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAG 1545
Db 11527 CAGCTGGTCACCACCTTCTGTCGCGGCGCCATGACTGAGAGGTCCGGCGCTTTACAGGAG 11586
Qy 1546 GATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAA 1605
Db 11587 GATCCCCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAA 11646
Qy 1606 GAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGA 1665
Db 11647 GAAGGGGGCGGGGAAGAAGAGGAAGGGGGTGGAGAAGCTGAGGCCGAGGACGAAGGCAGA 11706
Qy 1666 GCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTG 1725
Db 11707 GCCAGTATACACGAACAAGAGATGGAGAAACAGAAGCTTCTATTCCACCAAGCGCGACTG 11766
Qy 1726 GCGGACCGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCC 1785
Db 11767 GCAGACCGCGGTGTTGCCGAGATGGTGTTGCTGCATATCTCCGCGTCTAAAGGCCTGCCC 11826
Qy 1786 AGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATT 1845
Db 11827 AGCGAGATGGTCATGAAGACATTACAGCTCGGTATTAGTATACTGAGAGGAGGCAATATT 11886
Qy 1846 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACG 1905
Db 11887 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGATTCTTCACG 11946
Qy 1906 TCCATCGCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAAC 1965
Db 11947 TCCATCGCCGGCCTCATGAACTCCTGCTCAGTGCTCGATCTTGACGCCTTCGAGAGGAAC 12006
Qy 1966 ACCAAGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCAT 2025
Db 12007 ACCAAAGCTGAAGGTCTGGGCGTGGGTCTGGAAGGCGCCGCAGGAGAGAAGAACATGCAT 12066
Qy 2026 GACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 2085
Db 12067 GACGCCGAGTTCACCTGCGCACTCTTTAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 12126
Qy 2086 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTC 2145
Db 12127 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGGCGGCAGTGAACGTGGTC 12186
Qy 2146 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 2205
Db 12187 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 12246
Qy 2206 TACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGC 2265
Db 12247 TACTCTAGCAAGGAACTGATCGACCCGGCCGGCAAGGCGAATTTCTTCAAGGCCATTGGC 12306
Qy 2266 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAAT 2325
Db 12307 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACTCAGAAC 12366
Qy 2326 CAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTC 2385
Db 12367 CAGCAGGCTTTAGCTCACTCTAGGTTATGGGACGCTGTCGGTGGTTTCTTGTTCCTATTC 12426
Qy 2386 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 2445
Db 12427 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 12486
Qy 2446 CTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 2505
Db 12487 CTCAATCTGCAGAAGGACATGATCACCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 12546
Qy 2506 AATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAA 2565
Db 12547 AATGGTACAATCGGCAAGCAAATGGTGGACACTCTAGTAGAATCGGCCTCCAACGTGGAA 12606
Qy 2566 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGC 2625
Db 12607 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACTTCCAGCGCCAGC 12666
Qy 2626 TTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAA 2685
Db 12667 TTCCAAGAGATAGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAG 12726
Qy 2686 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAG 2745
Db 12727 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCTTAGCTTGCTGCGAG 12786
Qy 2746 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 2805
Db 12787 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 12846
Qy 2806 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 2865
Db 12847 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 12906
Qy 2866 GAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCA 2925
Db 12907 GAGCCTAGATTGGCTCGTTTCCTGGAGACGGCGGGTTCAGTCCTGAACTACTTCGAACCA 12966
Qy 2926 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAG 2985

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Db      12967 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCTAAGCGCATCGAGCGAGTCTACTTCGAG 13026

Qy       2986 ATCAAGGAGTCTAATA 3001
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Db      13027 ATCAAGGAGTCTAATA 13042


RESULT 6
US-11-097-143-22562
; Sequence 22562, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22562
;   LENGTH: 15606
;   TYPE: DNA
;   ORGANISM: DROSOPHILA
US-11-097-143-22562

  Query Match             57.3%;  Score 1718.2;  DB 10;  Length 15606;
  Best Local Similarity   73.9%;  Pred. No. 0;
  Matches 2236;  Conservative    0;  Mismatches  753;  Indels   36;  Gaps    3;

Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
              |||| |||  |||| ||| | || || || || ||  |||| || || ||||| |||
Db       9922 CAGTACTCGCTGCTCAACCGTATTGCGGATCACTCACTGGAGGCGCAGGACATTATGGTC 9981

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
              || |||||    || ||||| |  |||||||| ||   | | |||||| ||||| || |||
Db       9982 AAGATGGAGAGCTGTATGCCAAATCTAGAGACCATTCTCGCCGAGGTCGACCAGTTTGTG 10041

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
              ||||| ||||||||  ||||| || |||||  |||||  |||||  ||| | |||||   | ||
Db      10042 GAGTCGGACAAGACATACAATGATGCGCCTCATATTATCGACGTGATCCTGCCGCTGCTT 10101

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
              ||  | ||| | ||||| |||||| | |||||  || ||||||||  | |||  ||  | ||
Db      10102 TGCGCCTATCTACCGTTTTGGTGGTCCCAGGGACCGGATAATGTCAGTCCCACCAGTGGC 10161

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
              ||||||||  || |||||  |||||  || |||||||| | | | ||      |||||  || ||
Db      10162 AACCACGTGACCATGGTCACAGCCGATCACATGAATCCGTTGCTGCGAAATGTGCTTAAA 10221

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
              | |||||  |||||||| |||||  || |||||  || ||||||||  |||||  |||  ||||
Db      10222 ATGATCAAGAAGAACATTGGCAACGATAACGCCCCTTGGATGACTCGCATTGCCGCCTAT 10281

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
              |||||||||||  |||||||| |  || |||||  |||||  | ||||  | |||  |||||||
Db      10282 ACGCAGCAGATTATCATCAATACGTCGGAGGAGCTGCTCAAGGATCCGTTCTTGCCGCTG 10341

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
              || || || ||    || ||||| || || ||| | || |||||||| ||| || | ||
Db      10342 GCGGAGCGGGTGAAGAAGCGCACTGAGAACATGCTGCACAAGGAGGACAGCATGCGAGGA 10401

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
              || || |||||| | || |||||||| || ||||| ||| | ||| | || || ||||||
Db      10402 TTCATCAAGTCGGCCACGGACGACACTTCGCAGGTGGAGACCCAGCTGCAGGAGGACTGG 10461

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
              | ||||| ||  |||||| |||||  ||||| ||| |||||||||||||||||| || |||
Db      10462 AATCTGCTAGTGCGAGACATATACTCGTTCTATCCCCTGCTCATCAAGTACGTGGATCTG 10521

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
              ||| | |||||||||||  | | ||||  | || ||||| || ||||| ||||||||  |||
Db      10522 CAGCGAAACCACTGGCTGAAGGACAACATACCGGAGGCCGAGGAGCTCTACAACCATGTG 10581

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
              || || |||||||| || ||||| ||||||||||||||| | |||||||| |||||||||
Db      10582 GCAGAGATCTTCAATATATGGTCTAAGAGCCAGTACTTCCTTAAGGAGGAGCAGAACTTC 10641

Qy        721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
              |||||||||||  || ||  || |||||||    |||| ||||||| ||||| || ||    |
Db      10642 ATCTCTGCCAATGAGATCGACAACATGGCCTTGATCATGCCAACTGCAACCAGGAGGTCG 10701

Qy        781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGG---TGGAAAGAAAAAGAAGAAGCACCGT 837
              |          || ||  | || ||   |||||     | |||||| |||||||||  || |
Db      10702 GCCATCTCGGAAGGTGCTCCTGCTGTGGGTGGCAAGGTAAAGAAGAAGAAGAAGAACAGG 10761

Qy        838 GATAAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAG 897
              || ||||| |||||||| |||||||| || || ||     || ||||| || || |||||
Db      10762 GACAAGAAGCGCGACAAGGACAAGGAGGTGCAGGCCAGTCTGATGGTGGCCTGCCTGAAA 10821

Qy        898 AGGTTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCAT 957
              |  |  |||| ||||| || || || ||||| ||  |||| || ||||||||||||||||
Db      10822 CGCCTCCTACCCGTTGGACTGAATCTGTTCGCGGGTCGAGAGCAGGAACTGGTGCAGCAC 10881

Qy        958 TGTAAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACC 1017
              || || ||  ||| ||||||||| ||| | ||  | ||||||    || |||||     | |
Db      10882 TGCAAGGATCGGTACCTGAAGAAGATGCCCGAGTACGATGTGATCGAGTTCGCCCGCAAC 10941

Qy       1018 CAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTACTTG 1077
              |||||||| || || |||||  | || |||  | |||||  ||||| |||||  |||||| |
Db      10942 CAGCTGACCCTGCCGGATAAGCTGGACCCGTCGGACGAGATGTCCTGGCAGCATTACCTT 11001

Qy       1078 TATAGCAAGTTAGGTTCGA--------------------AGAGTAAGAGCAATATAACT 1116
              ||     ||| | ||   ||                    ||     |   ||    | |
Db      11002 TACTCAAAGCTGGGCAAGACGGAGGAACCGGTGGACGAACAGGCGCTGGAGAAGGCCAAT 11061

Qy       1117 GTGGAAACTGCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCT 1176
              ||  |  |    || ||          | |  |  | || || || ||  | ||||| ||
Db      11062 GTTAACTCCAACGAGAAGGGCAAGGACAAAACCCAGGAGACAGTGGATCGCATCGTGGCG 11121

Qy       1177 ATGAGTAAAGTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAAC 1236
              |||    || || || || ||  |||| ||||||||||||||| |||||    ||| |||||
Db      11122 ATGGCCAAGGTTCTGTTTGGCCTGCACATGATCGACCATCCACAACAGCAGAGCAAGAAT 11181

Qy       1237 GTGTACCGGTCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAA 1296
              || ||| ||   || |||||||| ||| | |||||  |||||  |||||||| ||||||| ||
Db      11182 GTCTACAGGAGCGTTGTGTCGATCCAAAGGAAGCGTGCCGTAATCGCATGCTTCCGTCAG 11241

Qy       1297 ACTTCACTACATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTAC 1356
              || || || |||||||| || |||||||| || || ||||||||||| ||  ||||||||
Db      11242 ACATCGCTGCATTCTCTACCCAGACATCGGGCCTGCAACATCTTCGCACGATCGTACTAC 11301

Qy       1357 GAGCTCTGGTTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAA 1416
              ||||  ||| || | |||||||||| | || ||||| || ||| | |||||||| || ||
Db      11302 GAGCAGTGGCTGCAGGAGGAGAACGTGGGCCAAGAGGTGATGGTCGAAGATCTGACGCAG 11361

Qy       1417 TCATTCGAAGACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGAC 1476
              | ||||| ||| | |||      ||||  || |  | ||||   |     ||||| ||
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Db      11362 ACGTTCGAGGACTCCGAGAAATCCAAGAAGGAGGGCGAGGAGACGGACAGCAAGCCGGAT 11421

Qy       1477 CCCCTCACGCAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCT 1536

Db      11422 CCGCTAACCCAACTGGTTACCACTTTCTGCCGCGGCGCCATGACGGAACGCAGCGGTGCC 11481

Qy       1537 TTGCAGGAGGATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAA 1596

Db      11482 CTCCAGGAGGATCTGCTCTACATGTCCTATGCCCAGATCGCGGCCAAGTCCACGGGCAAG 11541

Qy       1597 GAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGAC 1656

Db      11542 GAGGAGGAGGAAGGCGGCGACGAGGAAGGCGGTGAGGGTGG------------CGAAGAG 11589

Qy       1657 GAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAA 1716

Db      11590 GGCGAAGGCACCAGCATCCATGAACAAGAGATGGAGAAGCAGAAGCTGCTCTTCCATCAG 11649

Qy       1717 GCGCGGCTGGCGGACCGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAA 1776

Db      11650 GCACGTCTCTCCAATCGTGGCGTTGCCGAAATGGTGCTGTTGCACATTTCCGCCTCCAAA 11709

Qy       1777 GGCCTGCCCAGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGC 1836

Db      11710 GGTATACCTTCGGAGATGGTAATGACGACACTCAATCTCGGCATCGCCATTTTGCGCGGC 11769

Qy       1837 GGCAATATTGATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGC 1896

Db      11770 GGCAACATCGACATCCAAATGGGCATGCTGAACCACTTGAAGGAAAAGAAGGACGTTGGC 11829

Qy       1897 TTCTTTACGTCCATCGCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTC 1956

Db      11830 TTCTTTACCTCCATCGCCGGACTGATGAACTCCTGCAGTGTACTGGACCTGGACGCCTTT 11889

Qy       1957 GAGAGGAACACCAAGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAG 2016

Db      11890 GAGCGAAACACCAAAGCAGAGGGTCTTGGTGTAGGTTCCGAAGGCGCCGCGGGCGAGAAG 11949

Qy       2017 AACATGCATGACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAA 2076

Db      11950 AACATGCACGACGCGGAGTTCACCTGTGCGCTGTTCCGGTTCATCCAGCTGACCTGCGAG 12009

Qy       2077 GGACACAACTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTG 2136

Db      12010 GGCCACAACTTGGAATGGCAAAACTATTTGAGGACCCAGGCGGGTAACACCACCACCGTG 12069

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Db      12190 GCCATCGAAGTGGCTAGCCAAGTATTTAACACCCTCACTGAAGTCATCCAGGGTCCGTGT 12249

Qy       2317 ACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTG 2376

Db      12250 ACCCTCAATCAGCAGGCCTTGGCACACTCGAGGTTGTGGGATGCAGTTGGTGGCTTCCTC 12309

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Qy       2437 AAGGAACTCCTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGA 2496

Db      12370 AAGGAACTGCTGAATCTGCAAAAGGACATGATCACCATGATGCTTTCCATGCTGGAAGGA 12429

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Qy       2617 AGCGCCAGCTTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTC 2676

Db      12550 TCGCCCAGCTTCCACGAAGTGGACATGAAGAACGAGGGTTGGGTGACCCCCAAAGACTTT 12609

Qy       2677 AAGGAGAAAATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCT 2736

Db      12610 AGGGAAAAGATGGAGCAATCCAAGAACTACACACCGGAAGAAATGGATTTCCTTTTGGCC 12669

Qy       2737 TGCTGCGAGACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCAC 2796

Db      12670 TGCTGCGAGCGCAACCACGAGGGCAAGATCGATTACCGGGCCTTCGTGGAGCACTTCCAC 12729

Qy       2797 GAGCCTGCCAAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACAT 2856

Db      12730 GAACCATCAAAGGAGATCGGTTTCAACCTGGCTGTGCTCCTGACCAACCTCAGCGAACAC 12789

Qy       2857 ATGCCGAACGAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTAC 2916

Db      12790 ATGCCAAACGAACCGCGCCTGGCGCGCTTCCTGGAGACCGCCGGCTCGGTGCTCAACTAC 12849

Qy       2917 TTCGAACCATTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTC 2976

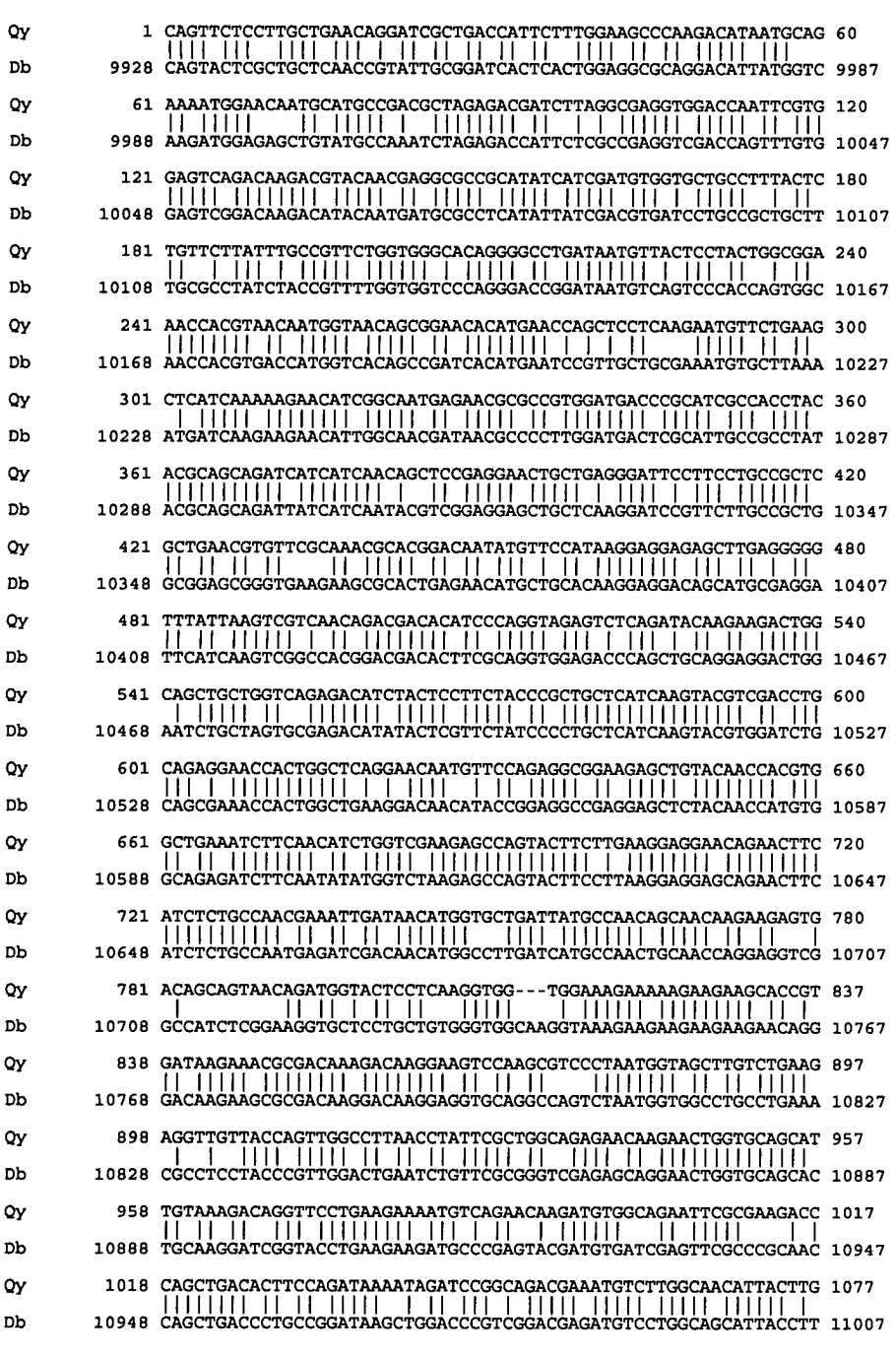
Db      12850 TTCGAGCCCTTCCTGGGCCGCATCGAGATTCTCGGCAGCTCCAAGCGCATCGAGCGCGTT 12909

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RESULT 7
US-10-668-767-9
; Sequence 9, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16363
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15890)..(15890)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(15327)
; OTHER INFORMATION:
US-10-668-767-9

Query Match 57.3%; Score 1718.2; DB 7; Length 16363;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 2236; Conservative 0; Mismatches 753; Indels 36; Gaps 3;


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Db 9928 CAGTACTCGCTGCTCAACCGTATTGCGGATCACTCACTGGAGGCGCAGGACATTATGGTC 9987
Qy 61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
Db 9988 AAGATGGAGAGCTGTATGCCAAATCTAGAGACCATTCTCGCCGAGGTCGACCAGTTTGTG 10047
Qy 121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
Db 10048 GAGTCGGACAAGACATACAATGATGCGCCTCATATTATCGACGTGATCCTGCCGCTGCTT 10107
Qy 181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
Db 10108 TGCGCCTATCTACCGTTTTGGTGGTCCCAGGGACCGGATAATGTCAGTCCCACCAGTGGC 10167
Qy 241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
Db 10168 AACCACGTGACCATGGTCACAGCCGATCACATGAATCCGTTGCTGCGAAATGTGCTTAAA 10227
Qy 301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
Db 10228 ATGATCAAGAAGAACATTGGCAACGATAACGCCCCTTGGATGACTCGCATTGCCGCCTAT 10287
Qy 361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
Db 10288 ACGCAGCAGATTATCATCAATACGTCGGAGGAGCTGCTCAAGGATCCGTTCTTGCCGCTG 10347
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Qy 661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
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Qy 781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGG---TGGAAAGAAAAAGAAGAAGCACCGT 837
Db 10708 GCCATCTCGGAAGGTGCTCCTGCTGTGGGTGGCAAGGTAAAGAAGAAGAAGAAGAACAGG 10767
Qy 838 GATAAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAG 897
Db 10768 GACAAGAAGCGCGACAAGGACAAGGAGGTGCAGGCCAGTCTAATGGTGGCCTGCCTGAAA 10827
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Db 10828 CGCCTCCTACCCGTTGGACTGAATCTGTTCGCGGGTCGAGAGCAGGAACTGGTGCAGCAC 10887
Qy 958 TGTAAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACC 1017
Db 10888 TGCAAGGATCGGTACCTGAAGAAGATGCCCGAGTACGATGTGATCGAGTTCGCCCGCAAC 10947
Qy 1018 CAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTACTTG 1077
Db 10948 CAGCTGACCCTGCCGGATAAGCTGGACCCGTCGGACGAGATGTCCTGGCAGCATTACCTT 11007
Qy 1078 TATAGCAAGTTAGGTTCGA----------AGAGTAAGAGCAATATAACT 1116
Db 11008 TACTCAAAGCTGGGCAAGACGGAGGAACCGGTGGACGAACAGGCGCTGGAGAAGGCCAAT 11067
Qy 1117 GTGGAAACTGCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCT 1176
Db 11068 GTTAACTCCAACGAGAAGGGCAAGGACAAAACCCAGGAGACAGTGGATCGCATCGTGGCG 11127
Qy 1177 ATGAGTAAAGTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAAC 1236
Db 11128 ATGGCCAAGGTTCTGTTTGGCCTGCACATGATCGACCATCCACAACAGCAGAGCAAGAAT 11187
Qy 1237 GTGTACCGGTCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAA 1296
Db 11188 GTCTACAGGAGCGTTGTGTCGATCCAAAGGAAGCGTGCCGTAATCGCATGCTTCCGTCAG 11247
Qy 1297 ACTTCACTACATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTAC 1356
Db 11248 ACATCGCTGCATTCTCTACCCAGACATCGGGCCTGCAACATCTTCGCACGATCGTACTAC 11307
Qy 1357 GAGCTCTGGTTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAA 1416
Db 11308 GAGCAGTGGCTGCAGGAGGAGAACGTGGGCCAAGAGGTGATGGTCGAAGATCTGACGCAG 11367
Qy 1417 TCATTCGAAGACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGAC 1476
Db 11368 ACGTTCGAGGACTCCGAGAAATCCAAGAAGGAGGGCGAGGAGACGGACAGCAAGCCGGAT 11427
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Db 11656 GCACGTCTCTCCAATCGTGGCGTTGCCGAAATGGTGCTGTTGCACGTTTCCGCCTCCAAA 11715
Qy 1777 GGCCTGCCCAGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGC 1836
Db 11716 GGTATACCTTCGGAGATGGTAATGACGACACTCAATCTCGGCATCGCCATTTTGCGCGGC 11775
Qy 1837 GGCAATATTGATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGC 1896
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Qy 1897 TTCTTTACGTCCATCGCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTC 1956
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Qy 2137 AACGTGGTCATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTC 2196

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Db      12076 AACGTGGTCATCTGTACTGTGGATTATTTGCTTCGTCTGCAAGAGTCCATCATGGACTTC 12135

Qy       2197 TACTGGCACTACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAG 2256

Db      12136 TACTGGCACTACTCCAGCAAAGAGATCATCGATCCCGCTGGAAAGGCCAACTTCTTCAAG 12195

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Qy       2317 ACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTG 2376

Db      12256 ACCCTCAATCAGCAGGCCTTGGCACACTCGAGGTTGTGGGATGCAGTTGGTGGCTTCCTC 12315

Qy       2377 TTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTG 2436

Db      12316 TTCCTGTTTTCCCACATGCAGGACAAGCTGTCAAAGCACTCCAGCCAAGTTGATCTGCTC 12375

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Db      12376 AAGGAACTGCTGAATCTGCAAAAGGACATGATCACCATGATGCTTTCCATGCTGGAAGGA 12435

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Db      12436 AATGTTGTTAACGGCACTATTGGCAAGCAGATGGTGGACACGCTGGTGGAGTCTGCCAGC 12495

Qy       2557 AACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCC 2616

Db      12496 AATGTGGAGCTGATTCTTAAGTACTTCGACATGTTCCTGAAGCTCGCCGACCTTATCGAA 12555

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; Sequence 7, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 15413
;   TYPE: DNA
;   ORGANISM: Peregrinus maidis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1264)
;   OTHER INFORMATION: n = a,c,g, or t
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (17)..(15397)
;   OTHER INFORMATION:
US-10-668-767-7

  Query Match           52.6%;  Score 1578.6;  DB 7;  Length 15413;
  Best Local Similarity  71.2%;  Pred. No. 0;
  Matches 2142;  Conservative    0;  Mismatches  829;  Indels   36;  Gaps    3;

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Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120

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Db      10133 GAGTCGGATAAAACCCATAACGATGCACCTCATATTATTGATGTGATAATGCCAATGCTA 10192

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240

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Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300

Db      10253 AATTATGTCACAACGGTGACGAGTGAACATATGAATCAACTTTTAAAGAATGTACTCAAA 10312

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360

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Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420

Db      10373 ACACAACAAATAATAATCAACTCTTCGGAGGAGTTGTTGAAAGATCCATTCCTCCCATTG 10432

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Db      10433 GCTGAAAGAGTGAAGAAACGGACTGATGCTATGTTTCATAAAGAGGAATCACTCAGGGGA 10492

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540

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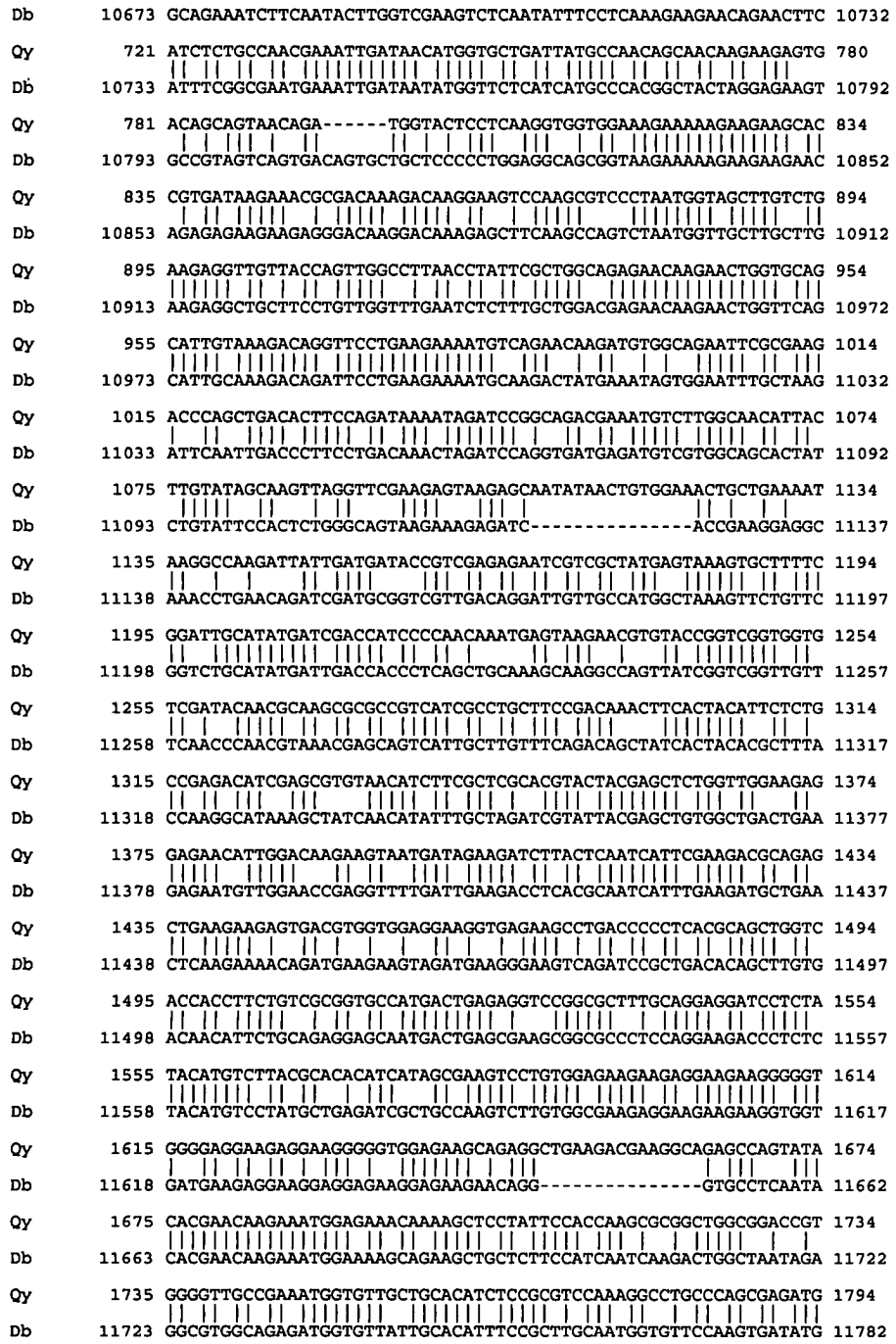
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Db      10553 CAACTTCTTGTGAGAGATATCTACTCATTCTATCCACTTCTCATCAAGTACGTTGACTTG 10612

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660

Db      10613 CAAAGGAATCATTGGTTGAGAAATAATATTTCTGAAGCTGAAGACTTGTATAATCATGTA 10672

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
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Db 10673 GCAGAAATCTTCAATACTTGGTCGAAGTCTCAATATTTCCTCAAAGAAGAACAGAACTTC 10732
Qy 721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
Db 10733 ATTTCGGCGAATGAAATTGATAATATGGTTCTCATCATGCCCACGGCTACTAGGAGAAGT 10792
Qy 781 ACAGCAGTAACAGA------TGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCAC 834
Db 10793 GCCGTAGTCAGTGACAGTGCTGCTCCCCCTGGAGGCAGCGGTAAGAAAAAGAAGAAGAAC 10852
Qy 835 CGTGATAAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTG 894
Db 10853 AGAGAGAAGAAGAGGGACAAGGACAAAGAGCTTCAAGCCAGTCTAATGGTTGCTTGCTTG 10912
Qy 895 AAGAGGTTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAG 954
Db 10913 AAGAGGCTGCTTCCTGTTGGTTTGAATCTCTTTGCTGGACGAGAACAAGAACTGGTTCAG 10972
Qy 955 CATTGTAAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAG 1014
Db 10973 CATTGCAAAGACAGATTCCTGAAGAAAATGCAAGACTATGAAATAGTGGAATTTGCTAAG 11032
Qy 1015 ACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTAC 1074
Db 11033 ATTCAATTGACCCTTCCTGACAAACTAGATCCAGGTGATGAGATGTCGTGGCAGCACTAT 11092
Qy 1075 TTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACTGCTGAAAAT 1134
Db 11093 CTGTATTCCACTCTGGGCAGTAAGAAAGAGATC--------------ACCGAAGGAGGC 11137
Qy 1135 AAGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAAGTGCTTTTC 1194
Db 11138 AAACCTGAACAGATCGATGCGGTCGTTGACAGGATTGTTGCCATGGCTAAAGTTCTGTTC 11197
Qy 1195 GGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGGTCGGTGGTG 1254
Db 11198 GGTCTGCATATGATTGACCACCCTCAGCTGCAAAGCAAGGCCAGTTATCGGTCGGTTGTT 11257
Qy 1255 TCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTACATTCTCTG 1314
Db 11258 TCAACCCAACGTAAACGAGCAGTCATTGCTTGTTTCAGACAGCTATCACTACACGCTTTA 11317
Qy 1315 CCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGGTTGGAAGAG 1374
Db 11318 CCAAGGCATAAAGCTATCAACATATTTGCTAGATCGTATTACGAGCTGTGGCTGACTGAA 11377
Qy 1375 GAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAAGACGCAGAG 1434
Db 11378 GAGAATGTTGGAACCGAGGTTTTGATTGAAGACCTCACGCAATCATTTGAAGATGCTGAA 11437
Qy 1435 CTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCAGCTGGTC 1494
Db 11438 CTCAAGAAAACAGATGAAGAAGTAGATGAAGGGAAGTCAGATCCGCTGACACAGCTTGTG 11497
Qy 1495 ACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGATCCTCTA 1554
Db 11498 ACAACATTCTGCAGAGGAGCAATGACTGAGCGAAGCGGCGCCCTCCAGGAAGACCCTCTC 11557
Qy 1555 TACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGT 1614
Db 11558 TACATGTCCTATGCTGAGATCGCTGCCAAGTCTTGTGGCGAAGAGGAAGAAGAAGGTGGT 11617
Qy 1615 GGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATA 1674
Db 11618 GATGAAGAGGAAGGAGGAGAAGGAGAAGAACAGG--------------GTGCCTCAATA 11662
Qy 1675 CACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGT 1734
Db 11663 CACGAACAAGAAATGGAAAAGCAGAAGCTGCTCTTCCATCAATCAAGACTGGCTAATAGA 11722
Qy 1735 GGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAGATG 1794
Db 11723 GGCGTGGCAGAGATGGTGTTATTGCACATTTCCGCTTGCAATGGTGTTCCAAGTGATATG 11782
Qy 1795 GTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAG 1854
Db 11783 GTGGAGAAAACGCTTCAACTTGGTATATCGATTCTTCGAGGTGGCAACATTGATATCCAA 11842
Qy 1855 ATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCC 1914
Db 11843 ATGGGAATGCTGAATCACCTAAAAGAAAAGAAAGATGTGGGATTTTTTACATCTATCGCT 11902
Qy 1915 GGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCT 1974
Db 11903 GGATTAATGAATTCCTGCAGTGTACTGGATTTGGACGCATTTGAGCGCAATACGAAGGCA 11962
Qy 1975 GAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAG 2034
Db 11963 GAGGGCTTGGGCGTGGGATCGGATGGCGCAGCTGGTGAGAAGAACATGCACGACGCTGAG 12022
Qy 2035 TTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGG 2094
Db 12023 TTCACCTGCACATTGTTCAGATTCATTCAATTGACATGTGAAGGTCACAATCTTGAATGG 12082
Qy 2095 CAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACC 2154
Db 12083 CAGAATTATTTGAGAACTCAAGCAGGAAACACTACAACCGTGAACGTTGTCATATGTACC 12142
Qy 2155 GTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGC 2214
Db 12143 GTAGATTATCTTCTGAGACTACAGGAATCAATCATGGACTTTTATTGGCATTATTCGAGC 12202
Qy 2215 AAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCC 2274
Db 12203 AAAGAATTGATTGACCCAGCAGGAAAAGCCAATTTTTTTAAAGCTATAGGAGTTGCTAGT 12262
Qy 2275 CAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCT 2334
Db 12263 CAGGTTTTCAACACATTGTCTGAGGTTATTCAAGGTGCTTGTACTCAGAACCAGCAAGCT 12322
Qy 2335 TTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATG 2394
Db 12323 TTGGCTCATTCCAAATTGTGGGACGCTGTCGGTGGTTTCCTATTTTTATTCTCTCATATG 12382
Qy 2395 CAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTG 2454
Db 12383 CAAGATAAGCTATCAAAGCATTCAAGTCAAGTCGACCTTCTCAAGGAACTGCTAAATCTA 12442
Qy 2455 CAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACA 2514
Db 12443 CAGAAAGACATGATCACCATGATGTTATCTATGCTTGAAGGAAATGTTGTAAATGGTACT 12502
Qy 2515 ATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTG 2574
Db 12503 ATTGGAAAACAGATGGTTGATACTTTGGTTGAATCTGCTTCAAATGTTGAGTTGATTCTG 12562
Qy 2575 AAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAG 2634
Db 12563 AAATATTTTGATATGTTCCTGAAACTAAAAGACATGACTGAAGCACCTAGCTTCTTGGAA 12622
Qy 2635 ATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAA 2694
Db 12623 ATCGATCCGAATCACGATGGTTGGGTTCTACCCAAAGATTTCAAAGAGAAAATGGAACAA 12682
Qy 2695 CAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCAC 2754
Db 12683 CAAAAGAGCTATACAACAGAAGAAATTAGCTTCATGCTGCAGTGTTGTGAAACTAATCAC 12742
Qy 2755 GACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATC 2814
Db 12743 GATGGAAAGGTTGATTACATTGGCTTCGTTGACAGATTCCATGAACCTTCCAAAGAAATC 12802
Qy 2815 GGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGA 2874
Db 12803 GGTTTCAACTTGGCTGTATTATTAACAAACCTATCTGAGCACATGCCGAATGAGCCCAGG 12862

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Qy       2875 TTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGC 2934
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Db      12863 TTGGCTAGATTTTTGGAAACTGCAGGCAGTGTACTAAATTACTTTGAACCATTCCTAGGA 12922

Qy       2935 CGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAG 2994
             ||||| || || |||||| ||    || || || ||  | || || || || |||||||||
Db      12923 CGTATTGAAATTATGGGCAGCAGTAAACGTATAGAAAGAGTGTATTTTGAAATCAAGGAG 12982

Qy       2995 TCTAATA 3001
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Db      12983 TCAAATA 12989


RESULT 9
US-10-668-767-5
; Sequence 5, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
;  APPLICANT: Caspar, Timothy
;  APPLICANT:  Cordova, Daniel
;  APPLICANT:  Gutteridge, Steven
;  APPLICANT:  Rauh, James
;  APPLICANT:  Smith, Rejane
;  APPLICANT:  Tao, Yong
;  APPLICANT:  Wu, Lihong
;  TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
;  FILE REFERENCE: BB1533 US NA
;  CURRENT APPLICATION NUMBER: US/10/668,767
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: 60/412,795
;  PRIOR FILING DATE: 2002-09-23
;  PRIOR APPLICATION NUMBER: 60/427,324
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 149
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 15315
;   TYPE: DNA
;   ORGANISM: Periplaneta americana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(15312)
;   OTHER INFORMATION:
US-10-668-767-5

  Query Match           49.6%;  Score 1489.6;  DB 7;  Length 15315;
  Best Local Similarity   69.3%;  Pred. No. 0;
  Matches 2083;  Conservative    0;  Mismatches  894;  Indels   27;  Gaps    3;

Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
              || |  ||  | || ||  |  | ||||||  ||| ||||||||| || || ||||||
Db       9967 CAATATTCGCTTCTTAATCGATTTGCTGACAGTTCATTGGAAGCTCAGGATATAATGTCT 10026

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
              | |||||||      |||||| || |||||| ||  | |||   || || |||||| || ||
Db      10027 AGAATGGAAGGCACTATGCCTACTCTAGAAACTGTATTAAATGAAGTTGACCAGTTTGTC 10086

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
              || |||||| || || ||     || || || || || || ||||||  |  | ||||||| |
Db      10087 GAATCAGAAAAAACATATGCTGATGCACCTCACATTATTGATGTTATTTTACCTTTATTG 10146

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
              ||||| || || |||| ||||||||||| || || |||||||||  |||   ||     ||
Db      10147 TGTTCATACTTACCGTACTGGTGGGCACAAGGTCCAGATAATGTTGCTCTGACCACAGGT 10206

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
              || || || |||||||| ||    |||||| ||||||    ||  | || ||||||| | |||
Db      10207 AATCATGTTACAATGGTGACCAGCGAACATATGAACTGTCTATTAAAAAATGTTTTAAAG 10266

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
               | || ||||| || || || ||||| || || || |||||||| |  || ||  | ||
Db      10267 TTAATAAAAAAAAATATTGGAAATGATAATGCCCCTTGGATGACACAAATAGCAGCTTAT 10326

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
              || || || || || || ||    || || ||| |  | |  ||| | || || || ||
Db      10327 ACACAACAAATAATTATTAATTCTTCAGAAGAATTATTAAAAGATCCATTTCTACCACTT 10386

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
              || ||||| |||    |||||| || || |  | | |||||| || ||     || || ||
Db      10387 GCAGAACGAGTTAAAAAACGTACAGAAACATTATACCATAAAGAAGAATCATTAAGAGGA 10446

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
              ||||| || || || || || || || ||||| | ||  | || |||||||||| |||
Db      10447 TTTATAAAATCATCTACTGATGATACGTCCCAAATCGAAGCACAAATACAAGAAGATTGG 10506

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
              ||  || | || || || || || | || || || || ||||| || ||||| || | |
Db      10507 CAATTGGTTGTTAGGGATATTTATGCTTTTTATCCACTCCTCATAAAATACGTGGATCCT 10566

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
              ||| | || |||||||| | || ||  | || | || ||||| | ||||| || ||
Db      10567 CAGCGCAATCACTGGCTACGTAATAACATATCAAATGCTGAAGATTTATACAATCATGTC 10626

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
              ||||||| || ||||| ||||| ||    || ||||| ||    || ||||| |||||
Db      10627 TCTGAAATATTTAACATTTGGTCCAAATCGCAATACTTTTTACGTGAAGAACAAAACTTT 10686

Qy        721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
              || ||||| || |||||||||||| | || |||||||||| ||||| | ||| |
Db      10687 ATATCTGCAAATGAAATTGATAACATGATACTTATTATGCCAACGGCAACTCGGAGATCG 10746

Qy        781 ACAGCAGTAACAGATGGTACTCCTCAAGG---TGGTGGAAAGAAAAAGAAGAAGCACCGT 837
              | |   || ||||   | |      |||      |||||||||||||| || ||| |
Db      10747 GCTGTTATATCAGAAACTTCGTTAGGAGGGTCATCTGGAAAGAAAAAGAAAAAACACAGG 10806

Qy        838 GATAAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAG 897
              ||||| ||||| |||||||| || ||| | ||||| ||  | ||||| |||||||| ||
Db      10807 GATAAAAAAACGTGACAAAGAAAAAGAAATTCAAGCTTCATTGATGGTGGCTTGTCTTAAA 10866

Qy        898 AGGTTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCAT 957
              | ||  | |||||||| | ||  | ||||| || |||||||||||| | || || |||
Db      10867 CGATTACTGCCAGTTGGTTTAAATTTGTTCGCGGGAAGAGAACAAGAATTAGTTCAACAT 10926

Qy        958 TGTAAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACC 1017
              || || || || ||| | || |||||| |||| | |||||| | |||| |  || |
Db      10927 TGCAAGGATAGATTCTTAAAAAAAATGCCAGATTATGATGTGATACAATTTGTCAAAATT 10986

Qy       1018 CAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTACTTG 1077
              || ||||| | || |||||| |||| || || |||||||||| ||||| || || ||
Db      10987 CAATTGACATTACCCGATAAATTAGACCCAGCTGACGAAATGTCCTGGCAGCACTATTTA 11046

Qy       1078 TATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACTGCTGAAAATAAG 1137
              ||  ||||||||||     || |                  | || | |||||| |||
Db      11047 TACTCCAAGTTAGGAAGCAAAA------------------AAGGAAATACTGAAATTAAA 11088

Qy       1138 GCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAAGTGCTTTTCGGA 1197
              | |   | || ||    |  || ||||| |||||||||  |||||| ||||  |||
Db      11089 CCACAACAAGTCGACGAGGTAGCGGATAGAATTGTCGCTATGGCTAAAGTTCTTTATGGA 11148

Qy       1198 TTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGGTCGGTGGTGTCG 1257
              |||||||||| || ||||| || |     || |||       || || || || || |||
Db      11149 TTGCATATGATTGATCATCCTCAGCTTCAAAGCAAGGCGACTTATCGATCTGTTGTATCG 11208

Qy       1258 ATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTACATTCTCTGCCG 1317
              |  ||||| ||| | ||||| || || |||||||||  ||||| || || || |  | |
Db      11209 ACGCAACGTAAGAGAGCCGTAATTGCTTGTTTCCGACAACTCTCACTCCACGCTTTGACC 11268

Qy       1318 AGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGGTTGGAAGAGGAG 1377
              ||||| || ||    || || |||| |||  |||  ||||| || ||| |  |||| ||
Db      11269 AGACACCGTGCAGTAAATATATTCGTTCGTTCGTTTTACGAACTTTGGCTTCAAGATGAA 11328

Qy       1378 AACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAAGACGCAGAGCTG 1437
              || |||||||||||||| ||||| |||||||| || |||||||| ||||| || || ||
Db      11329 AATATTGGACAAGAAGTTATGATTGAAGATCTCACACAATCATTTGAAGAAGCGGAACTT 11388

Qy       1438 AAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACC 1497
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Db      11389 AAAAAACGTGACAAGGAAGAAGAAGAAGGAATGGCAGACCCATTAAATCAAATGGTTACA 11448

Qy       1498 ACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGATCCTCTATAC 1557

Db      11449 ACTTTCTGCCGAGGAGCCATGACTGAAAGAAGTGGTGCTTTACAAGAGGACCCTCTTTAC 11508

Qy       1558 ATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGG 1617

Db      11509 ATGTCTTATGCTGATATTTTGGCTAAGTCCTGCGGCGAAGAAGAAGAAGAA------GGT 11562

Qy       1618 GAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACAC 1677

Db      11563 AATAACGAAGAAGAAGGTTCAAATGGTAACGGAGATGAAGAAGGCGGTGCTTCTATCCAT 11622

Qy       1678 GAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGTGGG 1737

Db      11623 GAGCAAGAAATGGAAAAACAAAAGCTTTTGTTTCACCAAGCTCGATTGGCTAACCGTGGT 11682

Qy       1738 GTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAGATGGTC 1797

Db      11683 GTCGCAGAAATGGTTTTATTACACATATCAGCTTGCAAAGGTATACCCAGTGAAATGGTT 11742

Qy       1798 ATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAGATG 1857

Db      11743 ATGAAAACGCTTCAATTGGGAATCGCAGTTCTCCGTGGTGGTAATTTAGACATTCAAATG 11802

Qy       1858 GGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGC 1917

Db      11803 GGAATGTTAAATCATTTAAAAGAAAAGAAAGATGTTGGATTTTTTACTTCAGTTGCTGGT 11862

Qy       1918 CTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAA 1977

Db      11863 TTAATGAACTCATGCAGCGTTCTTGATTTGGACGCTTTTGAGAGAAATACCAAAGCAGAA 11922

Qy       1978 GGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTC 2037

Db      11923 GGTTTGGGAGTAGGATCGGAAGGTGCTGCTGGTGAAAAAAATATGCATGATGCAGAGTTC 11982

Qy       2038 ACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAG 2097

Db      11983 ACGTGTACTCTATTTAGATTTATTCAATTAACTTGTGAAGGACATAATTTAGAATGGCAA 12042

Qy       2098 AACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTC 2157

Db      12043 AATTGTTTAAGAACCCAAGCAGGAAATACCACAACTGTAAATGTTGCAATTTGTACAGTG 12102

Qy       2158 GACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAG 2217

Db      12103 GATTATTTACTTAGGCTTCAGGAATCTATAATGGATTTTTATTGGCATTATTCGAGTAAA 12162

Qy       2218 GAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAA 2277

Db      12163 GAGTTAATCGATCCAGCAGGAAAAGCAAATTTCTTCAAAGCAATCGGTGTCGCCAGCCAA 12222

Qy       2278 GTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTG 2337

Db      12223 GTGTTTAATACACTATCCGAAGTAATTCAAGGACCATGTACTCAAAATCAACAGGCCCTA 12282

Qy       2338 GCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAG 2397

Db      12283 GCTCATTCCAGGTTGTGGGATGCTGTTGGAGGGTTTTTGTTTTTATTTTCACACATGCAA 12342

Qy       2398 GACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAG 2457

Db      12343 GATAAATTATCGAAACATTCTAGTCAAGTAGATTTACTAAAAGAACTTTTGAATTTACAA 12402

Qy       2458 AAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATC 2517

Db      12403 AAAGATATGATTACGATGATGCTGTCAATGTTAGAAGGAAATGTTGTTAATGGAACAATT 12462

Qy       2518 GGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAA 2577

Db      12463 GGTAAACAAATGGTTGACACTCTAGTAGAGTCGGCGTCAAATGTCGAGTTGATATTGAAA 12522

Qy       2578 TACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATT 2637

Db      12523 TATTTTGACATGTTCCTGAAACTTAAAGATTTAACGAGTTCAACAAGCTTTACGGAAATT 12582

Qy       2638 GATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAG 2697

Db      12583 GACCCCAATAACGATGGTTGGGTACATCCCAAAGATTTTAAAGAAAAAATGGAACAACAA 12642

Qy       2698 AAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGAC 2757

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Qy       2758 GGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGG 2817

Db      12703 GGAAAAATTGATTACATTGGCTTCACTGATCAATTCCACGAGCCATCTAAAGAAATTGGT 12762

Qy       2818 TTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTG 2877

Db      12763 TTTAATCTTGCCGTATTATTAACTAATCTATCAGAACATATGCCAAATGAACCTAGATTA 12822

Qy       2878 GCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGT 2937

Db      12823 ACAAGATTCCTAGAAACAGCTAGCAGTGTTTTGAACTATTTCCAACCGTTCCTGGGTAGA 12882

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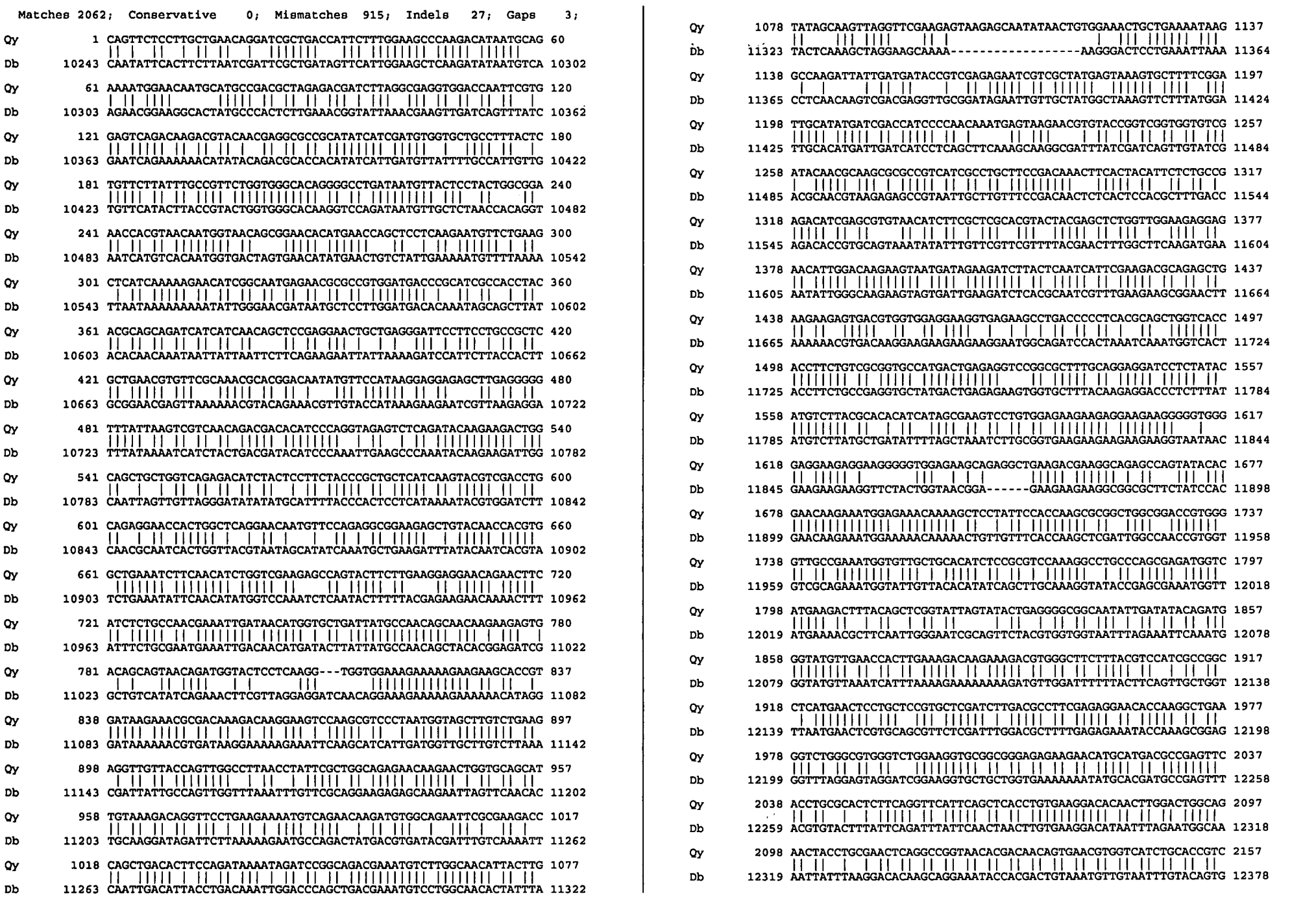
Db      12883 ATTGAAATTCTTGGAGGAAGTAAGCGTATAGAACGGGTGTACTTTGAAATTAAAGAATCA 12942

Qy       2998 AATA 3001

Db      12943 AATA 12946
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RESULT 10
US-10-668-767-3
; Sequence 3, Application US/10668767
; Publication No. US20040171114A1
; GENERAL INFORMATION:
; APPLICANT: Caspar, Timothy
; APPLICANT: Cordova, Daniel
; APPLICANT: Gutteridge, Steven
; APPLICANT: Rauh, James
; APPLICANT: Smith, Rejane
; APPLICANT: Tao, Yong
; APPLICANT: Wu, Lihong
; TITLE OF INVENTION: Isolation and Uses of Ryanodine Receptors
; FILE REFERENCE: BB1533 US NA
; CURRENT APPLICATION NUMBER: US/10/668,767
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/412,795
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/427,324
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 15845
; TYPE: DNA
; ORGANISM: Myzus persicae
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (36)..(37)
; OTHER INFORMATION: n = A, C, G, or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5807)
; OTHER INFORMATION: n = a or t
US-10-668-767-3

Query Match 48.5%; Score 1456; DB 7; Length 15845;
Best Local Similarity 68.6%; Pred. No. 0;


Matches 2062; Conservative 0; Mismatches 915; Indels 27; Gaps 3;
Qy 1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
Db 10243 CAATATTCACTTCTTAATCGATTCGCTGATAGTTCATTGGAAGCTCAAGATATAATGTCA 10302
Qy 61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
Db 10303 AGAACGGAAGGCACTATGCCCACTCTTGAAACGGTATTAAACGAAGTTGATCAGTTTATC 10362
Qy 121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
Db 10363 GAATCAGAAAAAACATATACAGACGCACCACATATCATTGATGTTATTTTGCCATTGTTG 10422
Qy 181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
Db 10423 TGTTCATACTTACCGTACTGGTGGGCACAAGGTCCAGATAATGTTGCTCTAACCACAGGT 10482
Qy 241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
Db 10483 AATCATGTCACAATGGTGACTAGTGAACATATGAACTGTCTATTGAAAAATGTTTTAAAA 10542
Qy 301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
Db 10543 TTAATAAAAAAAAATATTGGGAACGATAATGCTCCTTGGATGACACAAATAGCAGCTTAT 10602
Qy 361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
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Qy 421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
Db 10663 GCGGAACGAGTTAAAAAACGTACAGAAACGTTGTACCATAAAGAAGAATCGTTAAGAGGA 10722
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Db 10723 TTTATAAAATCATCTACTGACGATACATCCCAAATTGAAGCCCAAATACAAGAAGATTGG 10782
Qy 541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
Db 10783 CAATTAGTTGTTAGGGATATATATGCATTTTACCCACTCCTCATAAAATACGTGGATCTT 10842
Qy 601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
Db 10843 CAACGCAATCACTGGTTACGTAATAGCATATCAAATGCTGAAGATTTATACAATCACGTA 10902
Qy 661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
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Qy 721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
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Qy 781 ACAGCAGTAACAGATGGTACTCCTCAAGG---TGGTGGAAAGAAAAAGAAGAAGCACCGT 837
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Qy 958 TGTAAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACC 1017
Db 11203 TGCAAGGATAGATTCTTAAAAAGAATGCCAGACTATGACGTGATACGATTTGTCAAAATT 11262
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Qy 1078 TATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACTGCTGAAAATAAG 1137
Db 11323 TACTCAAAGCTAGGAAGCAAAA----------AAGGGACTCCTGAAATTAAA 11364
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Qy 1978 GGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTC 2037
Db 12199 GGTTTAGGAGTAGGATCGGAAGGTGCTGCTGGTGAAAAAAATATGCACGATGCCGAGTTT 12258
Qy 2038 ACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAG 2097
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Qy 2098 AACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTC 2157
Db 12319 AATTATTTAAGGACACAAGCAGGAAATACCACGACTGTAAATGTTGTAATTTGTACAGTG 12378

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Qy       2158 GACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAG 2217
Db      12379 GATTATTTACTTAGGCTTCAGGAATCTATAATGGATTTTTATTGGCATTATTCGAGCAAA 12438

Qy       2218 GAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAA 2277
Db      12439 GAGCTAATTGACCCAGCAGGAAAAGCAAATTTCTTCAAAGCAATCGGTGTAGCCAGCCTA 12498

Qy       2278 GTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTG 2337
Db      12499 GTTTTTAATACGCTATCCGAAGTAATTCAAGGACCGTGTACTCAAAATCAACAGGCCCTT 12558

Qy       2338 GCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAG 2397
Db      12559 GCTCATTCCAGATTGTGGGATGCCGTTGGAGGGTTTTTGTTTTTGTTTTCACACATGCAA 12618

Qy       2398 GACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAG 2457
Db      12619 GATAAATTATCGAAACATTCTAGTCAAGTAGATTTATTGAAAGAACTTTTAAATTTACAA 12678

Qy       2458 AAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATC 2517
Db      12679 AAAGATATGATTACGATGATGCTGTCCATGTTAGAAGGGAACGTTGTTAATGGAACAATT 12738

Qy       2518 GGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAA 2577
Db      12739 GGTAAACAGATGGTTGACACATTAGTAGAATCGGCGTCAAATGTCGAGTTGATTTTGAAA 12798

Qy       2578 TACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATT 2637
Db      12799 TATTTCGACATGTTCCTGAAACTTAAAGATTTAACTAGTTCAACAAGCTTTACGGAAATT 12858

Qy       2638 GATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAG 2697
Db      12859 GACCCCAACAATGATGGTTGGGTACATCCAAAAGATTTTAAAGAAAAAATGGAACAACAA 12918

Qy       2698 AAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGAC 2757
Db      12919 AAAAGTTACACTGCAGAGGAAATTGAATTTATGTTACAATGTTGTGAATCTAATCACGAT 12978

Qy       2758 GGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGG 2817
Db      12979 GGGAAAATTGATTACATTGGCTTTACCGATCAATTCCACGAGCCATCCAAAGAAATTGGT 13038

Qy       2818 TTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTG 2877
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Qy       2878 GCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGT 2937
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Qy       2938 ATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCT 2997
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Qy       2998 AATA 3001
Db      13219 AACA 13222


RESULT 11
US-10-887-553A-489
; Sequence 489, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
;  APPLICANT: Garza, Dan
;  APPLICANT:  Li, Hao
;  TITLE OF INVENTION: Method to treat conditions associated
;  TITLE OF INVENTION:  with insulin signalling dysregulation
;  FILE REFERENCE: 4-33262
;  CURRENT APPLICATION NUMBER: US/10/887,553A
;  CURRENT FILING DATE:  2004-07-08
;  PRIOR APPLICATION NUMBER: 60/485,883
;  PRIOR FILING DATE: 2003-08-07
;  NUMBER OF SEQ ID NOS: 1208
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 489
;   LENGTH: 15359
;   TYPE: DNA
;   ORGANISM: human
US-10-887-553A-489

  Query Match             25.7%;  Score 771.8;  DB 9;  Length 15359;
  Best Local Similarity   56.5%;  Pred. No. 9.2e-222;
  Matches 1691;  Conservative    0;  Mismatches 1187;  Indels  117;  Gaps    9;

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Db       9819 TGGGGCTCCCCAACAGTGTGGAGGAGATGTGTCCCGACATCCCGGTGCTGGAGCGGCTCA 9878

Qy         98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157
Db       9879 TGGCAGACATTGGGGGGCTGGCCGAGTCAGGTGCCCGCTACACAGAGATGCCGCATGTCA 9938

Qy        158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217
Db       9939 TCGAGATCACGCTGCCCATGCTATGCAGCTACCTGCCCCGATGGTGGGAGCGCGGGCCCG 9998

Qy        218 ATAATGTTACTCCTACT-----------GGCGGAAACCACGTAACAATGGTAACAGCGG 265
Db       9999 AGGCACCCCCTTCCGCCCTGCCCGCCGGCGCCCCCCCACCCTGCACAGCTGTCACCTCTG 10058

Qy        266 AACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATG 325
Db      10059 ACCACCTCAACTCCCTGCTGGGGAATATCCTGAGAATCATCGTCAACAACCTGGGCATTG 10118

Qy        326 AGAACGCGCCGTGGATGACCCGCATCGCCACCTACACGCAGCAGATCATCATCAACAGCT 385
Db      10119 ACGAGGCCTCCTGGATGAAGCGGCTGGCTGTGTTCGCACAGCCCATTGTGAGCCGTGCAC 10178

Qy        386 CCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGG 445
Db      10179 GGCCGGAGCTCCTGCAGTCCCACTTCATCCCAACTATCGGGCGGCTGCGCAAGAGGGCAG 10238

Qy        446 ACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACA 505
Db      10239 GGAAGGTGGTGTCCGAGGAGGAGCAGCTGCGCCTGGAGGCCAAGGCG---------GAGG 10289

Qy        506 CATCCCAGGTAGAGTCTCAGATACAAGAAGACTGGCAGCTGCTGGTCAGAGACATCTACT 565
Db      10290 CCCAGGAGGGCGAGCTGCTGGTGCGGGACGAGTTCTCTGTGCTCTGCCGGGACCTCTACG 10349

Qy        566 CCTTCTACCCGCTGCTCATCAAGTACGTCGACCTGCAGAGGAACCACTGGCTCAGGAACA 625
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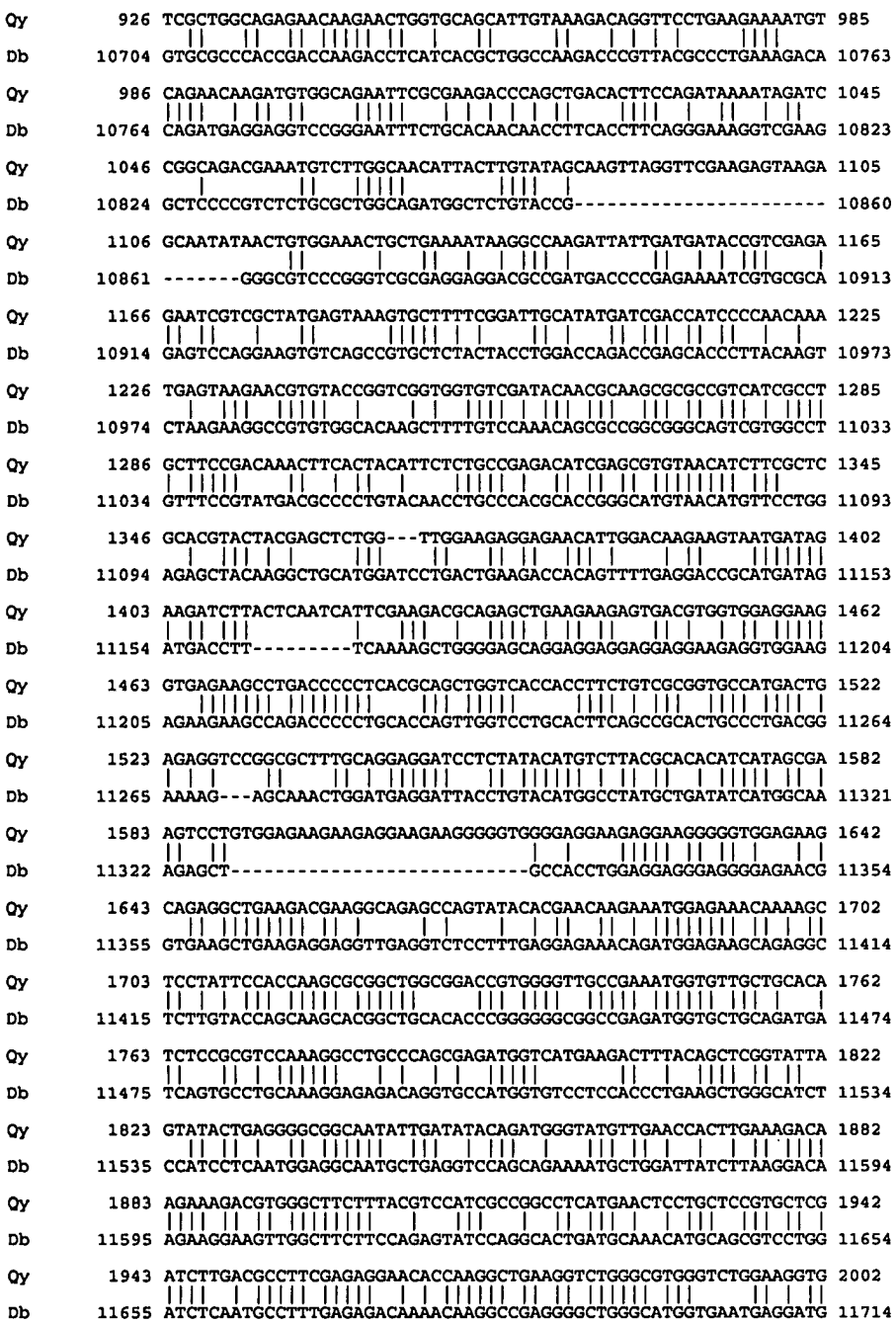
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Qy        686 AGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTCATCTCTGCCAACGAAATTGATAACA 745
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Qy        746 TGGTGCTGATTATGCCAACAGCAACAAGAAGAGTGACAGCAGTAACAGATGGTACTCCTC 805
Db      10530 TGTCCTTCCTGACTGCTGACAACAAAAGCAAAATGGCTAAGGCGGGAGATATA------C 10583

Qy        806 AAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGATAAGAAACGCGACAAAGACAAGGAAG 865
Db      10584 AGTCCGGTGGCTCGGACCAGGAACGCACCAAGAAGAAGCGCCGGGGGGACCGGTACTCTG 10643

Qy        866 TCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGGTTGTTACCAGTTGGCCTTAACCTAT 925
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RESULT 12
US-10-450-763-4960
; Sequence 4960, Application US/10450763
; Publication No. US20050196754A1

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; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 790CIP3/US
;  CURRENT APPLICATION NUMBER: US/10/450,763
;  CURRENT FILING DATE:  2003-06-11
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 4960
;   LENGTH: 15359
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (131)..(15244)
;   OTHER INFORMATION: 100% homologous to Homo sapiens skeletal muscle ryanodine
;   OTHER INFORMATION: receptor,accession number U48508,Smith-Waterman Score=26424.
US-10-450-763-4960

  Query Match             25.7%;  Score 771.8;  DB 9;  Length 15359;
  Best Local Similarity   56.5%;  Pred. No. 9.2e-222;
  Matches 1691;  Conservative    0;  Mismatches 1187;  Indels  117;  Gaps    9;

Qy         38 TGGAAGCCCAAGACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGATCT 97
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Qy         98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157
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Qy        158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217
Db       9939 TCGAGATCACGCTGCCCATGCTATGCAGCTACCTGCCCCGATGGTGGGAGCGCGGGCCCG 9998

Qy        218 ATAATGTTACTCCTACT-----------GGCGGAAACCACGTAACAATGGTAACAGCGG 265
Db       9999 AGGCACCCCCTTCCGCCCTGCCCGCCGGCGCCCCCCCACCCTGCACAGCTGTCACCTCTG 10058

Qy        266 AACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATG 325
Db      10059 ACCACCTCAACTCCCTGCTGGGGAATATCCTGAGAATCATCGTCAACAACCTGGGCATTG 10118

Qy        326 AGAACGCGCCGTGGATGACCCGCATCGCCACCTACACGCAGCAGATCATCATCAACAGCT 385
Db      10119 ACGAGGCCTCCTGGATGAAGCGGCTGGCTGTGTTCGCACAGCCCATTGTGAGCCGTGCAC 10178

Qy        386 CCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGG 445
Db      10179 GGCCGGAGCTCCTGCAGTCCCACTTCATCCCAACTATCGGGCGGCTGCGCAAGAGGGCAG 10238

Qy        446 ACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACA 505
Db      10239 GGAAGGTGGTGTCCGAGGAGGAGCAGCTGCGCCTGGAGGCCAAGGCG---------GAGG 10289

Qy        506 CATCCCAGGTAGAGTCTCAGATACAAGAAGACTGGCAGCTGCTGGTCAGAGACATCTACT 565
Db      10290 CCCAGGAGGGCGAGCTGCTGGTGCGGGACGAGTTCTCTGTGCTCTGCCGGGACCTCTACG 10349

Qy        566 CCTTCTACCCGCTGCTCATCAAGTACGTCGACCTGCAGAGGAACCACTGGCTCAGGAACA 625
Db      10350 CCCTGTATCCGCTGCTCATCCGCTACGTGGACAACAACAGGGCGCAGTGGCTGACGGAGC 10409

Qy        626 ATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTGGCTGAAATCTTCAACATCTGGTCGA 685
Db      10410 CGAATCCCAGCGCGGAGGAGCTGTTCAGGATGGTGGGCGAGATCTTCATCTACTGGTCCA 10469

Qy        686 AGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTCATCTCTGCCAACGAAATTGATAACA 745
Db      10470 AGTCCCACAACTTCAAGCGCGAGGAGCAGAACTTTGTGGTCCAGAATGAGATCAACAACA 10529

Qy        746 TGGTGCTGATTATGCCAACAGCAACAAGAAGAGTGACAGCAGTAACAGATGGTACTCCTC 805
Db      10530 TGTCCTTCCTGACTGCTGACAACAAAAGCAAAATGGCTAAGGCGGGAGATATA------C 10583

Qy        806 AAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGATAAGAAACGCGACAAAGACAAGGAAG 865
Db      10584 AGTCCGGTGGCTCGGACCAGGAACGCACCAAGAAGAAGCGCCGGGGGGGACCGGTACTCTG 10643

Qy        866 TCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGGTTGTTACCAGTTGGCCTTAACCTAT 925
Db      10644 TGCAGACGTCACTGATCGTGGCCACACTGAAGAAGATGCTGCCCATCGGCCTGAATATGT 10703

Qy        926 TCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGTAAAGACAGGTTCCTGAAGAAAATGT 985
Db      10704 GTGCGCCCACCGACCAAGACCTCATCACGCTGGCCAAGACCCGTTACGCCCTGAAAGACA 10763

Qy        986 CAGAACAAGATGTGGCAGAATTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATC 1045
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Qy       1046 CGGCAGACGAAATGTCTTGGCAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGA 1105
Db      10824 GCTCCCCGTCTCTGCGCTGGCAGATGGCTCTGTACCG---------------------- 10860

Qy       1106 GCAATATAACTGTGGAAACTGCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGA 1165
Db      10861 -------GGGCGTCCCGGGTCGCGAGGAGGACGCCGATGACCCCGAGAAAATCGTGCGCA 10913

Qy       1166 GAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAA 1225
Db      10914 GAGTCCAGGAAGTGTCAGCCGTGCTCTACTACCTGGACCAGACCGAGCACCCTTACAAGT 10973

Qy       1226 TGAGTAAGAACGTGTACCGGTCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCT 1285
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Qy       1346 GCACGTACTACGAGCTCTGG---TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAG 1402
Db      11094 AGAGCTACAAGGCTGCATGGATCCTGACTGAAGACCACAGTTTTGAGGACCGCATGATAG 11153

Qy       1403 AAGATCTTACTCAATCATTCGAAGACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAG 1462
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Qy       1463 GTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTG 1522
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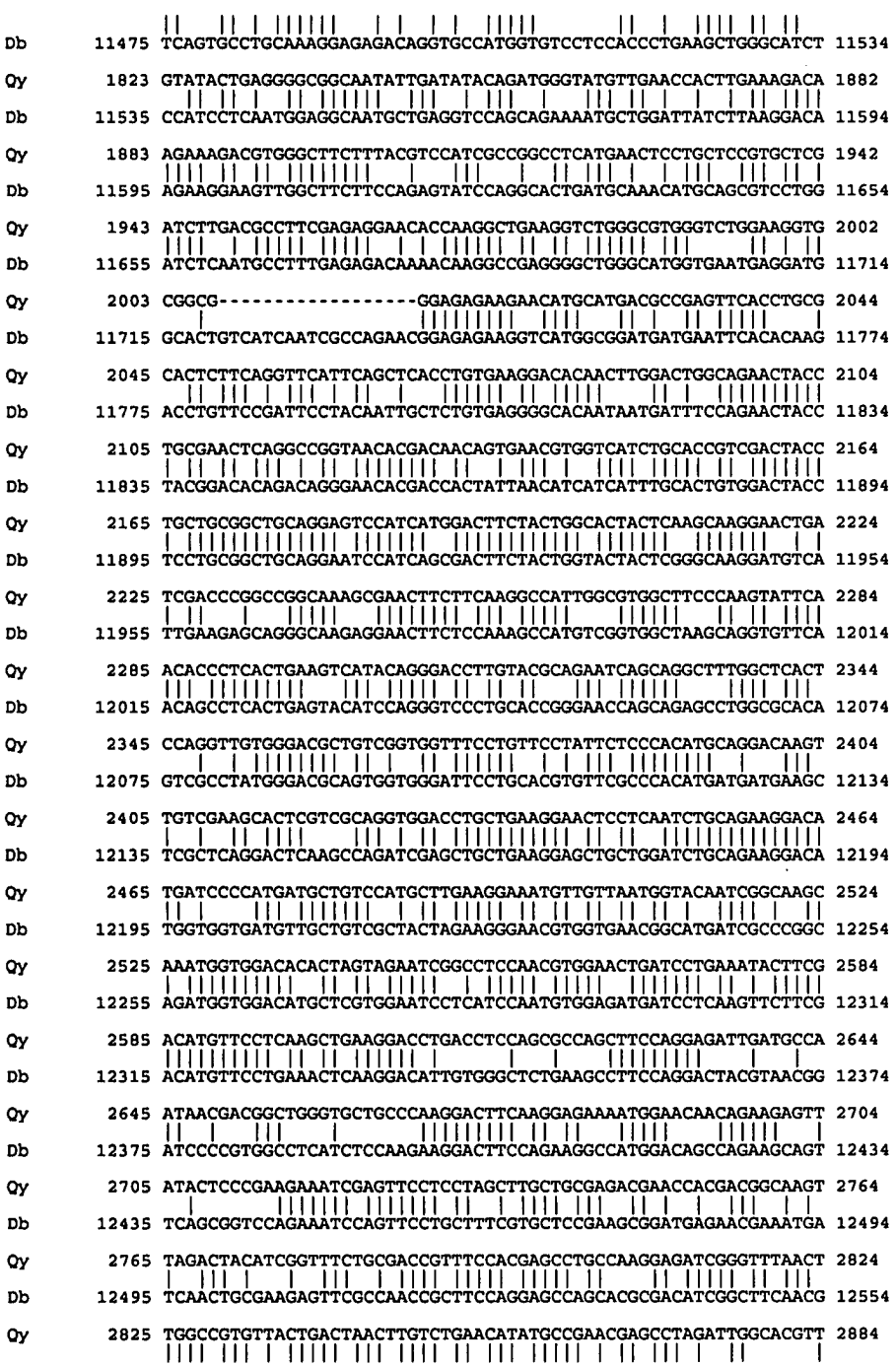
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Qy       1583 AGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAG 1642
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Qy       1643 CAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACAAAAGC 1702
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Qy       1763 TCTCCGCGTCCAAAGGCCTGCCCAGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTA 1822
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Qy       2003 CGGCG-----------------GGAGAGAAGAACATGCATGACGCCGAGTTCACCTGCG 2044

Db      11715 GCACTGTCATCAATCGCCAGAACGGAGAGAAGGTCATGGCGGATGATGAATTCACACAAG 11774

Qy       2045 CACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAACTACC 2104

Db      11775 ACCTGTTCCGATTCCTACAATTGCTCTGTGAGGGGCACAATAATGATTTCCAGAACTACC 11834

Qy       2105 TGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGACTACC 2164

Db      11835 TACGGACACAGACAGGGAACACGACCACTATTAACATCATCATTTGCACTGTGGACTACC 11894

Qy       2165 TGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAACTGA 2224

Db      11895 TCCTGCGGCTGCAGGAATCCATCAGCGACTTCTACTGGTACTACTCGGGCAAGGATGTCA 11954

Qy       2225 TCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCA 2284

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Qy       2345 CCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGACAAGT 2404

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Qy       2405 TGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAGGACA 2464

Db      12135 TCGCTCAGGACTCAAGCCAGATCGAGCTGCTGAAGGAGCTGCTGGATCTGCAGAAGGACA 12194

Qy       2465 TGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGCAAGC 2524

Db      12195 TGGTGGTGATGTTGCTGTCGCTACTAGAAGGGAACGTGGTGAACGGCATGATCGCCCGGC 12254

Qy       2525 AAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATACTTCG 2584

Db      12255 AGATGGTGGACATGCTCGTGGAATCCTCATCCAATGTGGAGATGATCCTCAAGTTCTTCG 12314

Qy       2585 ACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGATGCCA 2644

Db      12315 ACATGTTCCTGAAACTCAAGGACATTGTGGGCTCTGAAGCCTTCCAGGACTACGTAACGG 12374

Qy       2645 ATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAGAGTT 2704

Db      12375 ATCCCCGTGGCCTCATCTCCAAGAAGGACTTCCAGAAGGCCATGGACAGCCAGAAGCAGT 12434

Qy       2705 ATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGCAAGT 2764

Db      12435 TCAGCGGTCCAGAAATCCAGTTCCTGCTTTCGTGCTCCGAAGCGGATGAGAACGAAATGA 12494

Qy       2765 TAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTTAACT 2824

Db      12495 TCAACTGCGAAGAGTTCGCCAACCGCTTCCAGGAGCCAGCACGCGACATCGGCTTCAACG 12554

Qy       2825 TGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCACGTT 2884

Db      12555 TGGCGGTGCTGCTGACCAACCTGTCGGAGCATGTGCCGCATGACCCTCGCCTGCACAACT 12614

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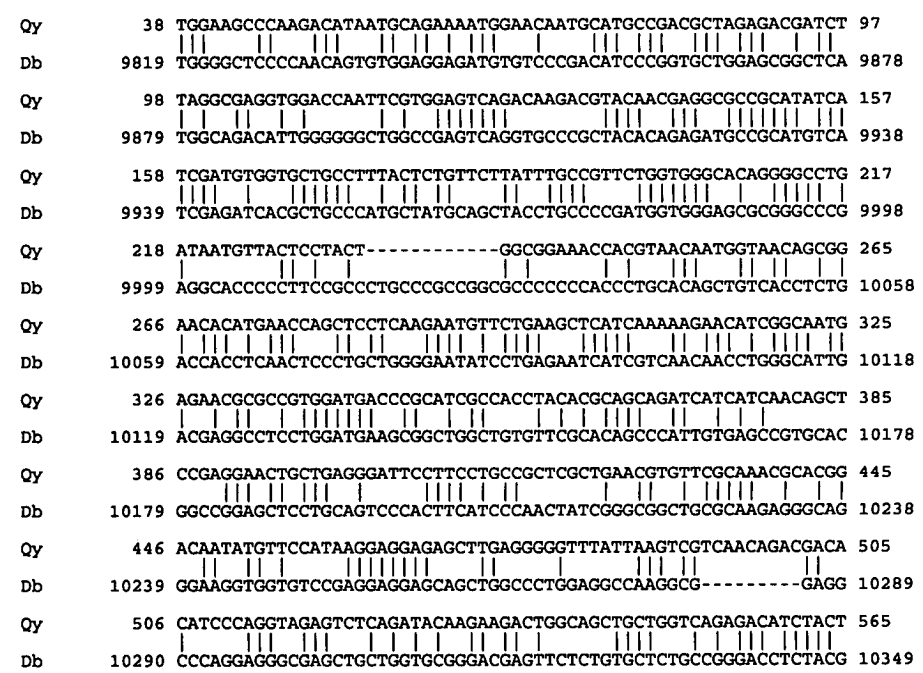
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Qy       2945 TCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAA 2999

Db      12675 TCATGGGCGCGTCACGCCGCATCGAGCGCATCTACTTCGAGATCTCAGAGACCAA 12729
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RESULT 13
US-10-276-774-500
; Sequence 500, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 500
; LENGTH: 15359
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-500

Query Match 25.7%; Score 770.2; DB 7; Length 15359;
Best Local Similarity 56.4%; Pred. No. 2.8e-221;
Matches 1690; Conservative 0; Mismatches 1188; Indels 117; Gaps 9;



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Qy         38 TGGAAGCCCAAGACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGATCT 97

Db       9819 TGGGGCTCCCCAACAGTGTGGAGGAGATGTGTCCCGACATCCCGGTGCTGGAGCGGCTCA 9878

Qy         98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157

Db       9879 TGGCAGACATTGGGGGGCTGGCCGAGTCAGGTGCCCGCTACACAGAGATGCCGCATGTCA 9938

Qy        158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217

Db       9939 TCGAGATCACGCTGCCCATGCTATGCAGCTACCTGCCCCGATGGTGGGAGCGCGGGCCCG 9998

Qy        218 ATAATGTTACTCCTACT-----------GGCGGAAACCACGTAACAATGGTAACAGCGG 265

Db       9999 AGGCACCCCCTTCCGCCCTGCCCGCCGGCGCCCCCCCACCCTGCACAGCTGTCACCTCTG 10058

Qy        266 AACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATG 325

Db      10059 ACCACCTCAACTCCCTGCTGGGGAATATCCTGAGAATCATCGTCAACAACCTGGGCATTG 10118

Qy        326 AGAACGCGCCGTGGATGACCCGCATCGCCACCTACACGCAGCAGATCATCATCAACAGCT 385

Db      10119 ACGAGGCCTCCTGGATGAAGCGGCTGGCTGTGTTCGCACAGCCCATTGTGAGCCGTGCAC 10178

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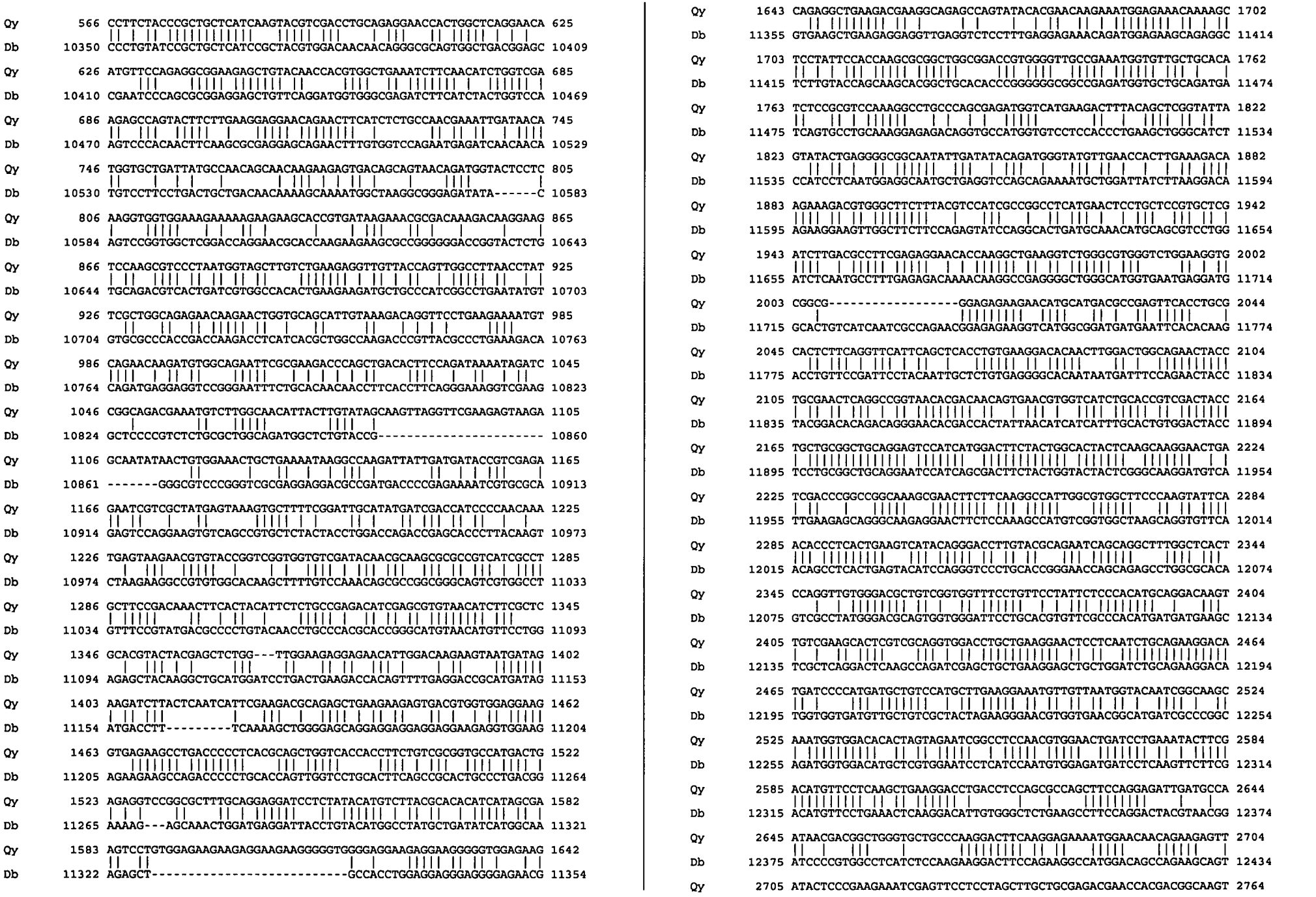
Db      10179 GGCCGGAGCTCCTGCAGTCCCACTTCATCCCAACTATCGGGCGGCTGCGCAAGAGGGCAG 10238

Qy        446 ACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACA 505

Db      10239 GGAAGGTGGTGTCCGAGGAGGAGCAGCTGGCCCTGGAGGCCAAGGCG---------GAGG 10289

Qy        506 CATCCCAGGTAGAGTCTCAGATACAAGAAGACTGGCAGCTGCTGGTCAGAGACATCTACT 565

Db      10290 CCCAGGAGGGCGAGCTGCTGGTGCGGGACGAGTTCTCTGTGCTCTGCCGGGACCTCTACG 10349
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Db      12435 TCAGCGGTCCAGAAATCCAGTTCCTGCTTTCGTGCTCCGAAGCGGATGAGAACGAAATGA 12494

Qy       2765 TAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTTAACT 2824

Db      12495 TCAACTGCGAAGAGTTCGCCAACCGCTTCCAGGAGCCAGCACGCGACATCGGCTTCAACG 12554

Qy       2825 TGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCACGTT 2884

Db      12555 TGGCGGTGCTGCTGACCAACCTGTCGGAGCATGTGCCGCATGACCCTCGCCTGCACAACT 12614

Qy       2885 TCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATCGAGA 2944

Db      12615 TCCTGGAGCTGGCCGAGAGCATCCTTGAGTACTTCCGCCCCTACCTGGGCCGCATCGAGA 12674

Qy       2945 TCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAA 2999

Db      12675 TCATGGGCGCGTCACGCCGCATCGAGCGCATCTACTTCGAGATCTCAGAGACCAA 12729


RESULT 14
US-10-276-774-552
; Sequence 552, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang, Y, Tom et al
;  TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-030
;  CURRENT APPLICATION NUMBER: US/10/276,774
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 2700
;  SOFTWARE: Custom
; SEQ ID NO 552
;   LENGTH: 14302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-276-774-552

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  Matches 1632;  Conservative    0;  Mismatches 1210;  Indels   96;  Gaps    7;

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Qy        130 AAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTCTGTTCTTAT 189

Db       9797 ATTCGCTACACTCAAATGCCACATGTCATGGAAGTCATACTGCCCATGCTTTGCAGCTAC 9856

Qy        190 TTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGAAACCACGTA 249

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Qy        250 ACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAA 309

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Qy        310 AAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTACACGCAGCAG 369

Db       9977 AATAACTTGGGGATTGATGAGGGAGCCTGGATGAAGAGGCTAGCAGTGTTTTCCCAGCCT 10036

Qy        370 ATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGT 429

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Qy        430 GTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAG 489

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Qy        490 TCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGGCAGCTGCTG 549

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Db      10208 GCCAGAGATCTCTATGCCTTCTACCCTCTCTTGATTAGATTTGTGGACTATAACAGGGCA 10267

Qy        610 CACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTGGCTGAAATC 669

Db      10268 AAGTGGCTAAAGGAGCCTAACCCAGAAGCAGAGGAGCTCTTCCGCATGGTGGCTGAAGTG 10327

Qy        670 TTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTCATCTCTGCC 729

Db      10328 TTTATCTACTGGTCGAAGTCCCATAATTTCAAAAGAGAAGAGCAGAACTTCGTTGTACAG 10387

Qy        730 AACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTGACAGCAGTA 789

Db      10388 AATGAAATCAACAATATGTCTTTCCTTATTACTGATACCAAGTCAAAGATGTCAAAGGCA 10447

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Db      10448 GCTGTTTCTGATCAGGAAAGGAAGAAAATGAAGCGCAAAGGAGATCGGTATTCCA----- 10502

Qy        850 GACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGGTTGTTACCA 909

Db      10503 ----------------TGCAGACCTCTCTGATTGTAGCAGCTCTGAAGCGGTTACTGCCC 10546

Qy        910 GTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGTAAAGACAGG 969

Db      10547 ATTGGGTTGAACATCTGTGCCCCTGGGGACCAGGAGCTCATTGCTCTGGCCAAAAATCGA 10606

Qy        970 TTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACCCAGCTGACACTT 1029

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Db      10667 CAAGGCAAGTTGGAGGATCCTGCTATTAGATGGCAAATGGCTCTTTACAAAGACTTACCA 10726

Qy       1081 AGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACTGCTGAAAATAAGGCC 1140

Db      10727 AACAGGACTGATGATACCTCAGATCCAGAGAAGACGGTAGAAAGAGTATTGGATATAGCA 10786

Qy       1141 AAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTG 1200

Db      10787 AATGTGCTTTTTCATCTTGAACAGAAGTCTAAACGTGTGGGTCGAAGACATTACTG---- 10842

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Db      10901 CAGAGGAAAAGGGCTGTTGTAGCCTGCTTCCGGATGGCCCCCTTATATAATCTGCCAAGG 10960

Qy       1321 CATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGGTTGGAAGAGGAGAAC 1380

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Db      11012 ACAGAAGAACATTACTTTGAAGATAAACTGATAGAAGATTTAGCAAAACCTGGGGCTGAA 11071

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Qy       1561 TCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAG 1620
Db      11189 GCCTATGCAGATATTATGGCAAAGAGTTGTCATGATGAGGAAGATGACGATGGTGAAGAG 11248

Qy       1621 GAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAA 1680
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Qy       1681 CAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGTGGGGTT 1740
Db      11270 AAAGAAATGGAAAAGCAAAAGCTTCTATACCAGCAAGCCCGACTCCACGATCGTGGCGCG 11329

Qy       1741 GCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAGATGGTCATG 1800
Db      11330 GCTGAGATGGTGCTACAGACAATCAGTGCCAGCAAAGGTGAAACTGGACCAATGGTAGCA 11389

Qy       1801 AAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAGATGGGT 1860
Db      11390 GCTACTCTGAAACTTGGAATTGCTATTTTAAATGGTGGGAACTCCACAGTACAGCAGAAA 11449

Qy       1861 ATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTC 1920
Db      11450 ATGCTTGACTACCTCAAGGAGAAAAAGGATGTGGGCTTCTTTCAGAGCCTGGCCGGCCTG 11509

Qy       1921 ATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGT 1980
Db      11510 ATGCAGTCATGTAGTGTCCTTGACCTAAATGCATTTGAGCGACAAAACAAAGCTGAAGGT 11569

Qy       1981 CTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACC 2040
Db      11570 CTTGGGATGGTGACAGAGGAAGGATCAGGAGAAAAGGTTCTGCAGGACGATGAGTTCACC 11629

Qy       2041 TGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAAC 2100
Db      11630 TGTGACCTCTTCCGATTCCTGCAACTACTCTGTGAGGGACACAACTCAGATTTTCAGAAT 11689

Qy       2101 TACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGAC 2160
Db      11690 TATCTGAGAACTCAGACTGGCAATAATACAACTGTCAACATAATTATCTCCACTGTAGAC 11749

Qy       2161 TACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAA 2220
Db      11750 TACCTACTGAGAGTTCAGGAATCAATTAGTGACTTTTATTGGTATTACTCTGGGAAAGAT 11809

Qy       2221 CTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTA 2280
Db      11810 GTTATTGATGAACAAGGACAACGGAATTTCTCCAAAGCTATCCAAGTGGCAAAACAAGTC 11869

Qy       2281 TTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCT 2340
Db      11870 TTTAACACTCTTACAGAGTATATTCAGGGTCCTTGCACTGGGAATCAACAGAGTTTGGCA 11929

Qy       2341 CACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGAC 2400
Db      11930 CACAGCAGGCTGTGGGATGCTGTGGTCGGCTTTCTTCATGTGTTTGCCCATATGCAGATG 11989

Qy       2401 AAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAG 2460
Db      11990 AAGCTGTCGCAGGATTCCAGTCAAATTGAGCTATTAAAAGAATTAATGGATCTGCAGAAG 12049

Qy       2461 GACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGC 2520
Db      12050 GATATGGTGGTCATGTTGCTGTCCATGTTAGAAGGTAATGTTGTTAATGGAACGATTGGC 12109

Qy       2521 AAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATAC 2580
Db      12110 AAACAGATGGTGGATATGCTTGTGGAATCTTCCAACAACGTGGAGATGATTCTCAAATTT 12169

Qy       2581 TTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGAT 2640
Db      12170 TTTGACATGTTCTTAAAACTAAAGGATTTGACGTCGTCTGATACTTTTAAAGAATATGAC 12229

Qy       2641 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 2700
Db      12230 CCCGATGGCAAGGGAGTCATTTCCAAGAGGGACTTCCACAAAGCGATGGAGAGCCATAAG 12289

Qy       2701 AGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGC 2760
Db      12290 CACTACACGCAGTCAGAAACGGAATTTCTTTTGTCTTGTGCGGAGACGGATGAGAATGAA 12349

Qy       2761 AAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTT 2820
Db      12350 ACCCTCGACTACGAAGAGTTCGTCAAACGCTTCCACGAACCTGCGAAGGACATCGGCTTC 12409

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Qy       2881 CGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATC 2940
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Qy       2941 GAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTA 2998
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RESULT 15
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; Sequence 490, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
;  APPLICANT: Garza, Dan
;  APPLICANT:  Li, Hao
;  TITLE OF INVENTION: Method to treat conditions associated
;  TITLE OF INVENTION:  with insulin signalling dysregulation
;  FILE REFERENCE: 4-33262
;  CURRENT APPLICATION NUMBER: US/10/887,553A
;  CURRENT FILING DATE:  2004-07-08
;  PRIOR APPLICATION NUMBER: 60/485,883
;  PRIOR FILING DATE: 2003-08-07
;  NUMBER OF SEQ ID NOS: 1208
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 490
;   LENGTH: 15731
;   TYPE: DNA
;   ORGANISM: human
US-10-887-553A-490

  Query Match             24.7%;  Score 740;  DB 9;  Length 15731;
  Best Local Similarity   55.5%;  Pred. No. 4.1e-212;
  Matches 1632;  Conservative    0;  Mismatches 1210;  Indels   96;  Gaps    7;

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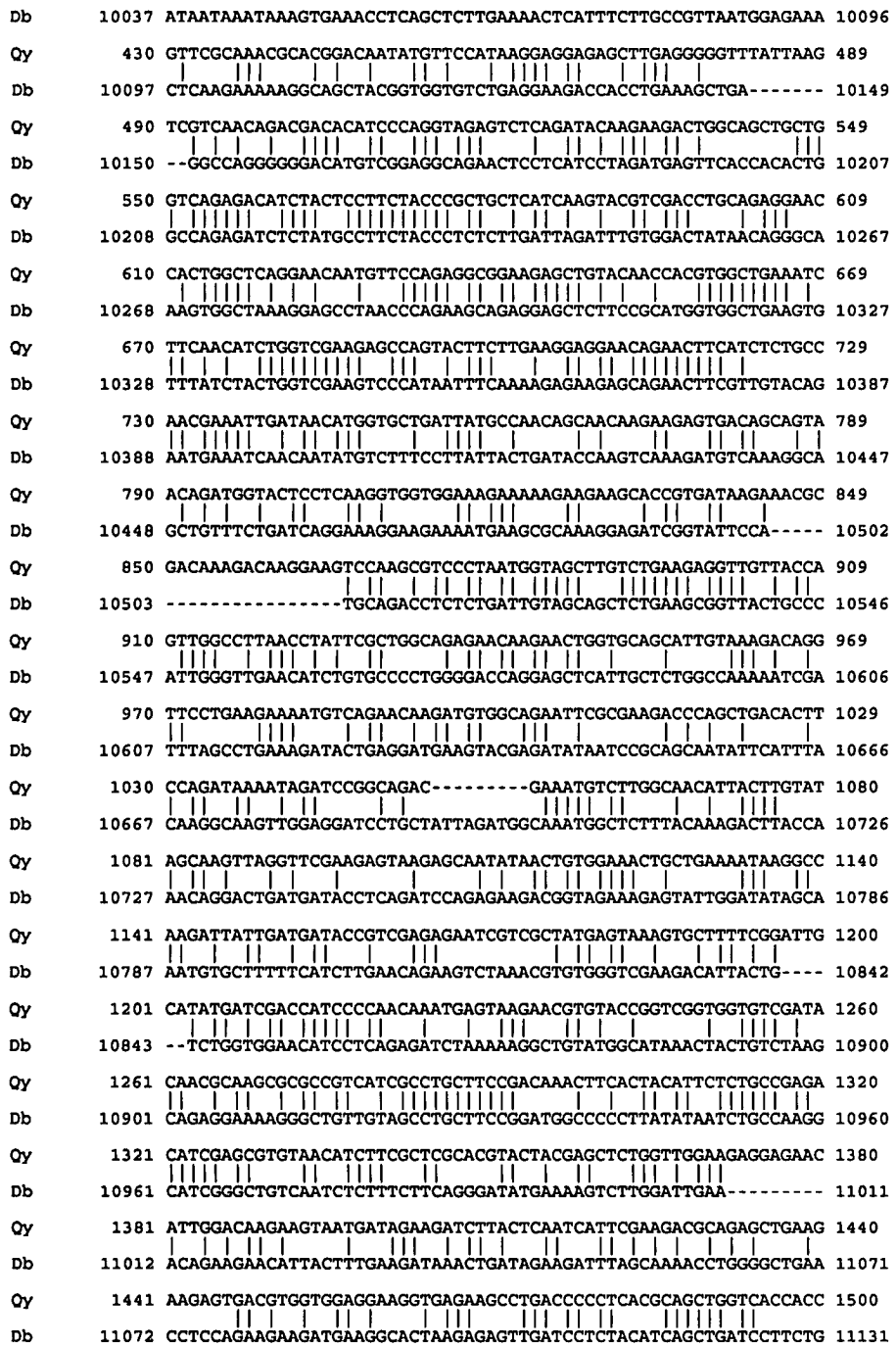
Qy        130 AAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTCTGTTCTTAT 189
Db       9797 ATTCGCTACACTCAAATGCCACATGTCATGGAAGTCATACTGCCCATGCTTTGCAGCTAC 9856

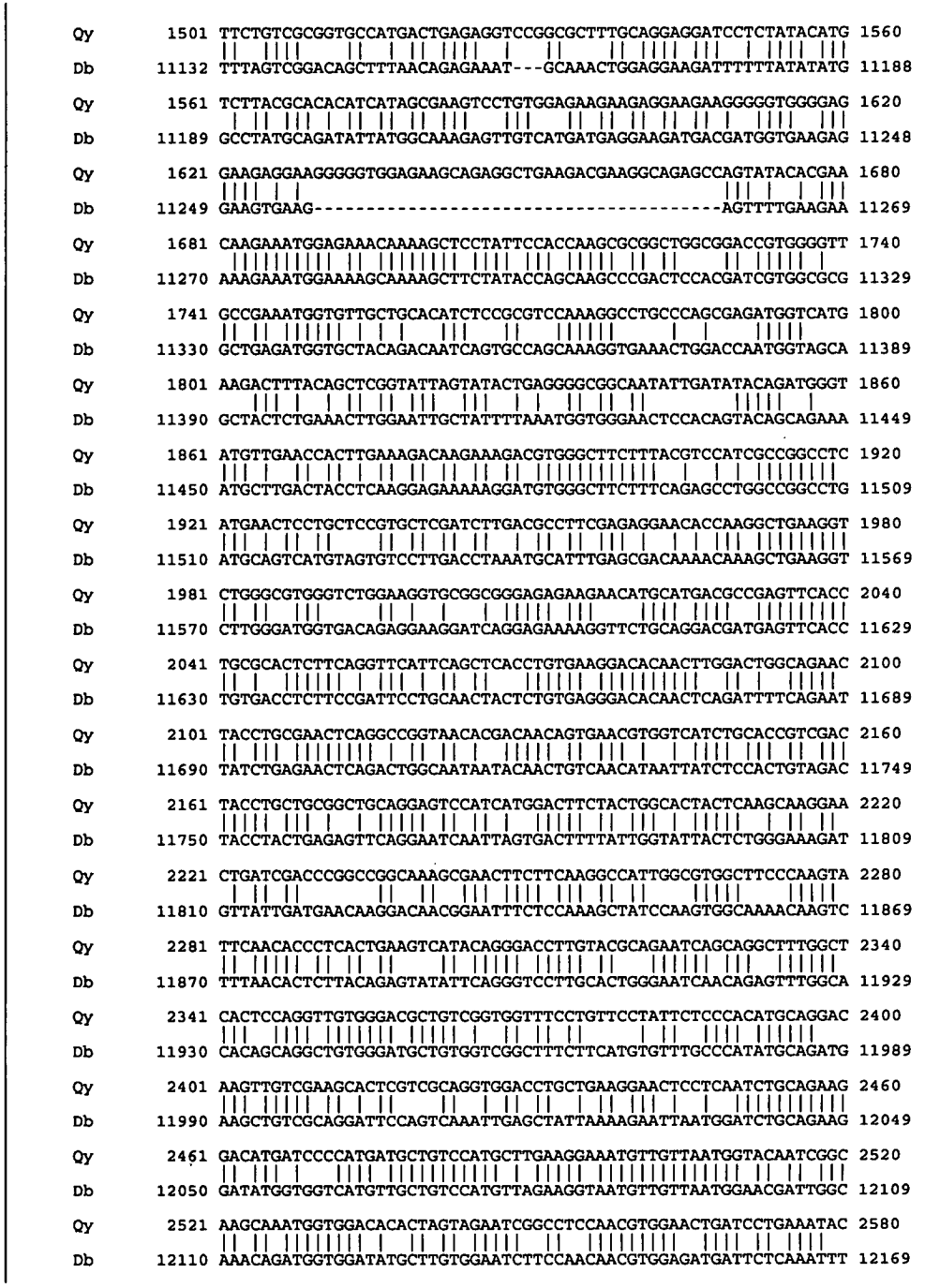
Qy        190 TTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGAAACCACGTA 249
Db       9857 ATGTCTCGTTGGTGGGAGCATGGACCTGAGAACAATCCAGAACGGGCCGAGATGTGCTGC 9916

Qy        250 ACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAA 309
Db       9917 ACAGCCCTGAACTCAGAGCACATGAACACACTTCTAGGGAACATATTGAAAATCATATAT 9976

Qy        310 AAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTACACGCAGCAG 369
Db       9977 AATAACTTGGGGATTGATGAGGGAGCCTGGATGAAGAGGCTAGCAGTGTTTTCCCAGCCT 10036

Qy        370 ATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGT 429
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Qy       2581 TTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGAT 2640
             || ||||||||| | || || ||||| |||| ||    |  | ||  | ||   |||
Db      12170 TTTGACATGTTCTTAAAACTAAAGGATTTGACGTCGTCTGATACTTTTAAAGAATATGAC 12229

Qy       2641 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 2700
              || ||  | | ||     |       | |||||||| |  |    |||||    || |||
Db      12230 CCCGATGGCAAGGGAGTCATTTCCAAGAGGGACTTCCACAAAGCGATGGAGAGCCATAAG 12289

Qy       2701 AGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGC 2760
                || || |    |||||  || || ||   |  ||||    |||||| |  |  | |
Db      12290 CACTACACGCAGTCAGAAACGGAATTTCTTTTGTCTTGTGCGGAGACGGATGAGAATGAA 12349

Qy       2761 AAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTT 2820
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Db      12350 ACCCTCGACTACGAAGAGTTCGTCAAACGCTTCCACGAACCTGCGAAGGACATCGGCTTC 12409

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Db      12410 AACGTCGCCGTCCTTCTGACAAACCTCTCTGAGCACATGCCCAACGATACCCGACTTCAG 12469

Qy       2881 CGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATC 2940
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Db      12530 GAAATCATGGGAAGCGCCAAACGCATCGAGAGGGTCTATTTTGAAATCAGTGAGTCCA 12587
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GenCore version 5.1.7
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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3001	100.0	15387	12	ADM68883	Adm68883 Heliothis
2	2996.2	99.8	15303	12	ADM68901	Adm68901 Heliothis
3	2917.4	97.2	15679	12	ADM68757	Adm68757 Heliothis
4	2846.4	94.8	15405	12	ADM68885	Adm68885 Heliothis
5	2844.8	94.8	15429	12	ADM68899	Adm68899 Heliothis
6	1718.2	57.3	15606	4	ABL16881	Abl16881 Drosophil
7	1718.2	57.3	16363	12	ADM68765	Adm68765 Drosophil
8	1578.6	52.6	15413	12	ADM68763	Adm68763 Peregrinu
9	1489.6	49.6	15315	12	ADM68761	Adm68761 Periplane
10	1456	48.5	15845	12	ADM68759	Adm68759 Myzus per
11	787.4	26.2	15672	2	AAQ10613	Aaq10613 Rianodin
12	771.8	25.7	15359	5	AAS69156	Aas69156 DNA encod
13	771.8	25.7	15359	12	ADQ85750	Adq85750 Human tum
14	771.8	25.7	15359	13	ADQ84285	Adq84285 Human tum
15	771.8	25.7	15359	13	ADQ83605	Adq83605 Human tum
16	771.8	25.7	15359	13	ACN40554	Acn40554 Tumour-as
17	771.8	25.7	15359	14	ADY19485	Ady19485 DNA encod
18	771.8	25.7	15359	14	ADY15561	Ady15561 DNA encod
19	771.8	25.7	15359	14	ADZ49160	Adz49160 Insulin s
20	770.2	25.7	15359	4	ABA08724	Aba08724 Human rya
21	770.2	25.7	15359	12	ADQ86825	Adq86825 Human tum
22	756.2	25.2	15355	4	AAH57405	Aah57405 Human ske
23	756.2	25.2	15464	2	AAQ11415	Aaq11415 Ryanodine
24	741.6	24.7	15731	4	AAH98746	Aah98746 Human EST
25	740	24.7	14302	4	ABA08776	Aba08776 Human rya
26	740	24.7	15731	12	ADP21411	Adp21411 Gene RYR2
27	740	24.7	15731	14	ADZ49161	Adz49161 Insulin s
28	738.4	24.6	6807	4	ABA08669	Aba08669 Human rya
29	732.2	24.4	15563	12	ADP21412	Adp21412 Gene RYR3
30	732.2	24.4	15563	14	ADZ49162	Adz49162 Insulin s
31	732.2	24.4	15583	5	AAS76501	Aas76501 DNA encod
32	732.2	24.4	15583	10	ADF59841	Adf59841 Human con
33	731.8	24.4	15820	5	AAS87533	Aas87533 DNA encod
34	724.6	24.1	15377	2	AAQ25975	Aaq25975 MH mutant
35	723.4	24.1	15453	12	ADQ22976	Adq22976 Human sof
36	717	23.9	14800	5	AAS06039	Aas06039 Angiotens
37	715	23.8	15512	2	AAV59470	Aav59470 Human rya
c 38	632.2	21.1	24236	4	ABL16880	Abl16880 Drosophil
39	211.6	7.1	4278	5	AAS87531	Aas87531 DNA encod
40	137.4	4.6	323	4	AAI23165	Aai23165 Probe #13
41	137.4	4.6	323	4	ABA68268	Aba68268 Human foe
42	137.4	4.6	323	4	AAI48484	Aai48484 Probe #17
43	137.4	4.6	323	4	ABA50322	Aba50322 Human bre
44	137.4	4.6	323	4	ABA35276	Aba35276 Probe #13
45	137.4	4.6	323	4	AAK42407	Aak42407 Human bon

ALIGNMENTS

RESULT 1
ADM68883
ID ADM68883 standard; DNA; 15387 BP.
XX
AC ADM68883;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:127.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Heliothis virescens.
XX
FH Key Location/Qualifiers
FT CDS 1. .15387
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68884.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 127; 687pp; English.

XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15387 BP; 4065 A; 3845 C; 4182 G; 3295 T; 0 U; 0 Other;

Query Match 100.0%; Score 3001; DB 12; Length 15387;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
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Db      10000 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 10059

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10060 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 10119

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10120 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 10179

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10180 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 10239

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10240 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 10299

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10300 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 10359

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10360 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 10419

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10420 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 10479

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10480 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 10539

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10540 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 10599

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
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Db      10600 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 10659

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10660 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 10719

Qy        721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10720 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 10779

Qy        781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10780 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 10839

Qy        841 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10840 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 10899

Qy        901 TTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 960
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Db      10900 TTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 10959

Qy        961 AAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACCCAG 1020
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Db      10960 AAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACCCAG 11019

Qy       1021 CTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTACTTGTAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11020 CTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTACTTGTAT 11079

Qy       1081 AGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACTGCTGAAAATAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11080 AGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACTGCTGAAAATAAGGCC 11139

Qy       1141 AAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11140 AAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTG 11199

Qy       1201 CATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGGTCGGTGGTGTCGATA 1260
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Db      11200 CATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGGTCGGTGGTGTCGATA 11259

Qy       1261 CAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTACATTCTCTGCCGAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11260 CAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTACATTCTCTGCCGAGA 11319

Qy       1321 CATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGGTTGGAAGAGGAGAAC 1380
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Db      11320 CATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGGTTGGAAGAGGAGAAC 11379

Qy       1381 ATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAAGACGCAGAGCTGAAG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11380 ATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAAGACGCAGAGCTGAAG 11439

Qy       1441 AAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACCACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11440 AAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACCACC 11499

Qy       1501 TTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGATCCTCTATACATG 1560
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Qy       1561 TCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAG 1620
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Db      11560 TCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAG 11619
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Qy      1621 GAAGAGGAAGGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAA 1680
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Qy      1681 CAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGTGGGGTT 1740
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Db     11740 GCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAGATGGTCATG 11799

Qy      1801 AAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAGATGGGT 1860
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Db     11800 AAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAGATGGGT 11859

Qy      1861 ATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTC 1920
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Db     11860 ATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTC 11919

Qy      1921 ATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGT 1980
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Qy      1981 CTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACC 2040
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Qy      2041 TGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAAC 2100
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Db     12040 TGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAAC 12099

Qy      2101 TACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGAC 2160
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Db     12100 TACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGAC 12159

Qy      2161 TACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAA 2220
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Qy      2221 CTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTA 2280
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Db     12220 CTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTA 12279

Qy      2281 TTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCT 2340
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Db     12280 TTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCT 12339

Qy      2341 CACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGAC 2400
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Db     12340 CACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGAC 12399

Qy      2401 AAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAG 2460
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Db     12400 AAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAG 12459

Qy      2461 GACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGC 2520
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Db     12460 GACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGC 12519

Qy      2521 AAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATAC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12520 AAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATAC 12579

Qy      2581 TTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGAT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12580 TTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGAT 12639

Qy      2641 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12640 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 12699

Qy      2701 AGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12700 AGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGC 12759

Qy      2761 AAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTT 2820
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Db     12760 AAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTT 12819

Qy      2821 AACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCA 2880
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Db     12820 AACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCA 12879

Qy      2881 CGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATC 2940
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Db     12880 CGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATC 12939

Qy      2941 GAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAAT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12940 GAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAAT 12999

Qy      3001 A 3001
             |
Db     13000 A 13000
```

RESULT 2
ADM68901
ID ADM68901 standard; DNA; 15303 BP.
XX
AC ADM68901;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:145.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Heliothis virescens.
XX
FH Key Location/Qualifiers
FT CDS 1. .15303
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68902.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 145; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a

```
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 15303 BP; 4036 A; 3822 C; 4161 G; 3284 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 2996.2;  DB 12;  Length 15303;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2998;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9916 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 9975

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9976 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 10035

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10036 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 10095

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10096 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 10155

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10156 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 10215

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10216 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 10275

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10276 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 10335

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      10336 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGAGGG 10395

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10396 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 10455

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10456 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 10515

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10516 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 10575

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10576 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 10635

Qy        721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10636 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 10695

Qy        781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10696 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 10755

Qy        841 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10756 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 10815

Qy        901 TTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10816 TTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 10875

Qy        961 AAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACCCAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10876 AAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACCCAG 10935

Qy       1021 CTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTACTTGTAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10936 CTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTACTTGTAT 10995

Qy       1081 AGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACTGCTGAAAATAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10996 AGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACTGCTGAAAATAAGGCC 11055

Qy       1141 AAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11056 AAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTG 11115

Qy       1201 CATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGGTCGGTGGTGTCGATA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11116 CATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGGTCGGTGGTGTCGATA 11175

Qy       1261 CAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTACATTCTCTGCCGAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11176 CAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTACATTCTCTGCCGAGA 11235

Qy       1321 CATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGGTTGGAAGAGGAGAAC 1380
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      11236 CATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGGCTGGAAGAGGAGAAC 11295

Qy       1381 ATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAAGACGCAGAGCTGAAG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11296 ATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAAGACGCAGAGCTGAAG 11355

Qy       1441 AAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACCACC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11356 AAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACCACC 11415

Qy       1501 TTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGATCCTCTATACATG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11416 TTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGATCCTCTATACATG 11475

Qy       1561 TCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11476 TCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAG 11535

Qy       1621 GAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11536 GAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAA 11595

Qy       1681 CAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGTGGGGTT 1740
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Db      11596 CAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGTGGGGTT 11655

Qy       1741 GCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAGATGGTCATG 1800

Db      11656 GCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAGATGGTCATG 11715

Qy       1801 AAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAGATGGGT 1860

Db      11716 AAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAGATGGGT 11775

Qy       1861 ATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTC 1920

Db      11776 ATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTC 11835

Qy       1921 ATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGT 1980

Db      11836 ATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGT 11895

Qy       1981 CTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACC 2040

Db      11896 CTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACC 11955

Qy       2041 TGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAAC 2100

Db      11956 TGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAAC 12015

Qy       2101 TACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGAC 2160

Db      12016 TACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGAC 12075

Qy       2161 TACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAA 2220

Db      12076 TACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAA 12135

Qy       2221 CTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTA 2280

Db      12136 CTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTA 12195

Qy       2281 TTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCT 2340

Db      12196 TTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCT 12255

Qy       2341 CACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGAC 2400

Db      12256 CACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGAC 12315

Qy       2401 AAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAG 2460

Db      12316 AAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAG 12375

Qy       2461 GACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGC 2520

Db      12376 GACATGATCACCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGC 12435

Qy       2521 AAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATAC 2580

Db      12436 AAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATAC 12495

Qy       2581 TTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGAT 2640

Db      12496 TTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGAT 12555

Qy       2641 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 2700

Db      12556 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 12615

Qy       2701 AGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGC 2760

Db      12616 AGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGC 12675

Qy       2761 AAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTT 2820

Db      12676 AAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTT 12735

Qy       2821 AACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCA 2880

Db      12736 AACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCA 12795

Qy       2881 CGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATC 2940

Db      12796 CGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATC 12855

Qy       2941 GAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAAT 3000

Db      12856 GAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAAT 12915

Qy       3001 A 3001

Db      12916 A 12916
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RESULT 3
ADM68757
ID   ADM68757 standard; DNA; 15679 BP.
XX
AC   ADM68757;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:1.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS   Heliothis virescens.
XX
FH   Key             Location/Qualifiers
FT   CDS             251. .15679
FT                   /*tag= a
FT                   /product= "ryanodine receptor"
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
DR   P-PSDB; ADM68758.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Claim 6; SEQ ID NO 1; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
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CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 15679 BP; 4148 A; 3911 C; 4252 G; 3366 T; 0 U; 2 Other;

  Query Match             97.2%;  Score 2917.4;  DB 12;  Length 15679;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches 2964;  Conservative    0;  Mismatches   37;  Indels   15;  Gaps    1;

Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10277 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 10336

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      10337 AAAATGGAACAATGCATGCCGACGTTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 10396

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      10397 GAGTCAGACAAGACGTACAACGAAGCGCCGCATATCATCGATGTGGTGTTGCCTTTACTC 10456

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
              |||||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db      10457 TGTTCTTACTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTCACTCCTACTGGCGGA 10516

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10517 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 10576

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      10577 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATAGCCACCTAC 10636

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
              || |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db      10637 ACCCAGCAGATCATCATCAACAGCTCCGAGGAGTTGCTGAGGGATTCCTTCCTGCCGCTC 10696

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
              |||||||||||||||| |||||||||||||||||||||||||||||||||||| |||||||
Db      10697 GCTGAACGTGTTCGCAAGCGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGAGGG 10756

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
              |||||||||||||||||||||||||||||||||| || |||||||| ||||||||||||||
Db      10757 TTTATTAAGTCGTCAACAGACGACACATCTCAAGTAGAGTCACAGATACAAGAAGACTGG 10816

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db      10817 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTACTCATCAAGTACGTCGACCTG 10876

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10877 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 10936

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
              || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||

Db      10937 GCCGAAATCTTCAACATATGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 10996

Qy        721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db      10997 ATCTCTGCCAACGAGATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 11056

Qy        781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 840
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      11057 ACAGCAGTAACAGATGGTACTCCTCAAGGCGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 11116

Qy        841 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11117 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 11176

Qy        901 TTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 960
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11177 TTGCTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 11236

Qy        961 AAAGACAGGTTCCTG---------------AAGAAAATGTCAGAACAAGATGTGGCAGAA 1005
              |||||||||||||||               ||||||||||||||||||||||||||||||
Db      11237 AAAGACAGGTTCCTGAAGGTAGGGACCCTCAAGAAAATGTCAGAACAAGATGTGGCAGAA 11296

Qy       1006 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11297 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 11356

Qy       1066 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11357 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 11416

Qy       1126 GCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAA 1185
              |||||||||| |||||||||||||||||||| || || || ||||||||||||||||||||
Db      11417 GCTGAAAATAAAGCCAAGATTATTGATGATACTGTTGAAAGGATCGTCGCTATGAGTAAA 11476

Qy       1186 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11477 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 11536

Qy       1246 TCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTA 1305
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db      11537 TCGGTGGTGTCCATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTA 11596

Qy       1306 CATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 1365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11597 CATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 11656

Qy       1366 TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAA 1425
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      11657 TTGGAAGAGGAGAACATTAGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAA 11716

Qy       1426 GACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACG 1485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11717 GACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACG 11776

Qy       1486 CAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAG 1545
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      11777 CAGCTGGTCACCACCTCCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAG 11836

Qy       1546 GATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAA 1605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11837 GATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAA 11896

Qy       1606 GAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGA 1665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11897 GAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGA 11956

Qy       1666 GCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTG 1725
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db      11957 GCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCCG 12016

Qy       1726 GCGGACCGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCC 1785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12017 GCGGACCGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCC 12076
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Qy       1786 AGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATT 1845
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12077 AGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATT 12136

Qy       1846 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACG 1905
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12137 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACG 12196

Qy       1906 TCCATCGCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAAC 1965
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12197 TCCATCGCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAAC 12256

Qy       1966 ACCAAGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCAT 2025
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12257 ACCAAGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCAT 12316

Qy       2026 GACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 2085
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12317 GACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 12376

Qy       2086 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTC 2145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12377 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTC 12436

Qy       2146 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 2205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12437 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 12496

Qy       2206 TACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGC 2265
             ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      12497 TACTCAAGCAAGGAACTGATCGACCCGGCTGGCAAAGCGAACTTCTTCAAGGCCATTGGC 12556

Qy       2266 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAAT 2325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12557 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAAT 12616

Qy       2326 CAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTC 2385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12617 CAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTC 12676

Qy       2386 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 2445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12677 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 12736

Qy       2446 CTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 2505
             ||||||| |||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db      12737 CTCAATCCGCAGAAGGACATGATCACCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 12796

Qy       2506 AATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAA 2565
             |||||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db      12797 AATGGTACAATCGTCAAGCAAATGGTGGACACACTAGTAGGATCGGCCTCCAACGTGGAA 12856

Qy       2566 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGC 2625
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12857 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGC 12916

Qy       2626 TTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAA 2685
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12917 TTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAA 12976

Qy       2686 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAG 2745
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db      12977 ATGGAACAACAGAAGAGTTATACNCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAG 13036

Qy       2746 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 2805
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13037 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 13096

Qy       2806 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 2865
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13097 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 13156

Qy       2866 GAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCA 2925
             |||||||||||||||||||| |||||||||||||||||||||||| |||||||||||||
Db      13157 GAGCCTAGATTGGCACGTTTTCTGGAGACGGCAGGTTCAGTCCTGGACTACTTCGAACCA 13216

Qy       2926 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAG 2985
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13217 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAG 13276

Qy       2986 ATCAAGGAGTCTAATA 3001
             ||||||||||||||||
Db      13277 ATCAAGGAGTCTAATA 13292
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RESULT 4
ADM68885
ID ADM68885 standard; DNA; 15405 BP.
XX
AC ADM68885;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:129.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Heliothis virescens.
XX
FH Key Location/Qualifiers
FT CDS 1. .15405
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68895.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 129; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,

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CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 15405 BP; 4086 A; 3850 C; 4173 G; 3296 T; 0 U; 0 Other;

  Query Match            94.8%;  Score 2846.4;  DB 12;  Length 15405;
  Best Local Similarity  96.8%;  Pred. No. 0;
  Matches 2920;  Conservative    0;  Mismatches   81;  Indels   15;  Gaps    1;

Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10003 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 10062

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
              |||||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||
Db      10063 AAAATGGAACAATGCATGCCGACGTTAGAGGCGATCTTAGGCGAGGTGGACCAATTCGTG 10122

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
              |||||||||||||||||||||| |||||||||||||||||||||||| | |||||||||
Db      10123 GAGTCAGACAAGACGTACAACGAAGCGCCGCATATCATCGATGTGGTGTTACCTTTACTC 10182

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10183 TGTTCTTACTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 10242

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10243 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 10302

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      10303 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATAGCCACCTAC 10362

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
              || |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db      10363 ACCCAGCAGATCATCATCAACAGCTCCGAGGAGTTGCTGAGGGATTCCTTCCTGCCGCTC 10422

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
              |||||||||||||||| |||||||||||||||||||||||||||||||||||| |||||
Db      10423 GCTGAACGTGTTCGCAAGCGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGAGGG 10482

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
              |||||||||||||||||||||||||||||| || |||||||| ||||||||||||||||||
Db      10483 TTTATTAAGTCGTCAACAGACGACACATCTCAAGTAGAGTCACAGATACAAGAAGACTGG 10542

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db      10543 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTACTCATCAAGTACGTCGACCTG 10602

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10603 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 10662

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
              || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      10663 GCCGAAATCTTCAACATATGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 10722

Qy        721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      10723 ATCTCTGCCAACGAGATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 10782

Qy        781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 840
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      10783 ACAGCAGTAACAGATGGTACTCCTCAAGGCGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 10842

Qy        841 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10843 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 10902

Qy        901 TTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 960
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10903 TTGCTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 10962

Qy        961 AAAGACAGGTTCCTG---------------AAGAAAATGTCAGAACAAGATGTGGCAGAA 1005
              |||||||||||||||               ||||||||||||||||||||||||||||||
Db      10963 AAAGACAGGTTCCTGAAGGTAGGGACCCTCAAGAAAATGTCAGAACAAGATGTGGCAGAA 11022

Qy       1006 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11023 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 11082

Qy       1066 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11083 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 11142

Qy       1126 GCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAA 1185
              |||||||||| |||||||||||||||||||| || || || ||||||||||||||||||
Db      11143 GCTGAAAATAAAGCCAAGATTATTGATGATACTGTTGAAAGGATCGTCGCTATGAGTAAA 11202

Qy       1186 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11203 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 11262

Qy       1246 TCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTA 1305
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||| |||
Db      11263 TCGGTGGTGTCCATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCGCTA 11322

Qy       1306 CATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 1365
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db      11323 CATTCTCTGCCGAGACACCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 11382

Qy       1366 TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAA 1425
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      11383 TTGGAAGAGGAGAACATTGGACAAGAAGTTATGATAGAAGATCTTACTCAATCATTCGAA 11442

Qy       1426 GACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACG 1485
              |||||||| |||||||||||||||||||||||||||||||||||||||||||| |||||||
Db      11443 GACGCAGAACTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCCGACCCCCTCACG 11502

Qy       1486 CAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAG 1545
              |||||||||||||||||||||||||||||| |||||||||||||||||||||| ||||||
Db      11503 CAGCTGGTCACCACCTTCTGTCGCGGCGCCATGACTGAGAGGTCCGGCGCTTTACAGGAG 11562

Qy       1546 GATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAA 1605
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11563 GATCCCCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAA 11622

Qy       1606 GAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGA 1665
              |||||||| ||||| |||||||||||||||||||||||||| ||||| || ||||||||||
Db      11623 GAAGGGGGCGGGGAAGAAGAGGAAGGGGGTGGAGAAGCTGAGGCCGAGGACGAAGGCAGA 11682

Qy       1666 GCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTG 1725
              |||||||||||||||||| |||||||||| ||||| |||||||||||||||||| |||
Db      11683 GCCAGTATACACGAACAAGAGATGGAGAAACAGAAGCTTCTATTCCACCAAGCGCGACTG 11742

Qy       1726 GCGGACCGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCC 1785
              || ||||| || |||||||| |||||||||||||| |||||||||| ||||||||||||
Db      11743 GCAGACCGCGGTGTTGCCGAGATGGTGTTGCTGCATATCTCCGCGTCTAAAGGCCTGCCC 11802

Qy       1786 AGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATT 1845
              |||||||||||||||||| |||||||||||||||||||||||||| || |||||||||
Db      11803 AGCGAGATGGTCATGAAGACATTACAGCTCGGTATTAGTATACTGAGAGGAGGCAATATT 11862

Qy       1846 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACG 1905
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Db      11863 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGATTCTTCACG 11922

Qy       1906 TCCATCGCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAAC 1965

Db      11923 TCCATCGCCGGCCTCATGAACTCCTGCTCAGTGCTCGATCTTGACGCCTTCGAGAGGAAC 11982

Qy       1966 ACCAAGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCAT 2025

Db      11983 ACCAAAGCTGAAGGTCTGGGCGTGGGTCTGGAAGGCGCCGCAGGAGAGAAGAACATGCAT 12042

Qy       2026 GACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 2085

Db      12043 GACGCCGAGTTCACCTGCGCACTCTTTAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 12102

Qy       2086 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTC 2145

Db      12103 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACGACAGTGAACGTGGTC 12162

Qy       2146 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 2205

Db      12163 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 12222

Qy       2206 TACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGC 2265

Db      12223 TACTCTAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAATTTCTTCAAGGCCATTGGC 12282

Qy       2266 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAAT 2325

Db      12283 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACTCAGAAC 12342

Qy       2326 CAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTC 2385

Db      12343 CAGCAGGCTTTAGCTCACTCTAGGTTATGGGACGCTGTCGGTGGTTTCTTGTTCCTATTC 12402

Qy       2386 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 2445

Db      12403 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 12462

Qy       2446 CTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 2505

Db      12463 CTCAATCTGCAGAAGGACATGATCACCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 12522

Qy       2506 AATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAA 2565

Db      12523 AATGGTACAATCGGCAAGCAAATGGTGGACACTCTAGTAGAATCGGCCTCCAACGTGGAA 12582

Qy       2566 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGC 2625

Db      12583 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACTTCCAGCGCCAGC 12642

Qy       2626 TTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAA 2685

Db      12643 TTCCAAGAGATAGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAG 12702

Qy       2686 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAG 2745

Db      12703 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCTTAGCTTGCTGCGAG 12762

Qy       2746 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 2805

Db      12763 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 12822

Qy       2806 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 2865

Db      12823 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 12882

Qy       2866 GAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCA 2925

Db      12883 GAGCCTAGATTGGCTCGTTTCCTGGAGACGGCGGGTTCAGTCCTGAACTACTTCGAACCA 12942

Qy       2926 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAG 2985

Db      12943 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCTAAGCGCATCGAGCGAGTCTACTTCGAG 13002

Qy       2986 ATCAAGGAGTCTAATA 3001

Db      13003 ATCAAGGAGTCTAATA 13018
```

RESULT 5
ADM68899
ID ADM68899 standard; DNA; 15429 BP.
XX
AC ADM68899;
XX
DT 17-JUN-2004 (first entry)
XX
DE Heliothis virescens ryanodine receptor encoding DNA SEQ ID NO:143.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Heliothis virescens.
XX
FH Key Location/Qualifiers
FT CDS 1. .15429
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68900.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 143; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is

CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15429 BP; 4084 A; 3856 C; 4190 G; 3299 T; 0 U; 0 Other;

Query Match 94.8%; Score 2844.8; DB 12; Length 15429;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2919; Conservative 0; Mismatches 82; Indels 15; Gaps 1;

```
Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10027 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 10086

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      10087 AAAATGGAACAATGCATGCCGACGTTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 10146

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
              |||||||||||||||||||||||| |||||||||||||||||||||||||| ||||||||||
Db      10147 GAGTCAGACAAGACGTACAACGAAGCGCCGCATATCATCGATGTGGTGTTGCCTTTACTC 10206

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10207 TGTTCTTACTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 10266

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10267 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 10326

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      10327 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATAGCCACCTAC 10386

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
              || |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db      10387 ACCCAGCAGATCATCATCAACAGCTCCGAGGAGTTGCTGAGGGATTCCTTCCTGCCGCTC 10446

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||| |||
Db      10447 GCTGAACGTGTTCGCAAGCGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGAGGG 10506

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
              |||||||||||||||||||||||||||||||| || |||||||| ||||||||||||||||
Db      10507 TTTATTAAGTCGTCAACAGACGACACATCTCAAGTAGAGTCACAGATACAAGAAGACTGG 10566

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db      10567 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTACTCATCAAGTACGTCGACCTG 10626

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10627 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 10686

Qy        661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
              || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      10687 GCCGAAATCTTCAACATATGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 10746

Qy        721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      10747 ATCTCTGCCAACGAGATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 10806

Qy        781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 840
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      10807 ACAGCAGTAACAGATGGTACTCCTCAAGGCGGTGGAAAGAAAAAGAAGAAGCACCGTGAT 10866

Qy        841 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      10867 AAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGG 10926

Qy        901 TTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 960
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10927 TTGCTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGT 10986

Qy        961 AAAGACAGGTTCCTG----------------AAGAAAATGTCAGAACAAGATGTGGCAGAA 1005
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      10987 AAAGACAGGTTCCTGAAGGTAGGGACCCTCAAGAAAATGTCAGAACAAGATGTGGCAGAA 11046

Qy       1006 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11047 TTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGG 11106

Qy       1066 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11107 CAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACT 11166

Qy       1126 GCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAA 1185
              |||||||||| |||||||||||||||||||| || || || ||||||||||||||||||
Db      11167 GCTGAAAATAAAGCCAAGATTATTGATGATACTGTTGAAAGGATCGTCGCTATGAGTAAA 11226

Qy       1186 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11227 GTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGG 11286

Qy       1246 TCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTA 1305
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||| |||
Db      11287 TCGGTGGTGTCCATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCGCTA 11346

Qy       1306 CATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 1365
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      11347 CATTCTCTGCCGAGACACCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGG 11406

Qy       1366 TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAA 1425
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      11407 TTGGAAGAGGAGAACATTGGACAAGAAGTTATGATAGAAGATCTTACTCAATCATTCGAA 11466

Qy       1426 GACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACG 1485
              |||||||| |||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      11467 GACGCAGAACTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCCGACCCCCTCACG 11526

Qy       1486 CAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAG 1545
              |||||||||||||||||||||||| |||||||||||||||||||||||||||| ||||||
Db      11527 CAGCTGGTCACCACCTTCTGTCGCGGCGCCATGACTGAGAGGTCCGGCGCTTTACAGGAG 11586

Qy       1546 GATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAA 1605
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11587 GATCCCCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAA 11646

Qy       1606 GAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGA 1665
              |||||||| ||||| |||||||||||||||||||||||||||| ||||| || ||||||||
Db      11647 GAAGGGGGCGGGGAAGAAGAGGAAGGGGGTGGAGAAGCTGAGGCCGAGGACGAAGGCAGA 11706

Qy       1666 GCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTG 1725
              |||||||||||||||||| |||||||||| ||||| |||||||||||||||| |||||||
Db      11707 GCCAGTATACACGAACAAGAGATGGAGAAACAGAAGCTTCTATTCCACCAAGCGCGACTG 11766

Qy       1726 GCGGACCGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCC 1785
              || ||||| || |||||||| |||||||||||||| |||||||||| ||||||||||||||
Db      11767 GCAGACCGCGGTGTTGCCGAGATGGTGTTGCTGCATATCTCCGCGTCTAAAGGCCTGCCC 11826

Qy       1786 AGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATT 1845
              |||||||||||||||||||||||||||||||||||||||||||||| || |||||||||||
Db      11827 AGCGAGATGGTCATGAAGACATTACAGCTCGGTATTAGTATACTGAGAGGAGGCAATATT 11886

Qy       1846 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACG 1905
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Db      11887 GATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGATTCTTCACG 11946

Qy       1906 TCCATCGCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAAC 1965
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      11947 TCCATCGCCGGCCTCATGAACTCCTGCTCAGTGCTCGATCTTGACGCCTTCGAGAGGAAC 12006
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Qy       1966 ACCAAGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCAT 2025
             ||||| |||||||||||||||||||||||||||||| || || ||||||||||||||||||
Db      12007 ACCAAAGCTGAAGGTCTGGGCGTGGGTCTGGAAGGCGCCGCAGGAGAGAAGAACATGCAT 12066

Qy       2026 GACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 2085
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      12067 GACGCCGAGTTCACCTGCGCACTCTTTAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 12126

Qy       2086 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTC 2145
             |||||||||||||||||||||||||||||||||||||||||| |  ||||||||||||||
Db      12127 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGGCGGCAGTGAACGTGGTC 12186

Qy       2146 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 2205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12187 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 12246

Qy       2206 TACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGC 2265
             ||||| |||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db      12247 TACTCTAGCAAGGAACTGATCGACCCGGCCGGCAAGGCGAATTTCTTCAAGGCCATTGGC 12306

Qy       2266 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAAT 2325
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db      12307 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACTCAGAAC 12366

Qy       2326 CAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTC 2385
             |||||||||| |||||||| ||||| |||||||||||||||||| ||||||||||||
Db      12367 CAGCAGGCTTTAGCTCACTCTAGGTTATGGGACGCTGTCGGTGGTTTCTTGTTCCTATTC 12426

Qy       2386 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 2445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12427 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 12486

Qy       2446 CTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 2505
             ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db      12487 CTCAATCTGCAGAAGGACATGATCACCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 12546

Qy       2506 AATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAA 2565
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      12547 AATGGTACAATCGGCAAGCAAATGGTGGACACTCTAGTAGAATCGGCCTCCAACGTGGAA 12606

Qy       2566 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGC 2625
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      12607 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACTTCCAGCGCCAGC 12666

Qy       2626 TTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAA 2685
             ||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db      12667 TTCCAAGAGATAGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAG 12726

Qy       2686 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAG 2745
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      12727 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCTTAGCTTGCTGCGAG 12786

Qy       2746 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 2805
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12787 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCC 12846

Qy       2806 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 2865
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12847 AAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAAC 12906

Qy       2866 GAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCA 2925
             |||||||||||||| |||||||||||||||| ||||||||||||||||||||||||||||||
Db      12907 GAGCCTAGATTGGCTCGTTTCCTGGAGACGGCGGGTTCAGTCCTGAACTACTTCGAACCA 12966

Qy       2926 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAG 2985
             |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Db      12967 TTCCTGGGCCGTATCGAGATCATGGGCGGCTCTAAGCGCATCGAGCGAGTCTACTTCGAG 13026

Qy       2986 ATCAAGGAGTCTAATA 3001
             ||||||||||||||||
Db      13027 ATCAAGGAGTCTAATA 13042
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RESULT 6
ABL16881
ID   ABL16881 standard; DNA; 15606 BP.
XX
AC   ABL16881;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 2116.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 2116; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 15606 BP; 3731 A; 4275 C; 4399 G; 3201 T; 0 U; 0 Other;

  Query Match             57.3%;  Score 1718.2;  DB 4;  Length 15606;
  Best Local Similarity   73.9%;  Pred. No. 0;
  Matches 2236;  Conservative    0;  Mismatches  753;  Indels   36;  Gaps    3;

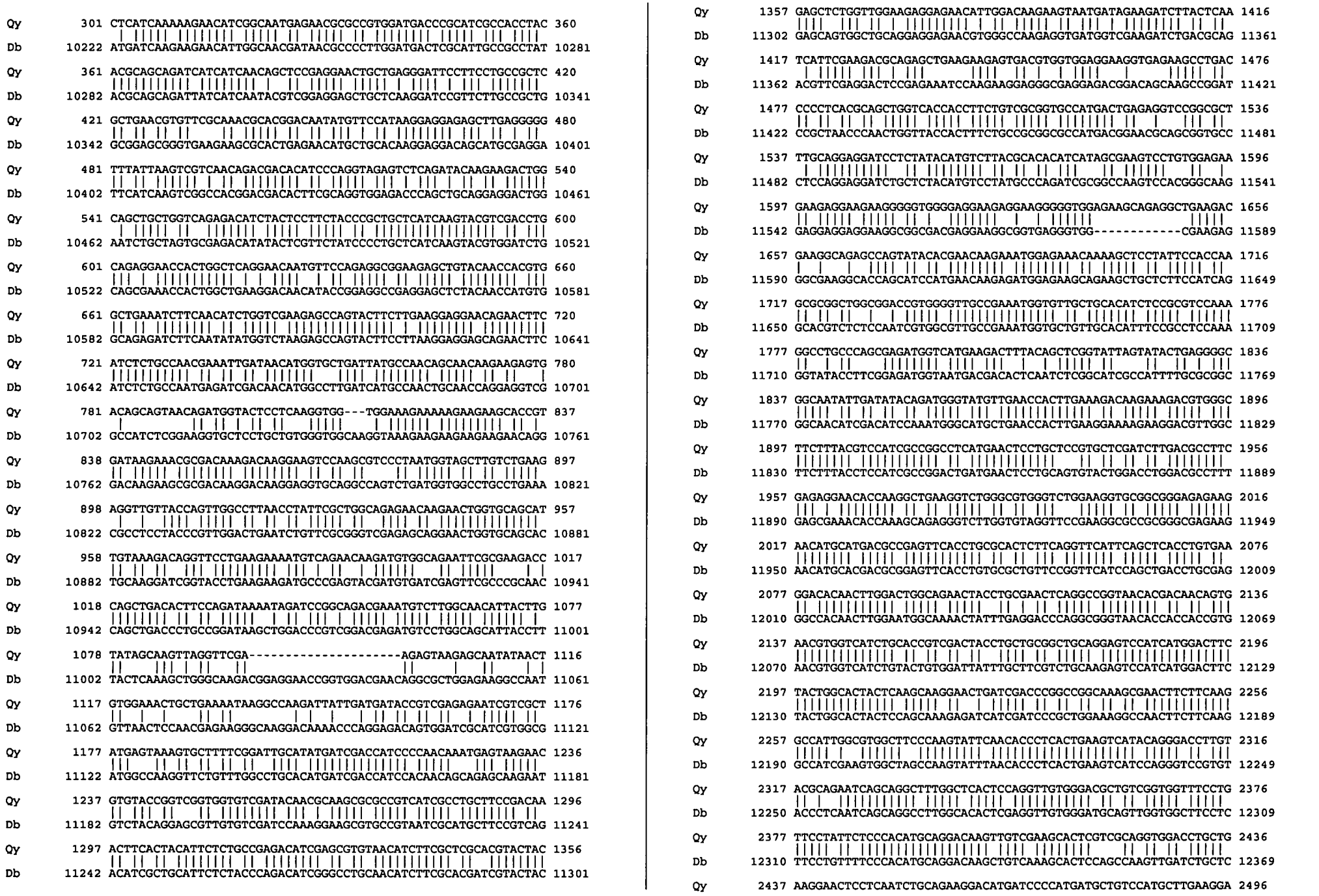
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              |||| |||  |||| ||| | || || || || ||  |||| || || ||||| |||
Db       9922 CAGTACTCGCTGCTCAACCGTATTGCGGATCACTCACTGGAGGCGCAGGACATTATGGTC 9981

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
              || |||||    || ||||| |  |||||||| ||  | | |||||| ||||| || |||
Db       9982 AAGATGGAGAGCTGTATGCCAAATCTAGAGACCATTCTCGCCGAGGTCGACCAGTTTGTG 10041

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
              ||||| |||||||| ||||| || ||||| ||||| ||||| ||| | ||||| | ||
Db      10042 GAGTCGGACAAGACATACAATGATGCGCCTCATATTATCGACGTGATCCTGCCGCTGCTT 10101

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
              ||  | ||| | ||||| |||||| | ||||| || ||||||||| | ||| ||  | ||
Db      10102 TGCGCCTATCTACCGTTTTGGTGGTCCCAGGGACCGGATAATGTCAGTCCCACCAGTGGC 10161

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
              |||||||| || ||||| ||||| || |||||||| | | | ||    ||||| || ||
Db      10162 AACCACGTGACCATGGTCACAGCCGATCACATGAATCCGTTGCTGCGAAATGTGCTTAAA 10221
```



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Db      12370 AAGGAACTGCTGAATCTGCAAAAGGACATGATCACCATGATGCTTTCCATGCTGGAAGGA 12429

Qy       2497 AATGTTGTTAATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCC 2556

Db      12430 AATGTTGTTAACGGCACTATTGGCAAGCAGATGGTGGACACGCTGGTGGAGTCTGCCAGC 12489

Qy       2557 AACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCC 2616

Db      12490 AATGTGGAGCTGATTCTTAAGTACTTCGACATGTTCCTGAAGCTCGCCGACCTTATCGAA 12549

Qy       2617 AGCGCCAGCTTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTC 2676

Db      12550 TCGCCCAGCTTCCACGAAGTGGACATGAAGAACGAGGGTTGGGTGACCCCCAAAGACTTT 12609

Qy       2677 AAGGAGAAAATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCT 2736

Db      12610 AGGGAAAAGATGGAGCAATCCAAGAACTACACACCGGAAGAAATGGATTTCCTTTTGGCC 12669

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Db      12670 TGCTGCGAGCGCAACCACGAGGGCAAGATCGATTACCGGGCCTTCGTGGAGCACTTCCAC 12729

Qy       2797 GAGCCTGCCAAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACAT 2856

Db      12730 GAACCATCAAAGGAGATCGGTTTCAACCTGGCTGTGCTCCTGACCAACCTCAGCGAACAC 12789

Qy       2857 ATGCCGAACGAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTAC 2916

Db      12790 ATGCCAAACGAACCGCGCCTGGCGCGCTTCCTGGAGACCGCCGGCTCGGTGCTCAACTAC 12849

Qy       2917 TTCGAACCATTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTC 2976

Db      12850 TTCGAGCCCTTCCTGGGCCGCATCGAGATTCTCGGCAGCTCCAAGCGCATCGAGCGCGTT 12909

Qy       2977 TACTTCGAGATCAAGGAGTCTAATA 3001

Db      12910 TACTTTGAGATCAAGGACTCGAACA 12934
```

```
RESULT 7
ADM68765
ID   ADM68765 standard; DNA; 16363 BP.
XX
AC   ADM68765;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Drosophila melanogaster ryanodine receptor encoding DNA SEQ ID NO:9.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS   Drosophila melanogaster.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15330
FT                   /*tag= a
FT                   /product= "ryanodine receptor"
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
DR   P-PSDB; ADM68766.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Claim 6; SEQ ID NO 9; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 16363 BP; 3940 A; 4448 C; 4559 G; 3414 T; 0 U; 2 Other;
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  Query Match             57.3%;  Score 1718.2;  DB 12;  Length 16363;
  Best Local Similarity   73.9%;  Pred. No. 0;
  Matches 2236;  Conservative    0;  Mismatches  753;  Indels   36;  Gaps    3;

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Db       9928 CAGTACTCGCTGCTCAACCGTATTGCGGATCACTCACTGGAGGCGCAGGACATTATGGTC 9987

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120

Db       9988 AAGATGGAGAGCTGTATGCCAAATCTAGAGACCATTCTCGCCGAGGTCGACCAGTTTGTG 10047

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180

Db      10048 GAGTCGGACAAGACATACAATGATGCGCCTCATATTATCGACGTGATCCTGCCGCTGCTT 10107

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240

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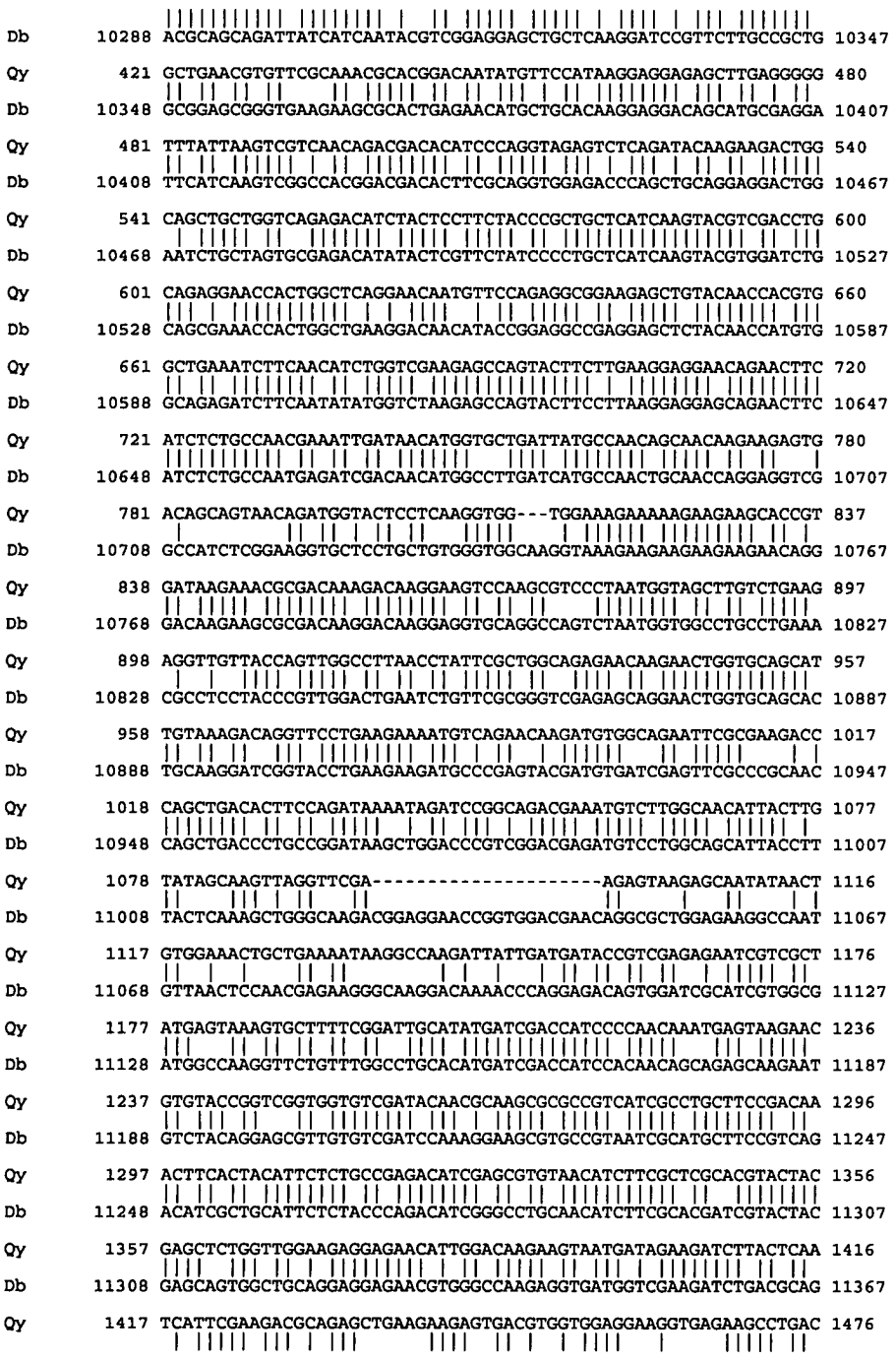
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Db      10168 AACCACGTGACCATGGTCACAGCCGATCACATGAATCCGTTGCTGCGAAATGTGCTTAAA 10227

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360

Db      10228 ATGATCAAGAAGAACATTGGCAACGATAACGCCCCTTGGATGACTCGCATTGCCGCCTAT 10287

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
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Db 10288 ACGCAGCAGATTATCATCAATACGTCGGAGGAGCTGCTCAAGGATCCGTTCTTGCCGCTG 10347
Qy 421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
Db 10348 GCGGAGCGGGTGAAGAAGCGCACTGAGAACATGCTGCACAAGGAGGACAGCATGCGAGGA 10407
Qy 481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
Db 10408 TTCATCAAGTCGGCCACGGACGACACTTCGCAGGTGGAGACCCAGCTGCAGGAGGACTGG 10467
Qy 541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
Db 10468 AATCTGCTAGTGCGAGACATATACTCGTTCTATCCCCTGCTCATCAAGTACGTGGATCTG 10527
Qy 601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
Db 10528 CAGCGAAACCACTGGCTGAAGGACAACATACCGGAGGCCGAGGAGCTCTACAACCATGTG 10587
Qy 661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
Db 10588 GCAGAGATCTTCAATATATGGTCTAAGAGCCAGTACTTCCTTAAGGAGGAGCAGAACTTC 10647
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Db 10648 ATCTCTGCCAATGAGATCGACAACATGGCCTTGATCATGCCAACTGCAACCAGGAGGTCG 10707
Qy 781 ACAGCAGTAACAGATGGTACTCCTCAAGGTGG---TGGAAAGAAAAAGAAGAAGCACCGT 837
Db 10708 GCCATCTCGGAAGGTGCTCCTGCTGTGGGTGGCAAGGTAAAGAAGAAGAAGAAGAACAGG 10767
Qy 838 GATAAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAG 897
Db 10768 GACAAGAAGCGCGACAAGGACAAGGAGGTGCAGGCCAGTCTAATGGTGGCCTGCCTGAAA 10827
Qy 898 AGGTTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCAT 957
Db 10828 CGCCTCCTACCCGTTGGACTGAATCTGTTCGCGGGTCGAGAGCAGGAACTGGTGCAGCAC 10887
Qy 958 TGTAAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACC 1017
Db 10888 TGCAAGGATCGGTACCTGAAGAAGATGCCCGAGTACGATGTGATCGAGTTCGCCCGCAAC 10947
Qy 1018 CAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTACTTG 1077
Db 10948 CAGCTGACCCTGCCGGATAAGCTGGACCCGTCGGACGAGATGTCCTGGCAGCATTACCTT 11007
Qy 1078 TATAGCAAGTTAGGTTCGA----------AGAGTAAGAGCAATATAACT 1116
Db 11008 TACTCAAAGCTGGGCAAGACGGAGGAACCGGTGGACGAACAGGCGCTGGAGAAGGCCAAT 11067
Qy 1117 GTGGAAACTGCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCT 1176
Db 11068 GTTAACTCCAACGAGAAGGGCAAGGACAAAACCCAGGAGACAGTGGATCGCATCGTGGCG 11127
Qy 1177 ATGAGTAAAGTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAATGAGTAAGAAC 1236
Db 11128 ATGGCCAAGGTTCTGTTTGGCCTGCACATGATCGACCATCCACAACAGCAGAGCAAGAAT 11187
Qy 1237 GTGTACCGGTCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAA 1296
Db 11188 GTCTACAGGAGCGTTGTGTCGATCCAAAGGAAGCGTGCCGTAATCGCATGCTTCCGTCAG 11247
Qy 1297 ACTTCACTACATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTAC 1356
Db 11248 ACATCGCTGCATTCTCTACCCAGACATCGGGCCTGCAACATCTTCGCACGATCGTACTAC 11307
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Db 11308 GAGCAGTGGCTGCAGGAGGAGAACGTGGGCCAAGAGGTGATGGTCGAAGATCTGACGCAG 11367
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Db 11368 ACGTTCGAGGACTCCGAGAAATCCAAGAAGGAGGGCGAGGAGACGGACAGCAAGCCGGAT 11427
Qy 1477 CCCCTCACGCAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCT 1536
Db 11428 CCGCTAACCCAACTGGTTACCACTTTCTGCCGCGGCGCCATGACGGAACGCAGCGGTGCC 11487
Qy 1537 TTGCAGGAGGATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAA 1596
Db 11488 CTCCAGGAGGATCTGCTCTACATGTCCTATGCCCAGATCGCGGCCAAGTCCACGGGCAAG 11547
Qy 1597 GAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGAC 1656
Db 11548 GAGGAGGAGGAAGGCGGCGACGAAGAAGGCGGTGAGGGTGG----------CGAAGAG 11595
Qy 1657 GAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAA 1716
Db 11596 GCCGAAGGCACCAGCATCCATGAACAAGAGATGGAGAAGCAGAAGCTGCTCTTCCATCAG 11655
Qy 1717 GCGCGGCTGGCGGACCGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAA 1776
Db 11656 GCACGTCTCTCCAATCGTGGCGTTGCCGAAATGGTGCTGTTGCACGTTTCCGCCTCCAAA 11715
Qy 1777 GGCCTGCCCAGCGAGATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGC 1836
Db 11716 GGTATACCTTCGGAGATGGTAATGACGACACTCAATCTCGGCATCGCCATTTTGCGCGGC 11775
Qy 1837 GGCAATATTGATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGC 1896
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Qy 1957 GAGAGGAACACCAAGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAG 2016
Db 11896 GAGCGAAACACCAAAGCAGAGGGTCTTGGTGTAGGTTCCGAAGGCGCCGCGGGCGAGAAG 11955
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Db 12016 GGCCACAACTTGGAATGGCAAAACTATTTGAGGACCCAGGCGGGTAACACCACCACCGTG 12075
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Db 12076 AACGTGGTCATCTGTACTGTGGATTATTTGCTTCGTCTGCAAGAGTCCATCATGGACTTC 12135
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Db 12136 TACTGGCACTACTCCAGCAAAGAGATCATCGATCCCGCTGGAAAGGCCAACTTCTTCAAG 12195
Qy 2257 GCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGT 2316
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Qy 2317 ACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTG 2376
Db 12256 ACCCTCAATCAGCAGGCCTTGGCACACTCGAGGTTGTGGGATGCAGTTGGTGGCTTCCTC 12315
Qy 2377 TTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTG 2436
Db 12316 TTCCTGTTTTCCCACATGCAGGACAAGCTGTCAAAGCACTCCAGCCAAGTTGATCTGCTC 12375
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Db 12376 AAGGAACTGCTGAATCTGCAAAAGGACATGATCACCATGATGCTTTCCATGCTGGAAGGA 12435
Qy 2497 AATGTTGTTAATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCC 2556
Db 12436 AATGTTGTTAACGGCACTATTGGCAAGCAGATGGTGGACACGCTGGTGGAGTCTGCCAGC 12495

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Qy       2557 AACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCC 2616
Db      12496 AATGTGGAGCTGATTCTTAAGTACTTCGACATGTTCCTGAAGCTCGCCGACCTTATCGAA 12555

Qy       2617 AGCGCCAGCTTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTC 2676
Db      12556 TCGCCCAGCTTCCACGAAGTGGACATGAAGAACGAGGGTTGGGTGACCCCCAAAGACTTT 12615

Qy       2677 AAGGAGAAAATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCT 2736
Db      12616 AGGGAAAAGATGGAGCAATCCAAGAACTACACACCGGAAGAAATGGATTTCCTTTGGCC 12675

Qy       2737 TGCTGCGAGACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCAC 2796
Db      12676 TGCTGCGAGCGCAACCACGAGGGCAAGATCGATTACCGGGCCTTCGTGGAGCACTTCCAC 12735

Qy       2797 GAGCCTGCCAAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACAT 2856
Db      12736 GAACCATCAAAGGAGATCGGTTTCAACCTGGCTGTGCTCCTGACCAACCTCAGCGAACAC 12795

Qy       2857 ATGCCGAACGAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTAC 2916
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Qy       2917 TTCGAACCATTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTC 2976
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Qy       2977 TACTTCGAGATCAAGGAGTCTAATA 3001
Db      12916 TACTTTGAGATCAAGGACTCGAACA 12940
```

RESULT 8
ADM68763
ID ADM68763 standard; DNA; 15413 BP.
XX
AC ADM68763;
XX
DT 17-JUN-2004 (first entry)
XX
DE Peregrinus maidis ryanodine receptor encoding DNA SEQ ID NO:7.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 17. .15400
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68764.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 7; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15413 BP; 4666 A; 2966 C; 3619 G; 4160 T; 0 U; 2 Other;

 Query Match 52.6%; Score 1578.6; DB 12; Length 15413;
 Best Local Similarity 71.2%; Pred. No. 0;
 Matches 2142; Conservative 0; Mismatches 829; Indels 36; Gaps 3;

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Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
Db      10073 CGAATGGAAAGTACAATGCCAACTTTAGACAACATTTTGAGTGAAGTTGATCAGTTTGTA 10132

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
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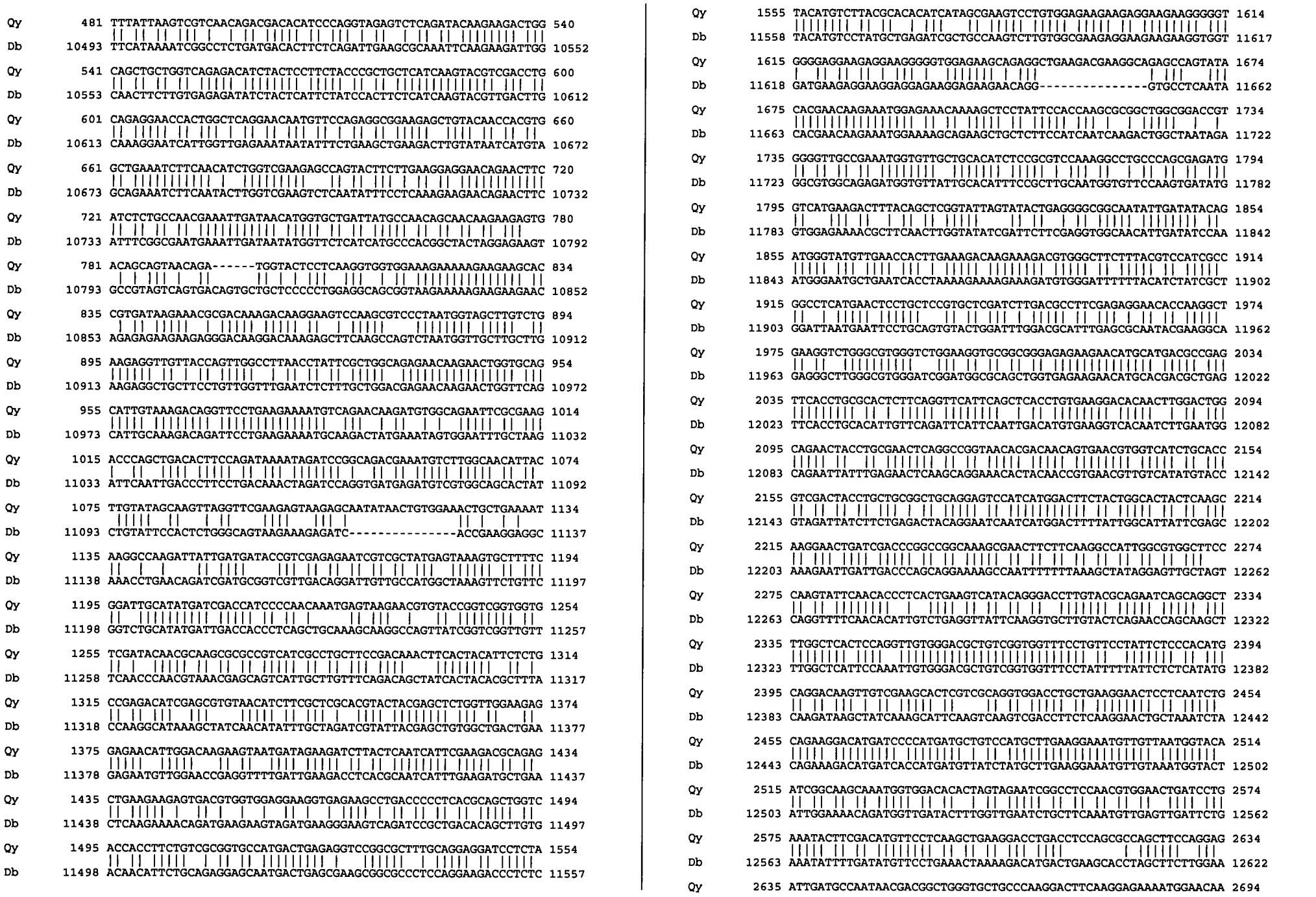
Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
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Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
Db      10253 AATTATGTCACAACGGTGACGAGTGAACATATGAATCAACTTTTAAAGAATGTACTCAAA 10312

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
Db      10313 ATGATTAAGAAAAATATTGGAAATGAAAGCGCTCCATGGATGACTAGGATAGCAGCATAT 10372

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
Db      10373 ACACAACAAATAATAATCAACTCTTCGGAGGAGTTGTTGAAAGATCCATTCCTCCCATTG 10432

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
Db      10433 GCTGAAAGAGTGAAGAAACGGACTGATGCTATGTTTCATAAAGAGGAATCACTCAGGGGA 10492
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Qy       2755 GACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATC 2814

Db      12743 GATGGAAAGGTTGATTACATTGGCTTCGTTGACAGATTCCATGAACCTTCCAAAGAAATC 12802

Qy       2815 GGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGA 2874

Db      12803 GGTTTCAACTTGGCTGTATTATTAACAAACCTATCTGAGCACATGCCGAATGAGCCCAGG 12862

Qy       2875 TTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGC 2934

Db      12863 TTGGCTAGATTTTTGGAAACTGCAGGCAGTGTACTAAATTACTTTGAACCATTCCTAGGA 12922

Qy       2935 CGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAG 2994

Db      12923 CGTATTGAAATTATGGGCAGCAGTAAACGTATAGAAAGAGTGTATTTTGAAATCAAGGAG 12982

Qy       2995 TCTAATA 3001

Db      12983 TCAAATA 12989


RESULT 9
ADM68761
ID   ADM68761 standard; DNA; 15315 BP.
XX
AC   ADM68761;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Periplaneta americana ryanodine receptor encoding DNA SEQ ID NO:5.
XX
KW   ryanodine receptor; insect ion channel; insecticide; pesticide;
KW   calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS   Periplaneta americana.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .15315
FT                   /*tag= a
FT                   /product= "ryanodine receptor"
XX
PN   WO2004027042-A2.
XX
PD   01-APR-2004.
XX
PF   23-SEP-2003; 2003WO-US029834.
XX
PR   23-SEP-2002; 2002US-0412795P.
PR   18-NOV-2002; 2002US-0427324P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Caspar T,  Cordova D,  Gutteridge S,  Rauh JJ,  Smith RM,  Wu L;
PI   Tao Y;
XX
DR   WPI; 2004-295411/27.
DR   P-PSDB; ADM68762.
XX
PT   New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT   for isolating other pest ryanodine receptors and in developing screens to
PT   identify insecticidally active compounds.
XX
PS   Claim 6; SEQ ID NO 5; 687pp; English.
XX
CC   The present invention describes an isolated nucleotide fragment (I)
CC   comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC   having an amino acid sequence identity of at least 80% when compared to a
CC   polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC   128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC   nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC   1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC   construct comprising (I) operably linked to at least one regulatory
CC   sequence; (2) a transformed host cell comprising the recombinant
CC   construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC   related polypeptides; (4) an isolated polypeptide having ryanodine
CC   receptor activity; (5) a method for evaluating at least one compound for
CC   its ability to modulate calcium homeostasis; (6) a method for evaluating
CC   at least one compound which modulates ryanodine receptor activity; (7) an
CC   isolated nucleic acid fragment encoding an insect ion channel comprising
CC   at least two fully defined polypeptide sequences selected from SEQ ID
CC   NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC   120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC   insect ion channel; (9) a method for expressing an isolated nucleic acid
CC   fragment encoding a toxic insect ion channel; and (10) recombinant
CC   construct comprising in the 5' to 3' direction a promoter operably linked
CC   to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC   The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC   useful for the isolation of other pest ryanodine receptors and developing
CC   of screens to identify insecticidally active compounds. The nucleic acid
CC   fragments are useful as pesticides, fragments of protein for antibody
CC   production, fragments of protein for determination of the structure of
CC   insecticide binding sites and in the identification of insecticides that
CC   disrupt the calcium balance in cells through other messengers that
CC   interact with the receptor calcium release mechanism. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 15315 BP; 5206 A; 2494 C; 3141 G; 4474 T; 0 U; 0 Other;

  Query Match             49.6%;  Score 1489.6;  DB 12;  Length 15315;
  Best Local Similarity   69.3%;  Pred. No. 0;
  Matches 2083;  Conservative    0;  Mismatches  894;  Indels   27;  Gaps    3;

Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60

Db       9967 CAATATTCGCTTCTTAATCGATTTGCTGACAGTTCATTGGAAGCTCAGGATATAATGTCT 10026

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120

Db      10027 AGAATGGAAGGCACTATGCCTACTCTAGAAACTGTATTAAATGAAGTTGACCAGTTTGTC 10086

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180

Db      10087 GAATCAGAAAAAACATATGCTGATGCACCTCACATTATTGATGTTATTTTACCTTTATTG 10146

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240

Db      10147 TGTTCATACTTACCGTACTGGTGGGCACAAGGTCCAGATAATGTTGCTCTGACCACAGGT 10206

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300

Db      10207 AATCATGTTACAATGGTGACCAGCGAACATATGAACTGTCTATTAAAAAATGTTTTAAAG 10266

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360

Db      10267 TTAATAAAAAAAAATATTGGAAATGATAATGCCCCTTGGATGACACAAATAGCAGCTTAT 10326

Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420

Db      10327 ACACAACAAATAATTATTAATTCTTCAGAAGAATTATTAAAAGATCCATTTCTACCACTT 10386

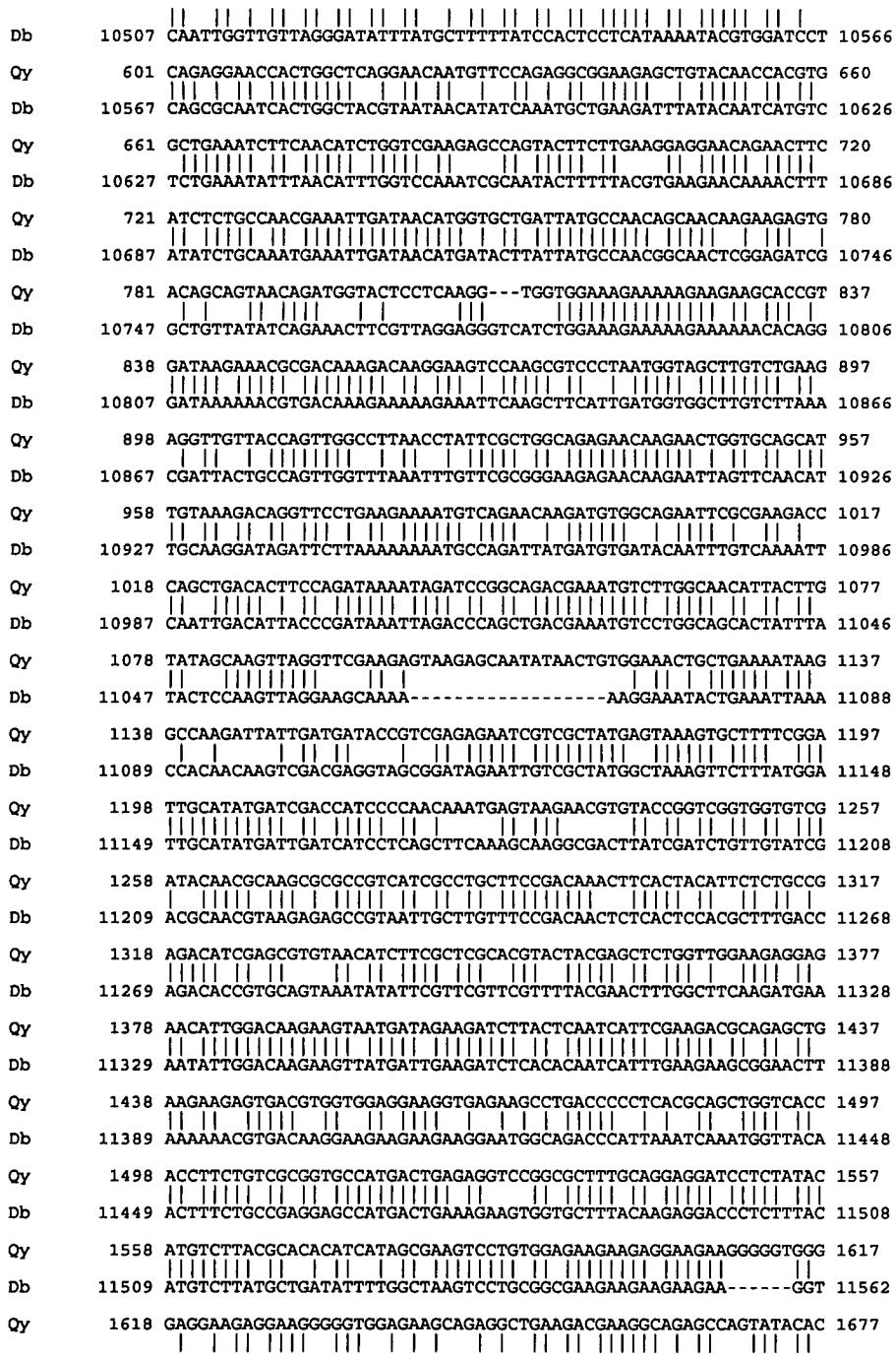
Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480

Db      10387 GCAGAACGAGTTAAAAAACGTACAGAAACATTATACCATAAAGAAGAATCATTAAGAGGA 10446

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540

Db      10447 TTTATAAAATCATCTACTGATGATACGTCCCAAATCGAAGCACAAATACAAGAAGATTGG 10506

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
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Db 10507 CAATTGGTTGTTAGGGATATTTATGCTTTTTATCCACTCCTCATAAAATACGTGGATCCT 10566
Qy 601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
Db 10567 CAGCGCAATCACTGGCTACGTAATAACATATCAAATGCTGAAGATTTATACAATCATGTC 10626
Qy 661 GCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTC 720
Db 10627 TCTGAAATATTTAACATTTGGTCCAAATCGCAATACTTTTTACGTGAAGAACAAAACTTT 10686
Qy 721 ATCTCTGCCAACGAAATTGATAACATGGTGCTGATTATGCCAACAGCAACAAGAAGAGTG 780
Db 10687 ATATCTGCAAATGAAATTGATAACATGATACTTATTATGCCAACGGCAACTCGGAGATCG 10746
Qy 781 ACAGCAGTAACAGATGGTACTCCTCAAGG---TGGTGGAAAGAAAAAGAAGAAGCACCGT 837
Db 10747 GCTGTTATATCAGAAACTTCGTTAGGAGGGTCATCTGGAAAGAAAAAGAAAAAACACAGG 10806
Qy 838 GATAAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTGAAG 897
Db 10807 GATAAAAAACGTGACAAAGAAAAAGAAATTCAAGCTTCATTGATGGTGGCTTGTCTTAAA 10866
Qy 898 AGGTTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAGCAT 957
Db 10867 CGATTACTGCCAGTTGGTTTAAATTTGTTCGCGGGAAGAGAACAAGAATTAGTTCAACAT 10926
Qy 958 TGTAAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGATGTGGCAGAATTCGCGAAGACC 1017
Db 10927 TGCAAGGATAGATTCTTAAAAAAAATGCCAGATTATGATGTGATACAATTTGTCAAAATT 10986
Qy 1018 CAGCTGACACTTCCAGATAAAATAGATCCGGCAGACGAAATGTCTTGGCAACATTACTTG 1077
Db 10987 CAATTGACATTACCCGATAAATTAGACCCAGCTGACGAAATGTCCTGGCAGCACTATTTA 11046
Qy 1078 TATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAACTGTGGAAACTGCTGAAAATAAG 1137
Db 11047 TACTCCAAGTTAGGAAGCAAAA----------AAGGAAATACTGAAATTAAA 11088
Qy 1138 GCCAAGATTATTGATGATACCGTCGAGAGAATCGTCGCTATGAGTAAAGTGCTTTTCGGA 1197
Db 11089 CCACAACAAGTCGACGAGGTAGCGGATAGAATTGTCGCTATGGCTAAAGTTCTTTATGGA 11148
Qy 1198 TTGCATATGATCGACCATCCCCAACAAATGAGTAAGAACGTGTACCGGTCGGTGGTGTCG 1257
Db 11149 TTGCATATGATTGATCATCCTCAGCTTCAAAGCAAGGCGACTTATCGATCTGTTGTATCG 11208
Qy 1258 ATACAACGCAAGCGCGCCGTCATCGCCTGCTTCCGACAAACTTCACTACATTCTCTGCCG 1317
Db 11209 ACGCAACGTAAGAGAGCCGTAATTGCTTGTTTCCGACAACTCTCACTCCACGCTTTGACC 11268
Qy 1318 AGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGGTTGGAAGAGGAG 1377
Db 11269 AGACACCGTGCAGTAAATATATTCGTTCGTTCGTTTTACGAACTTTGGCTTCAAGATGAA 11328
Qy 1378 AACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAAGACGCAGAGCTG 1437
Db 11329 AATATTGGACAAGAAGTTATGATTGAAGATCTCACACAATCATTTGAAGAAGCGGAACTT 11388
Qy 1438 AAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACC 1497
Db 11389 AAAAAACGTGACAAGGAAGAAGAAGAAGGAATGGCAGACCCATTAAATCAAATGGTTACA 11448
Qy 1498 ACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGATCCTCTATAC 1557
Db 11449 ACTTTCTGCCGAGGAGCCATGACTGAAAGAAGTGGTGCTTTACAAGAGGACCCTCTTTAC 11508
Qy 1558 ATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGG 1617
Db 11509 ATGTCTTATGCTGATATTTTGGCTAAGTCCTGCGGCGAAGAAGAAGAAGAA------GGT 11562
Qy 1618 GAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACAC 1677
Db 11563 AATAACGAAGAAGAAGGTTCAAATGGTAACGGAGATGAAGAAGGCGGTGCTTCTATCCAT 11622
Qy 1678 GAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGACCGTGGG 1737
Db 11623 GAGCAAGAAATGGAAAAACAAAAGCTTTTGTTTCACCAAGCTCGATTGGCTAACCGTGGT 11682
Qy 1738 GTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAGATGGTC 1797
Db 11683 GTCGCAGAAATGGTTTTATTACACATATCAGCTTGCAAAGGTATACCCAGTGAAATGGTT 11742
Qy 1798 ATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATACAGATG 1857
Db 11743 ATGAAAACGCTTCAATTGGGAATCGCAGTTCTCCGTGGTGGTAATTTAGACATTCAAATG 11802
Qy 1858 GGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGC 1917
Db 11803 GGAATGTTAAATCATTTAAAAGAAAAGAAAGATGTTGGATTTTTTACTTCAGTTGCTGGT 11862
Qy 1918 CTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAA 1977
Db 11863 TTAATGAACTCATGCAGCGTTCTTGATTTGGACGCTTTTGAGAGAAATACCAAAGCAGAA 11922
Qy 1978 GGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTC 2037
Db 11923 GGTTTGGGAGTAGGATCGGAAGGTGCTGCTGGTGAAAAAAATATGCATGATGCAGAGTTC 11982
Qy 2038 ACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAG 2097
Db 11983 ACGTGTACTCTATTTAGATTTATTCAATTAACTTGTGAAGGACATAATTTAGAATGGCAA 12042
Qy 2098 AACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTC 2157
Db 12043 AATTGTTTAAGAACCCAAGCAGGAAATACCACAACTGTAAATGTTGCAATTTGTACAGTG 12102
Qy 2158 GACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAG 2217
Db 12103 GATTATTTACTTAGGCTTCAGGAATCTATAATGGATTTTTATTGGCATTATTCGAGTAAA 12162
Qy 2218 GAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAA 2277
Db 12163 GAGTTAATCGATCCAGCAGGAAAAGCAAATTTCTTCAAAGCAATCGGTGTCGCCAGCCAA 12222
Qy 2278 GTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTG 2337
Db 12223 GTGTTTAATACACTATCCGAAGTAATTCAAGGACCATGTACTCAAAATCAACAGGCCCTA 12282
Qy 2338 GCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAG 2397
Db 12283 GCTCATTCCAGGTTGTGGGATGCTGTTGGAGGGTTTTTGTTTTTATTTTCACACATGCAA 12342
Qy 2398 GACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAG 2457
Db 12343 GATAAATTATCGAAACATTCTAGTCAAGTAGATTTACTAAAAGAACTTTTGAATTTACAA 12402
Qy 2458 AAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATC 2517
Db 12403 AAAGATATGATTACGATGATGCTGTCAATGTTAGAAGGAAATGTTGTTAATGGAACAATT 12462
Qy 2518 GGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAA 2577
Db 12463 GGTAAACAAATGGTTGACACTCTAGTAGAGTCGGCGTCAAATGTCGAGTTGATATTGAAA 12522
Qy 2578 TACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATT 2637
Db 12523 TATTTTGACATGTTCCTGAAACTTAAAGATTTAACGAGTTCAACAAGCTTTACGGAAATT 12582
Qy 2638 GATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAG 2697
Db 12583 GACCCCAATAACGATGGTTGGGTACATCCCAAAGATTTTAAAGAAAAAATGGAACAACAA 12642
Qy 2698 AAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGAC 2757
Db 12643 AAAAGTTATACTGCGGAGGAAATTGAATTTATGTTACAATGTTGTGAATCTAATCATGAT 12702

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Qy       2758 GGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGG 2817
Db      12703 GGAAAAATTGATTACATTGGCTTCACTGATCAATTCCACGAGCCATCTAAAGAAATTGGT 12762

Qy       2818 TTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTG 2877
Db      12763 TTTAATCTTGCCGTATTATTAACTAATCTATCAGAACATATGCCAAATGAACCTAGATTA 12822

Qy       2878 GCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGT 2937
Db      12823 ACAAGATTCCTAGAAACAGCTAGCAGTGTTTTGAACTATTTCCAACCGTTCCTGGGTAGA 12882

Qy       2938 ATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCT 2997
Db      12883 ATTGAAATTCTTGGAGGAAGTAAGCGTATAGAACGGGTGTACTTTGAAATTAAAGAATCA 12942

Qy       2998 AATA 3001
Db      12943 AATA 12946
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RESULT 10
ADM68759
ID ADM68759 standard; DNA; 15845 BP.
XX
AC ADM68759;
XX
DT 17-JUN-2004 (first entry)
XX
DE Myzus persicae ryanodine receptor encoding DNA SEQ ID NO:3.
XX
KW ryanodine receptor; insect ion channel; insecticide; pesticide;
KW calcium balance disruption; receptor calcium release mechanism; gene; ds.
XX
OS Myzus persicae.
XX
FH Key Location/Qualifiers
FT CDS 277. .15582
FT /*tag= a
FT /product= "ryanodine receptor"
XX
PN WO2004027042-A2.
XX
PD 01-APR-2004.
XX
PF 23-SEP-2003; 2003WO-US029834.
XX
PR 23-SEP-2002; 2002US-0412795P.
PR 18-NOV-2002; 2002US-0427324P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Caspar T, Cordova D, Gutteridge S, Rauh JJ, Smith RM, Wu L;
PI Tao Y;
XX
DR WPI; 2004-295411/27.
DR P-PSDB; ADM68760.
XX
PT New isolated nucleotide fragment encoding a ryanodine receptor, useful
PT for isolating other pest ryanodine receptors and in developing screens to
PT identify insecticidally active compounds.
XX
PS Claim 6; SEQ ID NO 3; 687pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising: (a) a nucleic acid sequence encoding a ryanodine receptor
CC having an amino acid sequence identity of at least 80% when compared to a
CC polypeptide selected from the group consisting of SEQ ID NO. 2, 4, 6, 8,
CC 128, 130, 144, or 146; or (b) the complement of (a). (I) comprises a
CC nucleotide sequence selected from 9 fully defined sequences (SEQ ID NO.
CC 1, 3, 5, 7, 9, 127, 129, 143, or 145). Also described: (1) a recombinant
CC construct comprising (I) operably linked to at least one regulatory
CC sequence; (2) a transformed host cell comprising the recombinant
CC construct; (3) a method to isolate (I) encoding ryanodine receptors and
CC related polypeptides; (4) an isolated polypeptide having ryanodine
CC receptor activity; (5) a method for evaluating at least one compound for
CC its ability to modulate calcium homeostasis; (6) a method for evaluating
CC at least one compound which modulates ryanodine receptor activity; (7) an
CC isolated nucleic acid fragment encoding an insect ion channel comprising
CC at least two fully defined polypeptide sequences selected from SEQ ID
CC NOs. 63-119 provided that the polypeptide sequences is not SEQ ID NO. 56,
CC 120-126; (8) a method for identifying a nucleic acid sequence encoding an
CC insect ion channel; (9) a method for expressing an isolated nucleic acid
CC fragment encoding a toxic insect ion channel; and (10) recombinant
CC construct comprising in the 5' to 3' direction a promoter operably linked
CC to an isolated nucleic acid fragment encoding a toxic insect ion channel.
CC The isolated nucleotide fragment (I) encoding a ryanodine receptor is
CC useful for the isolation of other pest ryanodine receptors and developing
CC of screens to identify insecticidally active compounds. The nucleic acid
CC fragments are useful as pesticides, fragments of protein for antibody
CC production, fragments of protein for determination of the structure of
CC insecticide binding sites and in the identification of insecticides that
CC disrupt the calcium balance in cells through other messengers that
CC interact with the receptor calcium release mechanism. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 15845 BP; 5273 A; 2716 C; 3325 G; 4528 T; 0 U; 3 Other;

Query Match 48.5%; Score 1456; DB 12; Length 15845;
Best Local Similarity 68.6%; Pred. No. 0;
Matches 2062; Conservative 0; Mismatches 915; Indels 27; Gaps 3;

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Qy          1 CAGTTCTCCTTGCTGAACAGGATCGCTGACCATTCTTTGGAAGCCCAAGACATAATGCAG 60
Db      10243 CAATATTCACTTCTTAATCGATTCGCTGATAGTTCATTGGAAGCTCAAGATATAATGTCA 10302

Qy         61 AAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGGACCAATTCGTG 120
Db      10303 AGAACGGAAGGCACTATGCCCACTCTTGAAACGGTATTAAACGAAGTTGATCAGTTTATC 10362

Qy        121 GAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGCTGCCTTTACTC 180
Db      10363 GAATCAGAAAAAACATATACAGACGCACCACATATCATTGATGTTATTTTGCCATTGTTG 10422

Qy        181 TGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTCCTACTGGCGGA 240
Db      10423 TGTTCATACTTACCGTACTGGTGGGCACAAGGTCCAGATAATGTTGCTCTAACCACAGGT 10482

Qy        241 AACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGAATGTTCTGAAG 300
Db      10483 AATCATGTCACAATGGTGACTAGTGAACATATGAACTGTCTATTGAAAAATGTTTTAAAA 10542

Qy        301 CTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCCACCTAC 360
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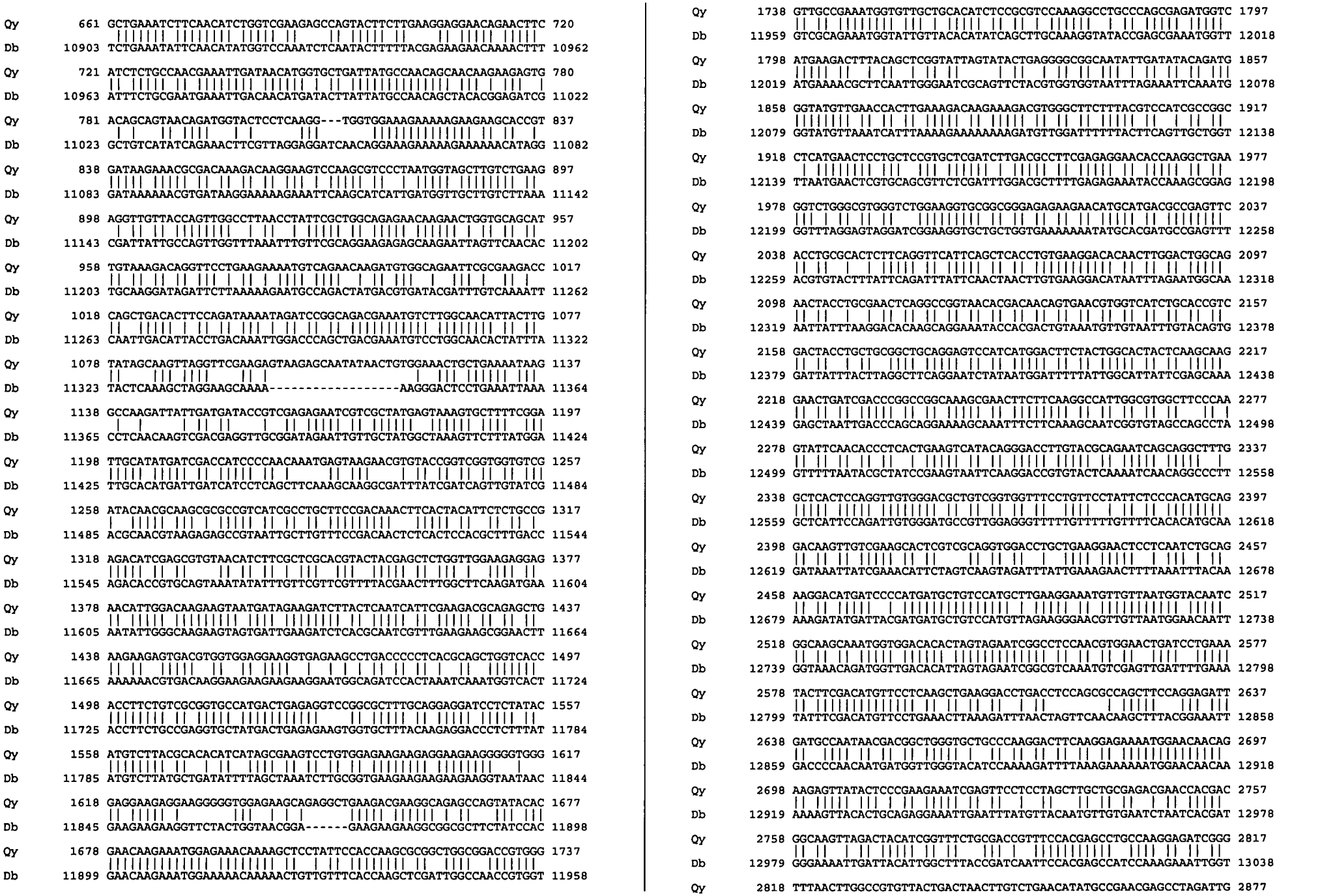
Qy        361 ACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTC 420
Db      10603 ACACAACAAATAATTATTAATTCTTCAGAAGAATTATTAAAAGATCCATTCTTACCACTT 10662

Qy        421 GCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGG 480
Db      10663 GCGGAACGAGTTAAAAAACGTACAGAAACGTTGTACCATAAAGAAGAATCGTTAAGAGGA 10722

Qy        481 TTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAAGACTGG 540
Db      10723 TTTATAAAATCATCTACTGACGATACATCCCAAATTGAAGCCCAAATACAAGAAGATTGG 10782

Qy        541 CAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTCGACCTG 600
Db      10783 CAATTAGTTGTTAGGGATATATATGCATTTTACCCACTCCTCATAAAATACGTGGATCTT 10842

Qy        601 CAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTG 660
Db      10843 CAACGCAATCACTGGTTACGTAATAGCATATCAAATGCTGAAGATTTATACAATCACGTA 10902
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Db      13039 TTCAATCTTGCCGTTTTGTTGACTAACCTATCAGAACACATGCCAAATGAACCTAGGTTA 13098

Qy       2878 GCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGT 2937

Db      13099 ACGAGATTCTTAGAAACAGCTAGCAGTGTTTTGAATTATTTCCAGCCATTCCTTGGAAGA 13158

Qy       2938 ATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCT 2997

Db      13159 ATTGAAATTCTCGGAGGAAGTAAACGCATAGAACGGGTGTACTTTGAAATTAAGGAATCA 13218

Qy       2998 AATA 3001

Db      13219 AACA 13222


RESULT 11
AAQ10613
ID   AAQ10613 standard; DNA; 15672 BP.
XX
AC   AAQ10613;
XX
DT   26-APR-1991  (first entry)
XX
DE   Rianodin receptor gene.
XX
KW   Rianodin receptor gene; calcium release modulator; tranquiliser;
KW   antagonist; ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers
FT   GC_signal       351. .356
FT                   /*tag= b
FT                   /note= "feature unlabelled in specification"
FT   CAAT_signal     392. .396
FT                   /*tag= d
FT                   /note= "feature unlabelled in specification"
FT   GC_signal       407. .452
FT                   /*tag= c
FT                   /note= "feature unlabelled in specification"
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FT   misc_feature    514. .521
FT                   /*tag= f
FT                   /note= "feature unlabelled in specification"
FT   CDS             593. .15553
FT                   /*tag= a
FT                   /product= "rianodin receptor"
FT   polyA_signal    15388. .15393
FT                   /*tag= g
XX
PN   JP03011098-A.
XX
PD   18-JAN-1991.
XX
PF   07-JUN-1989;   89JP-00144569.
XX
PR   07-JUN-1989;   89JP-00144569.
XX
PA   (MITU ) MITSUBISHI KASEI CORP.
XX
DR   WPI; 1991-062003/09.
DR   P-PSDB; AAR10834.
XX
PT   New rianodin receptor, genes encoding it and its prepn. - useful as
PT   calcium release modulator for tranquillisers and for assaying calcium
PT   antagonists.
XX
PS   Disclosure; Fig 1; 18pp; Japanese.
XX
CC   RNA contg. poly(A) was prepared from rabbit skeletal muscle endoplasmic
CC   reticulum. From the obtd. poly(A) mRNA, a cDNA bank corresp. to it was
CC   prepared by random primer method, oligo (dT) primer method, and primer
CC   extension method. A cDNA was obtained by screening with a DNA probe (see
CC   AAQ10614-15). By introducing the obtd. cDNA into an expression vector,
CC   vector pRRS7 was formed. The product is said to be involved in calcium
CC   release from sarcoplasmic reticulum which triggers constriction of
CC   skeletal muscle. Therefore, the receptor is useful as tranquilliser and
CC   assay series for screening of calcium antagonist
XX
SQ   Sequence 15672 BP; 3139 A; 4909 C; 4955 G; 2669 T; 0 U; 0 Other;

  Query Match             26.2%;  Score 787.4;  DB 2;  Length 15672;
  Best Local Similarity   56.8%;  Pred. No. 4.5e-196;
  Matches 1700;  Conservative    0;  Mismatches 1181;  Indels  114;  Gaps    9;

Qy         38 TGGAAGCCCAAGACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGATCT 97

Db      10131 TGGGGCTCCCCAACAGCGTGGAGGAGATGTGTCCTGACATCCCGGTGCTGGATCGGCTCA 10190

Qy         98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157

Db      10191 TGGCAGACATCGGGGGGCTGGCCGAGTCCGGGGCCCGCTACACGGAGATGCCGCACGTCA 10250

Qy        158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217

Db      10251 TCGAGATCACGCTGCCCATGCTCTGCAGCTACCTGCCCCGCTGGTGGGAGCGCGGGCCCG 10310

Qy        218 ATAATGTTACTCCTACT-----------GGCGGAAACCACGTAACAATGGTAACAGCGG 265

Db      10311 AGGCGCCCCCTCCCGCCCTGCCTGCCGGCGCCCCCCGCCCTGCACGGCTGTCACCTCCG 10370

Qy        266 AACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATG 325

Db      10371 ACCACCTCAACTCACTCTTGGGGAACATCTTGCGCATCATTGTCAACAACCTGGGCATTG 10430

Qy        326 AGAACGCGCCGTGGATGACCCGCATCGCCACCTACACGCAGCAGATCATCATCAACAGCT 385

Db      10431 ACGAGGCCACCTGGATGAAGCGGCTTGCTGTGTTCGCCCAGCCCATCGTGAGCCGGGCGC 10490

Qy        386 CCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGG 445

Db      10491 GGCCTGAGCTCCTGCATTCCCACTTCATCCCCACCATCGGGCGGCTGCGCAAGCGGGCAG 10550

Qy        446 ACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACA 505

Db      10551 GCAAGGTGGTGGCCGAGGAGGAGCAGCTGCGG---------CTGGAGGCCAAGGCCGAGG 10601

Qy        506 CATCCCAGGTAGAGTCTCAGATACAAGAAGACTGGCAGCTGCTGGTCAGAGACATCTACT 565

Db      10602 CCGAGGAGGGCGAGCTCCTGGTGCGGGACGAGTTCTCTGTGCTCTGCCGGGACCTGTACG 10661

Qy        566 CCTTCTACCCGCTGCTCATCAAGTACGTCGACCTGCAGAGGAACCACTGGCTCAGGAACA 625

Db      10662 CCCTCTACCCGCTGCTCATCCGCTACGTGGACAACAACAGGGCGCACTGGCTGACGGAGC 10721

Qy        626 ATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTGGCTGAAATCTTCAACATCTGGTCGA 685

Db      10722 CCAACGCCAACGCCGAGGAGCTGTTCAGGATGGTGGGCGAGATCTTCATCTACTGGTCCA 10781

Qy        686 AGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTCATCTCTGCCAACGAAATTGATAACA 745

Db      10782 AGTCCCACAACTTCAAGCGTGAGGAGCAGAACTTTGTGGTCCAGAACGAGATCAACAACA 10841

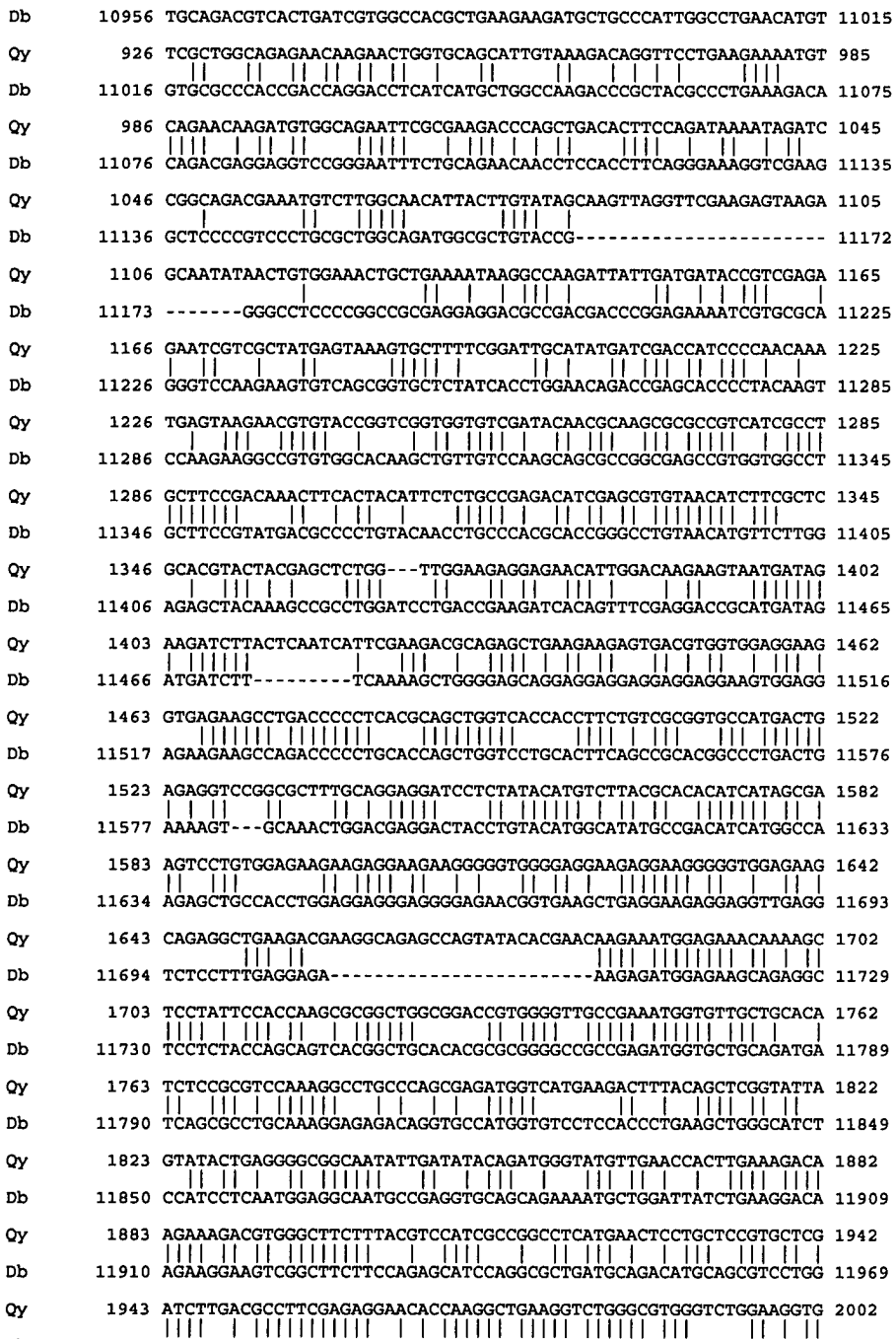
Qy        746 TGGTGCTGATTATGCCAACAGCAACAAGAAGAGTGACAGCAGTAACAGATGGTACTCCTC 805

Db      10842 TGTCCTTCCTGACGGCTGACAGCAAGAGCAAGATGGCCAAGGCGGGAGACG------CAC 10895

Qy        806 AAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGATAAGAAACGCGACAAAGACAAGGAAG 865

Db      10896 AGTCGGGCGGCTCGGACCAGGAACGCACCAAGAAGAAGCGCCGGGGGGACAGGTACTCCG 10955

Qy        866 TCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGGTTGTTACCAGTTGGCCTTAACCTAT 925
```



RESULT 12
AAS69156
ID AAS69156 standard; cDNA; 15359 BP.

XX
AC AAS69156;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #4960.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG04969.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 4960; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 15359 BP; 3251 A; 4580 C; 4716 G; 2812 T; 0 U; 0 Other;

Query Match 25.7%; Score 771.8; DB 5; Length 15359;
Best Local Similarity 56.5%; Pred. No. 5.8e-192;
Matches 1691; Conservative 0; Mismatches 1187; Indels 117; Gaps 9;

```
Qy         38 TGGAAGCCCAAGACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGATCT 97
Db       9819 TGGGGCTCCCCAACAGTGTGGAGGAGATGTGTCCCGACATCCCGGTGCTGGAGCGGCTCA 9878

Qy         98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157
Db       9879 TGGCAGACATTGGGGGGCTGGCCGAGTCAGGTGCCCGCTACACAGAGATGCCGCATGTCA 9938

Qy        158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217
```

```
Db       9939 TCGAGATCACGCTGCCCATGCTATGCAGCTACCTGCCCCGATGGTGGGAGCGCGGGCCCG 9998

Qy        218 ATAATGTTACTCCTACT-----------GGCGGAAACCACGTAACAATGGTAACAGCGG 265
Db       9999 AGGCACCCCCTTCCGCCCTGCCCGCCGGCGCCCCCCCACCCTGCACAGCTGTCACCTCTG 10058

Qy        266 AACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATG 325
Db      10059 ACCACCTCAACTCCCTGCTGGGGAATATCCTGAGAATCATCGTCAACAACCTGGGCATTG 10118

Qy        326 AGAACGCGCCGTGGATGACCCGCATCGCCACCTACACGCAGCAGATCATCATCAACAGCT 385
Db      10119 ACGAGGCCTCCTGGATGAAGCGGCTGGCTGTGTTCGCACAGCCCATTGTGAGCCGTGCAC 10178

Qy        386 CCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGG 445
Db      10179 GGCCGGAGCTCCTGCAGTCCCACTTCATCCCAACTATCGGGCGGCTGCGCAAGAGGGCAG 10238

Qy        446 ACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACA 505
Db      10239 GGAAGGTGGTGTCCGAGGAGGAGCAGCTGCGCCTGGAGGCCAAGGCG---------GAGG 10289

Qy        506 CATCCCAGGTAGAGTCTCAGATACAAGAAGACTGGCAGCTGCTGGTCAGAGACATCTACT 565
Db      10290 CCCAGGAGGGCGAGCTGCTGGTGCGGGACGAGTTCTCTGTGCTCTGCCGGGACCTCTACG 10349

Qy        566 CCTTCTACCCGCTGCTCATCAAGTACGTCGACCTGCAGAGGAACCACTGGCTCAGGAACA 625
Db      10350 CCCTGTATCCGCTGCTCATCCGCTACGTGGACAACAACAGGGCGCAGTGGCTGACGGAGC 10409

Qy        626 ATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTGGCTGAAATCTTCAACATCTGGTCGA 685
Db      10410 CGAATCCCAGCGCGGAGGAGCTGTTCAGGATGGTGGGCGAGATCTTCATCTACTGGTCCA 10469

Qy        686 AGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTCATCTCTGCCAACGAAATTGATAACA 745
Db      10470 AGTCCCACAACTTCAAGCGCGAGGAGCAGAACTTTGTGGTCCAGAATGAGATCAACAACA 10529

Qy        746 TGGTGCTGATTATGCCAACAGCAACAAGAAGAGTGACAGCAGTAACAGATGGTACTCCTC 805
Db      10530 TGTCCTTCCTGACTGCTGACAACAAAAGCAAAATGGCTAAGGCGGGAGATATA------C 10583

Qy        806 AAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGATAAGAAACGCGACAAAGACAAGGAAG 865
Db      10584 AGTCCGGTGGCTCGGACCAGGAACGCACCAAGAAGAAGCGCCGGGGGGGACCGGTACTCTG 10643

Qy        866 TCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGGTTGTTACCAGTTGGCCTTAACCTAT 925
Db      10644 TGCAGACGTCACTGATCGTGGCCACACTGAAGAAGATGCTGCCCATCGGCCTGAATATGT 10703

Qy        926 TCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGTAAAGACAGGTTCCTGAAGAAAATGT 985
Db      10704 GTGCGCCCACCGACCAAGACCTCATCACGCTGGCCAAGACCCGTTACGCCCTGAAAGACA 10763

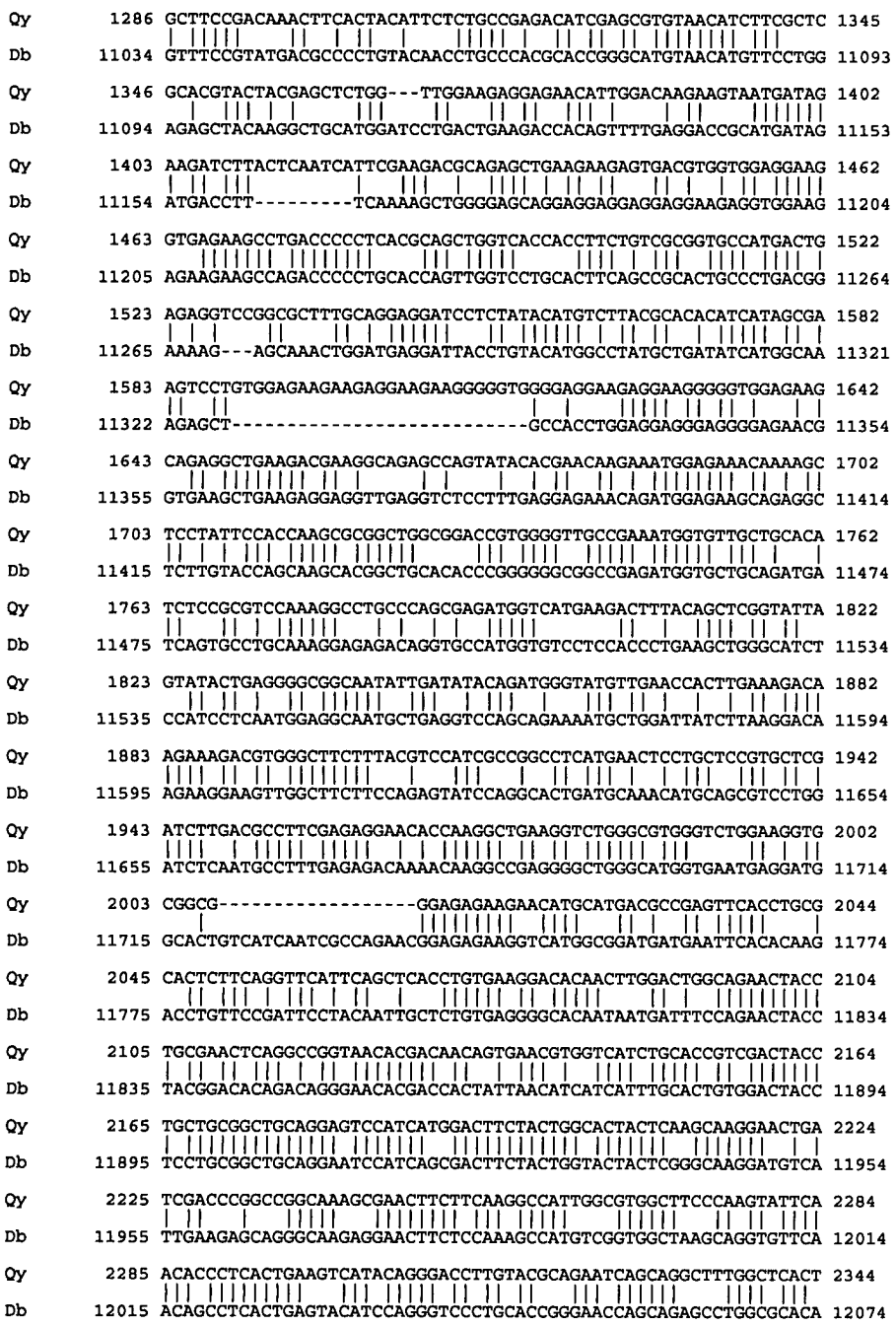
Qy        986 CAGAACAAGATGTGGCAGAATTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATC 1045
Db      10764 CAGATGAGGAGGTCCGGGAATTTCTGCACAACAACCTTCACCTTCAGGGAAAGGTCGAAG 10823

Qy       1046 CGGCAGACGAAATGTCTTGGCAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGA 1105
Db      10824 GCTCCCCGTCTCTGCGCTGGCAGATGGCTCTGTACCG---------------------- 10860

Qy       1106 GCAATATAACTGTGGAAACTGCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGA 1165
Db      10861 -------GGGCGTCCCGGGTCGCGAGGAGGACGCCGATGACCCCGAGAAAATCGTGCGCA 10913

Qy       1166 GAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAA 1225
Db      10914 GAGTCCAGGAAGTGTCAGCCGTGCTCTACTACCTGGACCAGACCGAGCACCCTTACAAGT 10973

Qy       1226 TGAGTAAGAACGTGTACCGGTCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCT 1285
Db      10974 CTAAGAAGGCCGTGTGGCACAAGCTTTTGTCCAAACAGCGCCGGCGGGCAGTCGTGGCCT 11033
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RESULT 13
ADQ85750
ID ADQ85750 standard; cDNA; 15359 BP.
XX
AC ADQ85750;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2564.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;

XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 2564; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 15359 BP; 3251 A; 4580 C; 4717 G; 2811 T; 0 U; 0 Other;

Query Match 25.7%; Score 771.8; DB 12; Length 15359;
Best Local Similarity 56.5%; Pred. No. 5.8e-192;
Matches 1691; Conservative 0; Mismatches 1187; Indels 117; Gaps 9;

```
Qy        38 TGGAAGCCCAAGACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGATCT 97
             ||| ||  |||  || || | |||  |  ||| |||  ||| |||  | ||
Db      9819 TGGGGCTCCCCAACAGTGTGGAGGAGATGTGTCCCGACATCCCGGTGCTGGAGCGGCTCA 9878

Qy        98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157
             | |  ||  | |      | |  |||||||          ||||  |||  ||||||| |||
Db      9879 TGGCAGACATTGGGGGGCTGGCCGAGTCAGGTGCCCGCTACACAGAGATGCCGCATGTCA 9938

Qy       158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217
             ||||  |  ||||||  | || ||   ||  ||||   |||||||  |  |||||
Db      9939 TCGAGATCACGCTGCCCATGCTATGCAGCTACCTGCCCCGATGGTGGGAGCGCGGGCCCG 9998

Qy       218 ATAATGTTACTCCTACT----------GGCGGAAACCACGTAACAATGGTAACAGCGG 265
             |       || | |               | |      | |   |||   || ||  | |
Db      9999 AGGCACCCCCTTCCGCCCTGCCCGCCGGCGCCCCCCCACCCTGCACAGCTGTCACCTCTG 10058

Qy       266 AACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATG 325
             | ||| | |||   || ||   |||| | ||||  |||||   || ||| | |||| ||
Db     10059 ACCACCTCAACTCCCTGCTGGGGAATATCCTGAGAATCATCGTCAACAACCTGGGCATTG 10118

Qy       326 AGAACGCGCCGTGGATGACCCGCATCGCCACCTACACGCAGCAGATCATCATCAACAGCT 385
             | | ||  | |||||||  ||  | ||    | | | ||||  ||  | | |
Db     10119 ACGAGGCCTCCTGGATGAAGCGGCTGGCTGTGTTCGCACAGCCCATTGTGAGCCGTGCAC 10178

Qy       386 CCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGG 445
               ||| || |||  |      |||| | ||        |  ||  | |||||  |  | |
Db     10179 GGCCGGAGCTCCTGCAGTCCCACTTCATCCCAACTATCGGGCGGCTGCGCAAGAGGGCAG 10238

Qy       446 ACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACA 505
               ||  || |     ||||||||    || |    |       ||| ||           ||
Db     10239 GGAAGGTGGTGTCCGAGGAGGAGCAGCTGCGCCTGGAGGCCAAGGCG---------GAGG 10289

Qy       506 CATCCCAGGTAGAGTCTCAGATACAAGAAGACTGGCAGCTGCTGGTCAGAGACATCTACT 565
             |      |||  |||   | | | |  || || |      ||||   | | ||| |||||
Db     10290 CCCAGGAGGGCGAGCTGCTGGTGCGGGACGAGTTCTCTGTGCTCTGCCGGGACCTCTACG 10349

Qy       566 CCTTCTACCCGCTGCTCATCAAGTACGTCGACCTGCAGAGGAACCACTGGCTCAGGAACA 625
             || | || ||||||||||||   ||||| |||     | |||   || ||||| | | |
Db     10350 CCCTGTATCCGCTGCTCATCCGCTACGTGGACAACAACAGGGCGCAGTGGCTGACGGAGC 10409

Qy       626 ATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTGGCTGAAATCTTCAACATCTGGTCGA 685
               |||   ||||| |||||| ||      ||||  || |||||| |  |||||| |
Db     10410 CGAATCCCAGCGCGGAGGAGCTGTTCAGGATGGTGGGCGAGATCTTCATCTACTGGTCCA 10469

Qy       686 AGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTCATCTCTGCCAACGAAATTGATAACA 745
             ||  |||  |||||  |  |||||  |||||||  |      || || ||  | ||||
Db     10470 AGTCCCACAACTTCAAGCGCGAGGAGCAGAACTTTGTGGTCCAGAATGAGATCAACAACA 10529

Qy       746 TGGTGCTGATTATGCCAACAGCAACAAGAAGAGTGACAGCAGTAACAGATGGTACTCCTC 805
             ||    | | |     | |||| | || |    |   ||||          |
Db     10530 TGTCCTTCCTGACTGCTGACAACAAAAGCAAAATGGCTAAGGCGGGAGATATA------C 10583

Qy       806 AAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGATAAGAAACGCGACAAAGACAAGGAAG 865
             |  |||||  | |  || |     |  | |||  || |  |  |  |  |  |  |
Db     10584 AGTCCGGTGGCTCGGACCAGGAACGCACCAAGAAGAAGCGCCGGGGGGACCGGTACTCTG 10643

Qy       866 TCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGGTTGTTACCAGTTGGCCTTAACCTAT 925
             | ||  |||| || || || ||    |||||| | || | ||  | ||||| ||  | |
Db     10644 TGCAGACGTCACTGATCGTGGCCACACTGAAGAAGATGCTGCCCATCGGCCTGAATATGT 10703

Qy       926 TCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGTAAAGACAGGTTCCTGAAGAAAATGT 985
               ||  ||  || ||||| ||  |  ||     ||  | | | |      ||||
Db     10704 GTGCGCCCACCGACCAAGACCTCATCACGCTGGCCAAGACCCGTTACGCCCTGAAAGACA 10763

Qy       986 CAGAACAAGATGTGGCAGAATTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATC 1045
             ||||  | || ||    |||||  | | | | | ||    ||||  |  ||  | ||
Db     10764 CAGATGAGGAGGTCCGGGAATTTCTGCACAACAACCTTCACCTTCAGGGAAAGGTCGAAG 10823

Qy      1046 CGGCAGACGAAATGTCTTGGCAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGA 1105
               |          ||  |||||          ||||  |
Db     10824 GCTCCCCGTCTCTGCGCTGGCAGATGGCTCTGTACCG---------------------- 10860

Qy      1106 GCAATATAACTGTGGAAACTGCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGA 1165
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Db     10861 -------GGGCGTCCCGGGTCGCGAGGAGGACGCCGATGACCCCGAGAAAATCGTGCGCA 10913

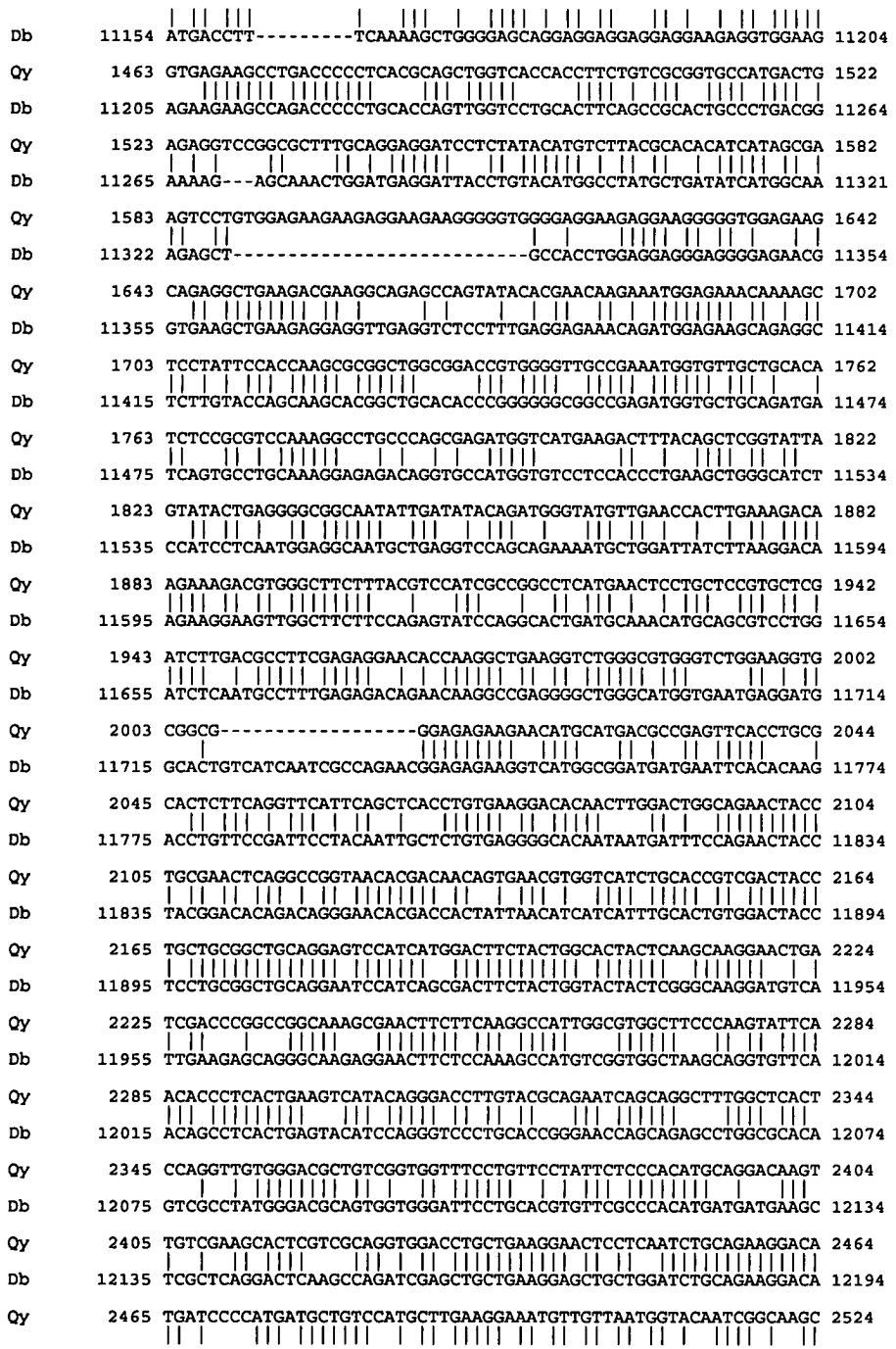
Qy      1166 GAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAA 1225
             || ||   |  ||      |||||  | |   || |   || ||| || ||  |  |
Db     10914 GAGTCCAGGAAGTGTCAGCCGTGCTCTACTACCTGGACCAGACCGAGCACCCTTACAAGT 10973

Qy      1226 TGAGTAAGAACGTGTACCGGTCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCT 1285
               |  |||  |||||  |  |  |||| | ||| |||  ||| | |||| |||||
Db     10974 CTAAGAAGGCCGTGTGGCACAAGCTTTTGTCCAAACAGCGCCGGCGGGCAGTCGTGGCCT 11033

Qy      1286 GCTTCCGACAAACTTCACTACATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTC 1345
             | |||||    ||  | ||  |      |||||  |  || || || |||||||| |||
Db     11034 GTTTCCGTATGACGCCCCTGTACAACCTGCCCACGCACCGGGCATGTAACATGTTCCTGG 11093

Qy      1346 GCACGTACTACGAGCTCTGG---TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAG 1402
               | ||| | |     |||    ||  || || |||  |     | ||    |||||||
Db     11094 AGAGCTACAAGGCTGCATGGATCCTGACTGAAGACCACAGTTTTGAGGACCGCATGATAG 11153

Qy      1403 AAGATCTTACTCAATCATTCGAAGACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAG 1462
```



RESULT 14
ADQ84285
ID ADQ84285 standard; cDNA; 15359 BP.
XX
AC ADQ84285;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1099.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;
XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 1099; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide

CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 15359 BP; 3251 A; 4580 C; 4717 G; 2811 T; 0 U; 0 Other;

Query Match 25.7%; Score 771.8; DB 13; Length 15359;
Best Local Similarity 56.5%; Pred. No. 5.8e-192;
Matches 1691; Conservative 0; Mismatches 1187; Indels 117; Gaps 9;

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Qy        38 TGGAAGCCCAAGACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGATCT 97
             |||    ||   |||   || || | |||   |    ||| |||  ||| |||  | ||
Db      9819 TGGGGCTCCCCAACAGTGTGGAGGAGATGTGTCCCGACATCCCGGTGCTGGAGCGGCTCA 9878

Qy        98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157
             | |  ||  | |     | |  |||||||        ||||  |||  ||||||| |||
Db      9879 TGGCAGACATTGGGGGGCTGGCCGAGTCAGGTGCCCGCTACACAGAGATGCCGCATGTCA 9938

Qy       158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217
             ||||  |   ||||||  | || ||    ||  ||||    |||||||  |  |||||  |
Db      9939 TCGAGATCACGCTGCCCATGCTATGCAGCTACCTGCCCCGATGGTGGGAGCGCGGGCCCG 9998

Qy       218 ATAATGTTACTCCTACT-----------GGCGGAAACCACGTAACAATGGTAACAGCGG 265
             |     || | |                | |     | |   |||   || ||  | |
Db      9999 AGGCACCCCCTTCCGCCCTGCCCGCCGGCGCCCCCCCACCCTGCACAGCTGTCACCTCTG 10058

Qy       266 AACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATG 325
             | ||| | |||   || ||   |||| | ||||   |||||   || ||| | |||| ||
Db     10059 ACCACCTCAACTCCCTGCTGGGGAATATCCTGAGAATCATCGTCAACAACCTGGGCATTG 10118

Qy       326 AGAACGCGCCGTGGATGACCCGCATCGCCACCTACACGCAGCAGATCATCATCAACAGCT 385
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Db     10119 ACGAGGCCTCCTGGATGAAGCGGCTGGCTGTGTTCGCACAGCCCATTGTGAGCCGTGCAC 10178

Qy       386 CCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGG 445
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Db     10179 GGCCGGAGCTCCTGCAGTCCCACTTCATCCCAACTATCGGGCGGCTGCGCAAGAGGGCAG 10238

Qy       446 ACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACA 505
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Db     10239 GGAAGGTGGTGTCCGAGGAGGAGCAGCTGCGCCTGGAGGCCAAGGCG---------GAGG 10289

Qy       506 CATCCCAGGTAGAGTCTCAGATACAAGAAGACTGGCAGCTGCTGGTCAGAGACATCTACT 565
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Db     10290 CCCAGGAGGGCGAGCTGCTGGTGCGGGACGAGTTCTCTGTGCTCTGCCGGGACCTCTACG 10349

Qy       566 CCTTCTACCCGCTGCTCATCAAGTACGTCGACCTGCAGAGGAACCACTGGCTCAGGAACA 625
             || | || ||||||||||||    |||||  |||     | |||   || |||||  | | |
Db     10350 CCCTGTATCCGCTGCTCATCCGCTACGTGGACAACAACAGGGCGCAGTGGCTGACGGAGC 10409

Qy       626 ATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTGGCTGAAATCTTCAACATCTGGTCGA 685
               |||    |||||  |||||||  ||      ||||  || |||||||  |  |||||| |
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Qy       686 AGAGCCAGTACTTCTTGAAGGAGGAACAGAACTTCATCTCTGCCAACGAAATTGATAACA 745
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Qy       746 TGGTGCTGATTATGCCAACAGCAACAAGAAGAGTGACAGCAGTAACAGATGGTACTCCTC 805
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Db     10530 TGTCCTTCCTGACTGCTGACAACAAAAGCAAAATGGCTAAGGCGGGAGATATA------C 10583

Qy       806 AAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGATAAGAAACGCGACAAAGACAAGGAAG 865
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Db     10584 AGTCCGGTGGCTCGGACCAGGAACGCACCAAGAAGAAGCGCCGGGGGGACCGGTACTCTG 10643

Qy       866 TCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGGTTGTTACCAGTTGGCCTTAACCTAT 925
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Qy       926 TCGCTGGCAGAGAACAAGAACTGGTGCAGCATTGTAAAGACAGGTTCCTGAAGAAAATGT 985
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Db     10704 GTGCGCCCACCGACCAAGACCTCATCACGCTGGCCAAGACCCGTTACGCCCTGAAAGACA 10763

Qy       986 CAGAACAAGATGTGGCAGAATTCGCGAAGACCCAGCTGACACTTCCAGATAAAATAGATC 1045
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Db     10764 CAGATGAGGAGGTCCGGGAATTTCTGCACAACAACCTTCACCTTCAGGGAAAGGTCGAAG 10823

Qy      1046 CGGCAGACGAAATGTCTTGGCAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGA 1105
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Db     10824 GCTCCCCGTCTCTGCGCTGGCAGATGGCTCTGTACCG---------------------- 10860

Qy      1106 GCAATATAACTGTGGAAACTGCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGA 1165
                      ||      | | | |||  |        ||  | |  |||    |
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Qy      1166 GAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAA 1225
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Db     10914 GAGTCCAGGAAGTGTCAGCCGTGCTCTACTACCTGGACCAGACCGAGCACCCTTACAAGT 10973

Qy      1226 TGAGTAAGAACGTGTACCGGTCGGTGGTGTCGATACAACGCAAGCGCGCCGTCATCGCCT 1285
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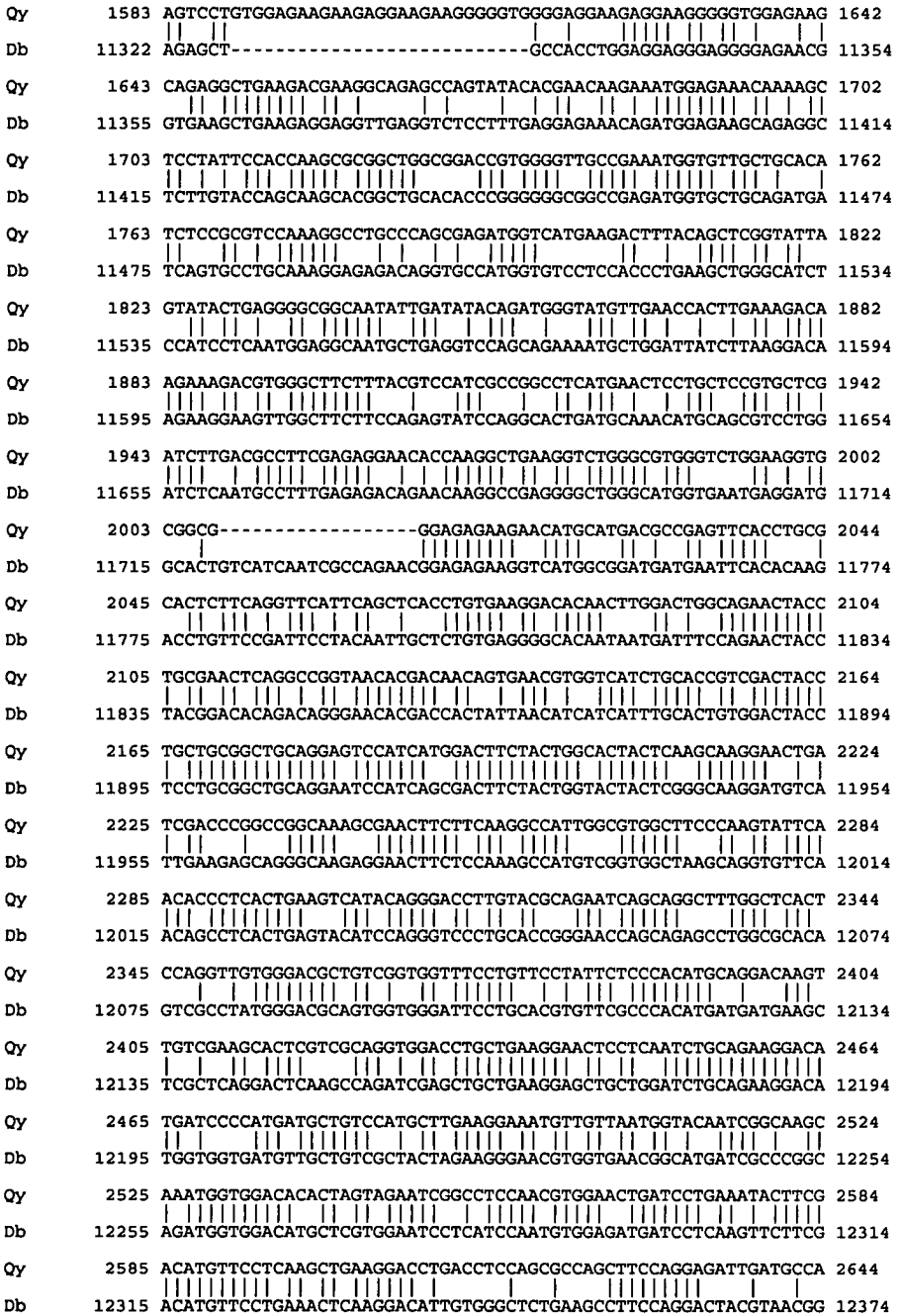
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Db     11034 GTTTCCGTATGACGCCCCTGTACAACCTGCCCACGCACCGGGCATGTAACATGTTCCTGG 11093

Qy      1346 GCACGTACTACGAGCTCTGG---TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAG 1402
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Qy      1403 AAGATCTTACTCAATCATTCGAAGACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAG 1462
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Qy      1463 GTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTG 1522
             |||||||  |||||||||     |||  ||||      |||| | |||  |||| |||| |
Db     11205 AGAAGAAGCCAGACCCCCTGCACCAGTTGGTCCTGCACTTCAGCCGCACTGCCCTGACGG 11264

Qy      1523 AGAGGTCCGGCGCTTTGCAGGAGGATCCTCTATACATGTCTTACGCACACATCATAGCGA 1582
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Db     11265 AAAAG---AGCAAACTGGATGAGGATTACCTGTACATGGCCTATGCTGATATCATGGCAA 11321
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RESULT 15
ADQ83605
ID ADQ83605 standard; cDNA; 15359 BP.
XX
AC ADQ83605;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #419.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;
XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 419; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide

CC comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

XX

SQ Sequence 15359 BP; 3251 A; 4580 C; 4717 G; 2811 T; 0 U; 0 Other;

Query Match 25.7%; Score 771.8; DB 13; Length 15359;
Best Local Similarity 56.5%; Pred. No. 5.8e-192;
Matches 1691; Conservative 0; Mismatches 1187; Indels 117; Gaps 9;

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Qy        38 TGGAAGCCCAAGACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGATCT 97
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Db      9819 TGGGGCTCCCCAACAGTGTGGAGGAGATGTGTCCCGACATCCCGGTGCTGGAGCGGCTCA 9878

Qy        98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157
             | |  ||  | |     | |  |||||||        ||||  |||  ||||||| |||
Db      9879 TGGCAGACATTGGGGGGCTGGCCGAGTCAGGTGCCCGCTACACAGAGATGCCGCATGTCA 9938

Qy       158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217
             ||||  |   ||||||  | || ||    ||  ||||   |||||||  |  |||||  |
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Qy       218 ATAATGTTACTCCTACT----------GGCGGAAACCACGTAACAATGGTAACAGCGG 265
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Qy       266 AACACATGAACCAGCTCCTCAAGAATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATG 325
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Db     10119 ACGAGGCCTCCTGGATGAAGCGGCTGGCTGTGTTCGCACAGCCCATTGTGAGCCGTGCAC 10178

Qy       386 CCGAGGAACTGCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGG 445
             |||  || |||  |      ||||  | ||          |  ||  |  |||||  |  | |
Db     10179 GGCCGGAGCTCCTGCAGTCCCACTTCATCCCAACTATCGGGCGGCTGCGCAAGAGGGCAG 10238

Qy       446 ACAATATGTTCCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACA 505
               ||  || |      ||||||||     ||  |   |     ||| ||          ||
Db     10239 GGAAGGTGGTGTCCGAGGAGGAGCAGCTGCGCCTGGAGGCCAAGGCG---------GAGG 10289

Qy       506 CATCCCAGGTAGAGTCTCAGATACAAGAAGACTGGCAGCTGCTGGTCAGAGACATCTACT 565
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Qy       566 CCTTCTACCCGCTGCTCATCAAGTACGTCGACCTGCAGAGGAACCACTGGCTCAGGAACA 625
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Qy       626 ATGTTCCAGAGGCGGAAGAGCTGTACAACCACGTGGCTGAAATCTTCAACATCTGGTCGA 685
             |||   |||||  |||||||  ||      ||||   ||  |||||||  |  ||||||  |
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Db     10530 TGTCCTTCCTGACTGCTGACAACAAAAGCAAAATGGCTAAGGCGGGAGATATA------C 10583

Qy       806 AAGGTGGTGGAAAGAAAAAGAAGAAGCACCGTGATAAGAAACGCGACAAAGACAAGGAAG 865
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Db     10584 AGTCCGGTGGCTCGGACCAGGAACGCACCAAGAAGAAGCGCCGGGGGGACCGGTACTCTG 10643

Qy       866 TCCAAGCGTCCCTAATGGTAGCTTGTCTGAAGAGGTTGTTACCAGTTGGCCTTAACCTAT 925
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Qy      1106 GCAATATAACTGTGGAAACTGCTGAAAATAAGGCCAAGATTATTGATGATACCGTCGAGA 1165
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Qy      1166 GAATCGTCGCTATGAGTAAAGTGCTTTTCGGATTGCATATGATCGACCATCCCCAACAAA 1225
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Db     10914 GAGTCCAGGAAGTGTCAGCCGTGCTCTACTACCTGGACCAGACCGAGCACCCTTACAAGT 10973

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Qy      1286 GCTTCCGACAAACTTCACTACATTCTCTGCCGAGACATCGAGCGTGTAACATCTTCGCTC 1345
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Db     11034 GTTTCCGTATGACGCCCCTGTACAACCTGCCCACGCACCGGGCATGTAACATGTTCCTGG 11093

Qy      1346 GCACGTACTACGAGCTCTGG---TTGGAAGAGGAGAACATTGGACAAGAAGTAATGATAG 1402
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Db     11094 AGAGCTACAAGGCTGCATGGATCCTGACTGAAGACCACAGTTTTGAGGACCGCATGATAG 11153

Qy      1403 AAGATCTTACTCAATCATTCGAAGACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAG 1462
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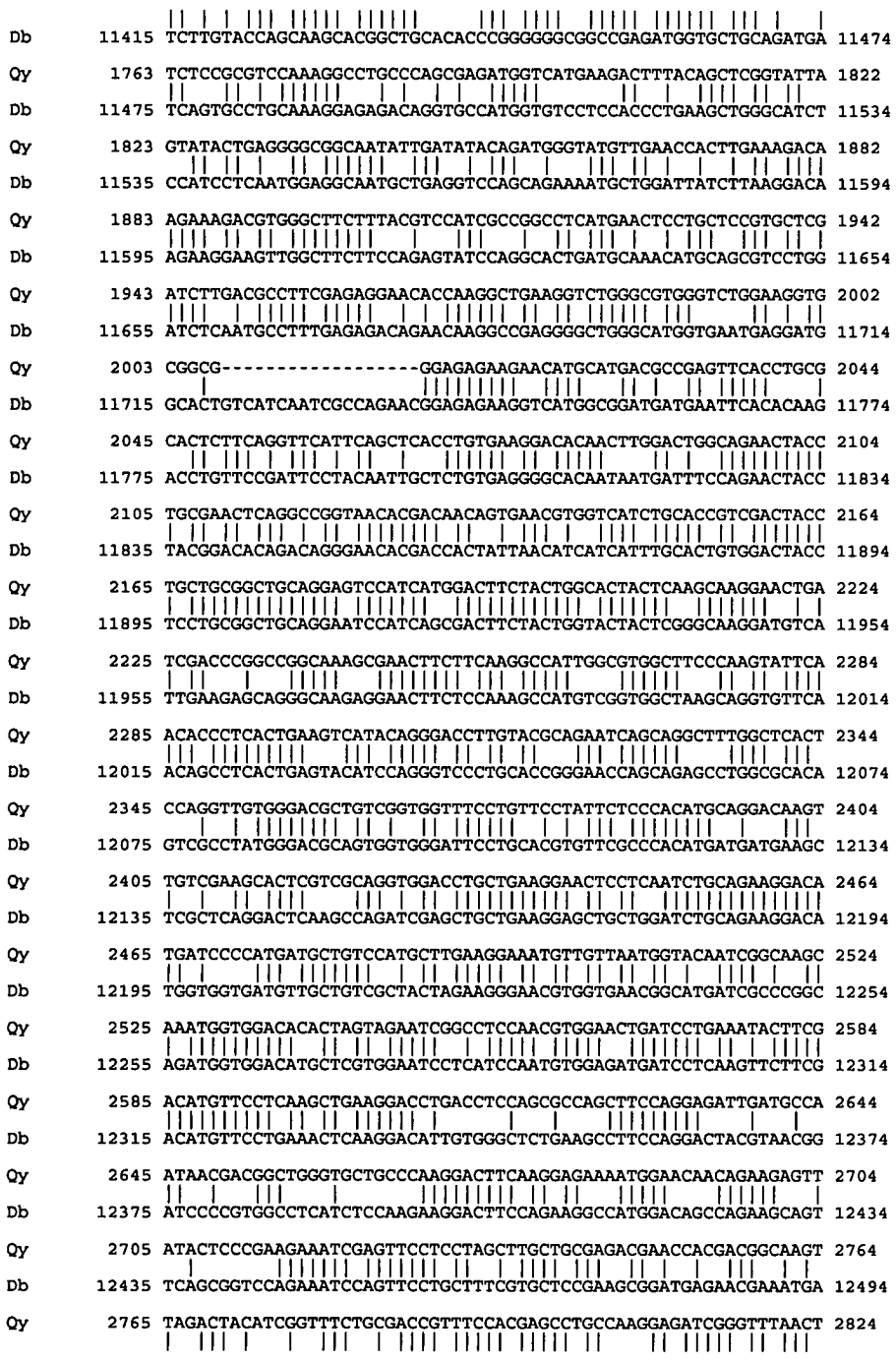
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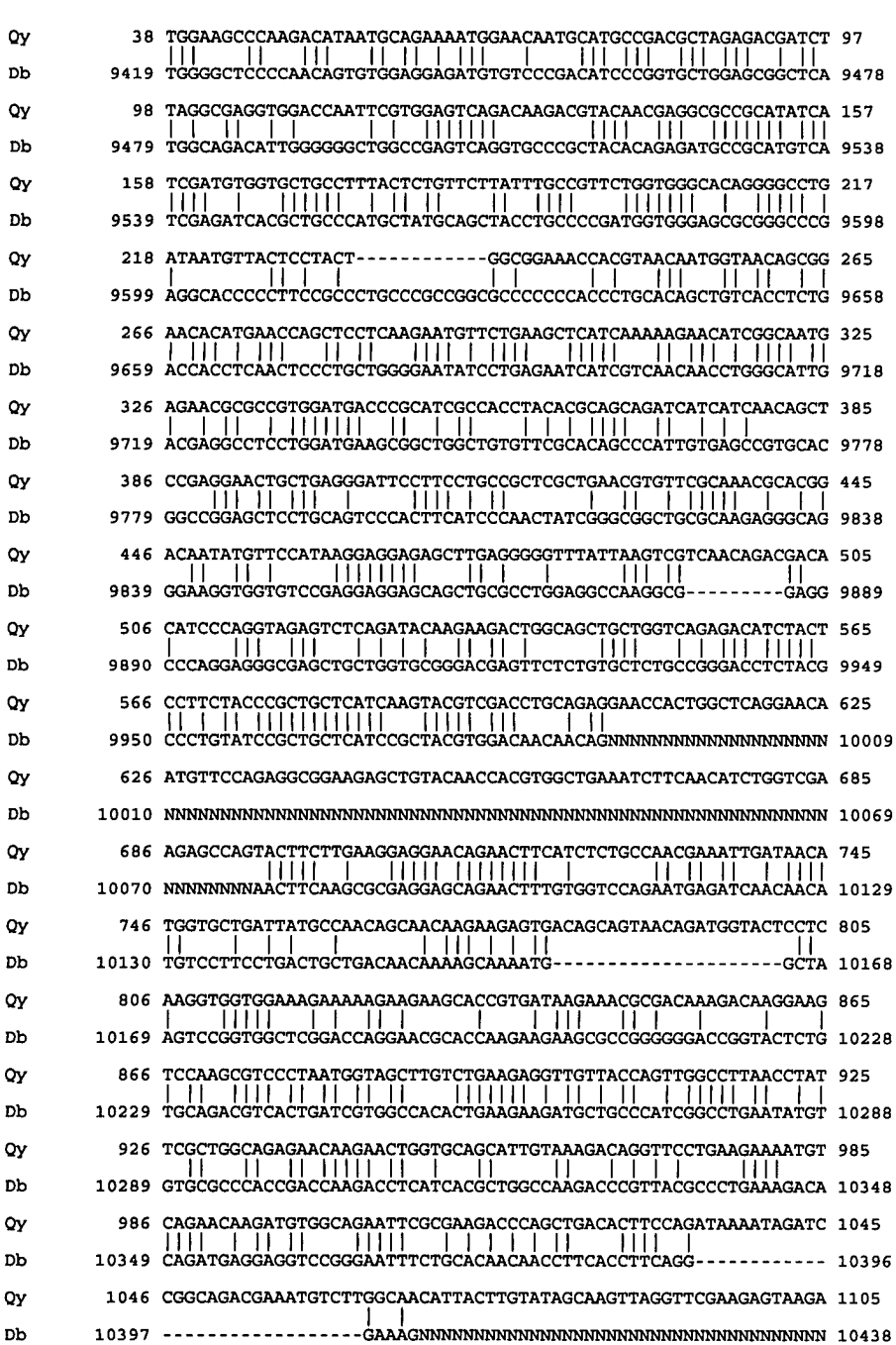
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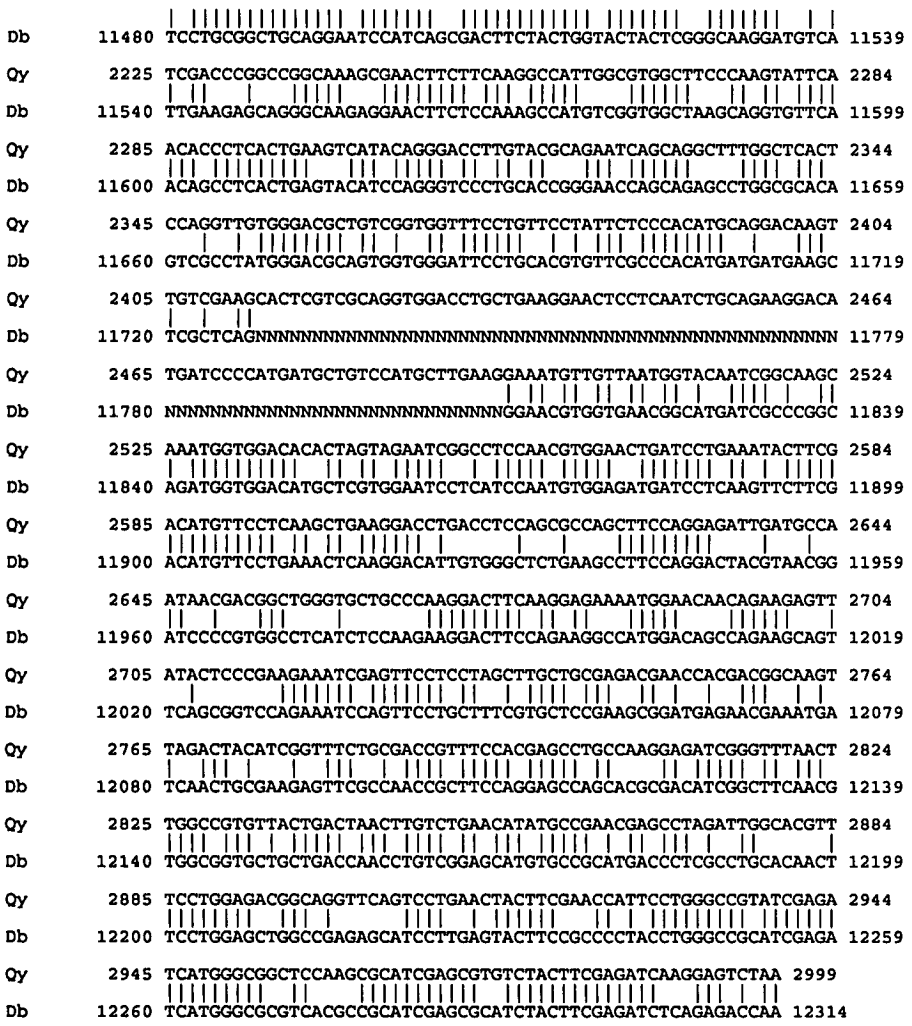
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	26	233.2	7.8	933	11	CNS03Z9F	AL267324 Tetraodon
	27	231.4	7.7	605	3	BM611222	BM611222 170006871
c	28	230	7.7	588	7	CR757066	CR757066 CR757066
	29	228.8	7.6	503	7	CN308890	CN308890 170004243
c	30	228.2	7.6	575	7	CR757030	CR757030 CR757030
c	31	223.2	7.4	700	5	BU724352	BU724352 SJMBGC04
	32	220.6	7.4	694	4	AY810313	AY810313 Schistoso
	33	216.8	7.2	460	5	BX502112	BX502112 DKFZp779O
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ALIGNMENTS

RESULT 1
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LOCUS DQ052093 14832 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens RYR1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION DQ052093
VERSION DQ052093.1 GI:66905537
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 14832)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 14832)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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/gene="RYR1"
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ORIGIN

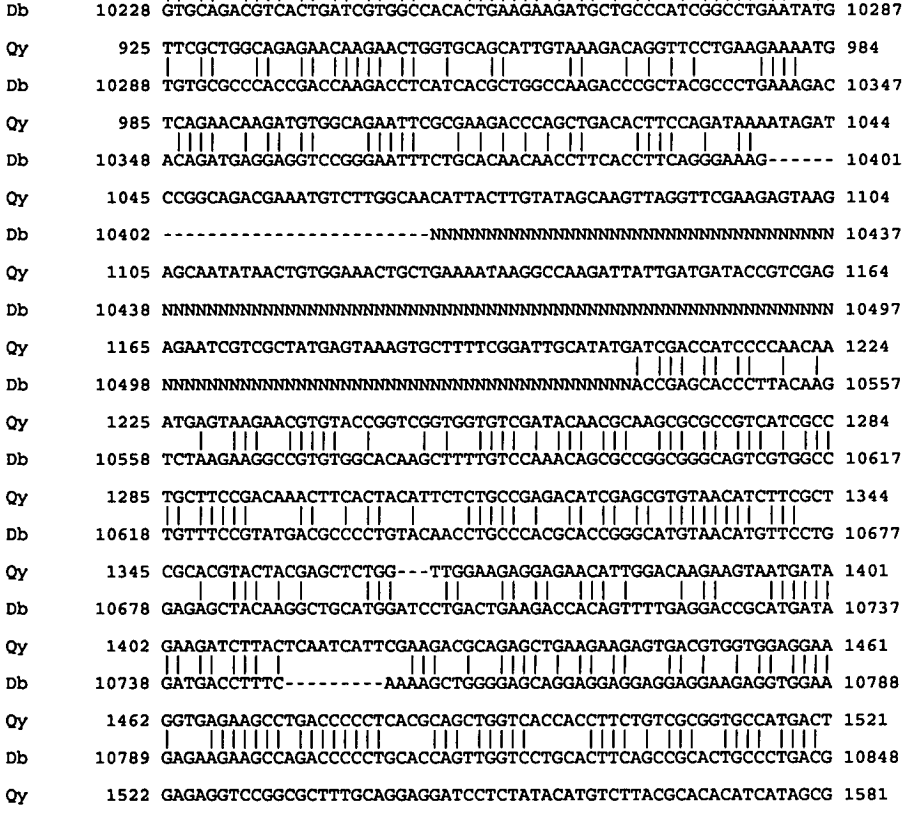
Query Match 21.4%; Score 642.6; DB 11; Length 14832;
Best Local Similarity 49.1%; Pred. No. 1.4e-157;
Matches 1470; Conservative 0; Mismatches 1393; Indels 132; Gaps 9;

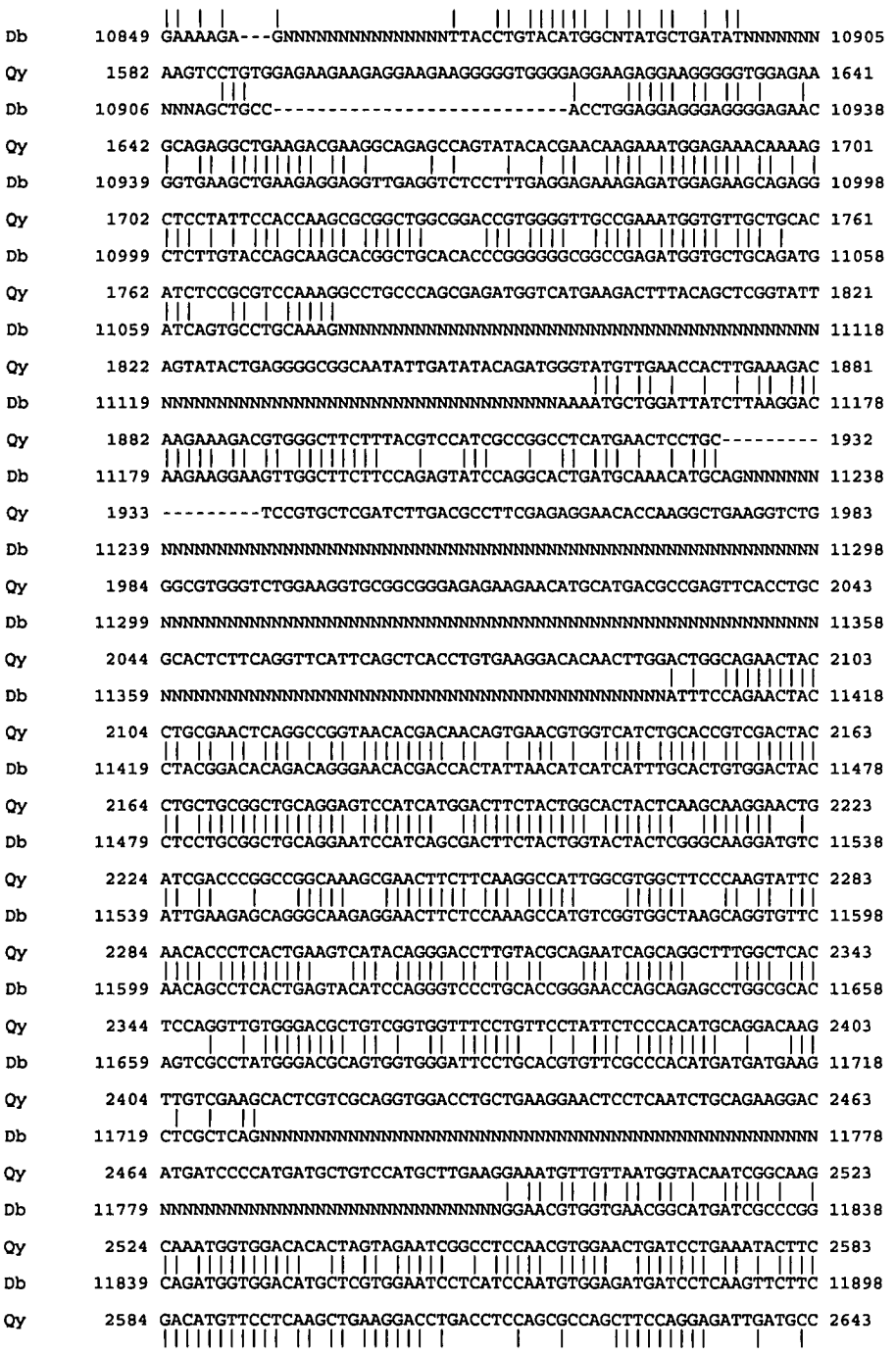

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Qy 98 TAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCA 157
Db 9479 TGGCAGACATTGGGGGGCTGGCCGAGTCAGGTGCCCGCTACACAGAGATGCCGCATGTCA 9538
Qy 158 TCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTG 217
Db 9539 TCGAGATCACGCTGCCCATGCTATGCAGCTACCTGCCCCGATGGTGGGAGCGCGGGCCCG 9598
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Qy 1463 GTGAGAAGCCTGACCCCCTCACGCAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTG 1522
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RESULT 2
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LOCUS       DQ052094               14736 bp    DNA     linear   GSS 02-JUN-2005
DEFINITION  Pan troglodytes RYR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ052094
VERSION     DQ052094.1  GI:66905538
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 14736)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
  PUBMED    15869325
REFERENCE   2  (bases 1 to 14736)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
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            alignment.
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RESULT 3
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LOCUS AK042482 3045 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630095L05 product:RYANODINE RECEPTOR 1 (SKELETAL MUSCLE-TYPE RYANODINE RECEPTOR) (RYR1) (RYR-1) (SKELETAL MUSCLE CALCIUM RELEASE CHANNEL) homolog [Homo sapiens], full insert sequence.
ACCESSION AK042482
VERSION AK042482.1 GI:26089063
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5

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  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3045)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
            Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
            Trust/MRC building Addenbrookes Hospital Cambridge) whose
            assistance we gratefully acknowledge.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES              Location/Qualifiers
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                      RYANODINE RECEPTOR) (RYR1) (RYR-1) (SKELETAL MUSCLE
                      CALCIUM RELEASE CHANNEL) homolog [Homo sapiens]
                      (SWISSPROT|P21817, evidence: FASTY, 99.2%ID, 7.2%length,
                      match=1092)"
ORIGIN

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Db         50 TTCGTCCTGGACCTCAATGCCTTCGAGAGGCAGAACAAGGCAGAGGGGCTGGGCATGGTG 109

Qy       1993 CTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACCTGCGCACTCTTC 2052
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Db        770 GGCCTCATCTCCAAGAAGGACTTCCAGAAGGCCATGGACAGCCAGAAGCAGTTCACTGGC 829

Qy       2713 GAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGCAAGTTAGACTAC 2772
              |||  ||| ||||||| ||  | || | |||  |  |  |  | |  | | | |||  |
Db        830 CCAGAGATCCAGTTCCTGCTCTCGTGTTCCGAAGCAGATGAGAATGAGATGATCAACTGC 889

Qy       2773 ATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTTAACTTGGCCGTG 2832
                |  ||     |||| ||||| || || ||   ||| || || || ||| |||| |||
Db        890 GAAGAGTTTGCGAACCGCTTCCAGGAACCAGCACGGGACATTGGCTTCAACGTGGCGGTG 949

Qy       2833 TTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCACGTTTCCTGGAG 2892
              | || || ||| |||| || ||| |||| |||| || |  ||       |||||||||
Db        950 CTGCTTACCAACCTGTCAGAGCATGTGCCCCACGACCCGCGCCTGCGCAACTTCCTGGAG 1009

Qy       2893 ACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATCGAGATCATGGGC 2952
              ||| |      ||||| | ||||||   || | ||||||||| |||| |||||||||
Db       1010 CTGGCTGAGAGCATCCTGGAGTACTTCCGGCCTTACCTGGGCCGCATCGAAATCATGGGC 1069

Qy       2953 GGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAA 2999
              |  ||    ||||| || ||  |||| || ||||||   ||| | ||
Db       1070 GCATCGCGTCGCATAGAACGGATCTATTTTGAGATCTCAGAGACCAA 1116


RESULT 4
BX402920
LOCUS       BX402920                1042 bp    mRNA    linear   EST 29-APR-2004
DEFINITION  BX402920 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK003YB21 5-PRIME, mRNA sequence.
ACCESSION   BX402920
VERSION     BX402920.2  GI:46877799
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1042)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 13, 2003 this sequence version replaced gi:30626911.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            2465.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS1AK001ZF11QP1&c=2465.f.
FEATURES             Location/Qualifiers
     source          1. .1042
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DK003YB21"
                     /cell_type="HELA CELLS COT 25-NORMALIZED"
                     /cell_line="HELA"
                     /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             15.1%;  Score 453.2;  DB 5;  Length 1042;
  Best Local Similarity   65.1%;  Pred. No. 6.8e-108;
  Matches  668;  Conservative    0;  Mismatches  358;  Indels    0;  Gaps    0;

Qy       1861 ATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATCGCCGGCCTC 1920
             ||| |  || || | || || || || || |||||||||||||  |  | | ||||||||
Db         14 ATGCTTGACTACCTCAAGGAGAAAAAGGATGTGGGCTTCTTTCAGAGCCTGGCCGGCCTG 73

Qy       1921 ATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGT 1980
             ||| | || ||     || || || ||  | || || ||| |  | | ||| ||||||||
Db         74 ATGCAGTCATGTAGTGTCCTTGACCTAAATGCATTTGAGCGACAAAACAAAGCTGAAGGT 133

Qy       1981 CTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACC 2040
             || ||  |||     || | |  | ||||| |||     |||| |||| |||||||||
Db        134 CTTGGGATGGTGACAGAGGAAGGATCAGGAGAAAAGGTTCTGCAGGACGATGAGTTCACC 193

Qy       2041 TGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAAC 2100
             || |  |||||| | ||| | || ||    |||||| |||||||||| || |  |||||
Db        194 TGTGACCTCTTCCGATTCCTGCAACTACTCTGTGAGGGACACAACTCAGATTTTCAGAAT 253

Qy       2101 TACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGAC 2160
             || ||| |||||||| | || || |  ||||| || ||| |  | |||| ||| || |||
Db        254 TATCTGAGAACTCAGACTGGCAATAATACAACTGTCAACATAATTATCTCCACTGTAGAC 313

Qy       2161 TACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAA 2220
             ||||| ||| |  | ||||| || || |  ||||| || ||| | |||||  | || ||
Db        314 TACCTACTGAGAGTTCAGGAATCAATTAGTGACTTTTATTGGTATTACTCTGGGAAAGAT 373

Qy       2221 CTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTA 2280
              | || ||        ||  ||  ||| |||| ||| || ||    |||||    |||||
Db        374 GTTATTGATGAACAAGGACAACGGAATTTCTCCAAAGCTATCCAAGTGGCAAAACAAGTC 433

Qy       2281 TTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCT 2340
             || ||||| || || ||    || ||||| ||||| ||   ||||||| |||  ||||||
Db        434 TTTAACACTCTTACAGAGTATATTCAGGGTCCTTGCACTGGGAATCAACAGAGTTTGGCA 493

Qy       2341 CACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGAC 2400
             |||  |||| ||||||| ||||| |  || || ||     | ||  |||| ||||||
Db        494 CACAGCAGGCTGTGGGATGCTGTGGTCGGCTTTCTTCATGTGTTTGCCCATATGCAGATG 553

Qy       2401 AAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAG 2460
             ||| ||||| || | ||    ||  | || ||  | || ||| |  |  ||||||||||
Db        554 AAGCTGTCGCAGGATTCCAGTCAAATTGAGCTATTAAAAGAATTAATGGATCTGCAGAAG 613

Qy       2461 GACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGC 2520
             || ||| |   |||| |||||||||||| | ||||| ||||||||||||||| || || |||
Db        614 GATATGGTGGTCATGTTGCTGTCCATGTTAGAAGGTAATGTTGTTAATGGAACGATTGGC 673

Qy       2521 AAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATAC 2580
             || || |||||||| |  || || |||||  ||  |||||||||  |||| || ||||
Db        674 AAACAGATGGTGGATATGCTTGTGGAATCTTCCAACAACGTGGAGATGATTCTCAAATTT 733

Qy       2581 TTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGAT 2640
             || ||||||||| | || || |||||  |||| ||    |  |  ||  | ||  |||
Db        734 TTTGACATGTTCTTAAAACTAAAGGATTTGACGTCGTCTGATACTTTTAAAGAATATGAC 793

Qy       2641 GCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAG 2700
              || ||  | | ||      |        | |||||||| |  |     |||||    || |||
Db        794 CCCGATGGCAAGGGAGTCATTTCCAAGAGGGACTTCCACAAAGCGATGGAGAGCCATAAG 853

Qy       2701 AGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGC 2760
              || || |    |||||  || || ||  |  ||||    ||||||  |  | | |
Db        854 CACTACACGCAGTCAGAAACGGAATTTCTTTTGTCTTGTGCGGAGACGGATGAGAATGAA 913

Qy       2761 AAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTT 2820
             |   | ||||||   |  ||| | | || |||||||| ||||| ||||| ||||| ||
Db        914 ACCCTCGACTACGAAGAGTTCGTCAAACGCTTCCACGAACCTGCGAAGGACATCGGCTTC 973

Qy       2821 AACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCA 2880
             ||| | |||||  | ||||| ||| | ||||| || ||||| |     ||    ||   |
Db        974 AACGTCGCCGTCCTTCTGACAAACCTCTCTGAGCACATGCCAACGATACCCGACTTCAGA 1033

Qy       2881 CGTTTC 2886
              | ||||
Db       1034 CTTTTC 1039


RESULT 5
BF488910
LOCUS       BF488910                605 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  AT24194.5prime AT Drosophila melanogaster adult testes pOTB7
            Drosophila melanogaster cDNA clone AT24194 5 similar to Rya-r44F:
            FBan0010844 GO:[endoplasmic reticulum membrane (GO:0005789);
            caffeine-sensitive calcium-release channel (GO:0005219);
            caffeine-sensitive calcium-release channel (GO:0005219); ion
            channel (GO:0005216)] located on: 2R 44F5-44F7;: 08/12/2002, mRNA
            sequence.
ACCESSION   BF488910
VERSION     BF488910.2  GI:13754362
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 605)
  AUTHORS   Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Baxter,E.,
            Berman,B., Carlson,J., Champe,M., Chavez,C., Chew,M., Dorsett,V.,
            Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N.,
            Li,P., Liao,G., Miranda,A., Misra,S., Mungall,C.J., Nunoo,J.,
            Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C.,
            Lewis,S.E., Celniker,S. and Rubin,G.M.
  TITLE     BDGP/HHMI AT Drosophila EST Project
  JOURNAL   Unpublished (2000)
COMMENT     On Dec 6, 2000 this sequence version replaced gi:11572211.
            Other_ESTs: AT24194.3prime
            Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic AE003835: arm:2R [3832656,4092515]
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           estimated-cyto:44F1-45A7: 04/09/2001
           Plate: AT.241  row: H  column: 10
           High quality sequence stop: 572.
FEATURES             Location/Qualifiers
     source          1. .605
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone="AT24194"
                     /sex="male"
                     /dev_stage="0-3 day old Ore-R males"
                     /lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
                     AT.121-AT.319: DH5-alpha TonA"
                     /clone_lib="AT Drosophila melanogaster adult testes pOTB7"
                     /note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: Xho1; The mRNA for the testis library was made
                     from testes and seminal vessicles hand dissected from 0-3
                     day old Ore-R males. RNA kindly provided by the lab of
                     Margaret Fuller. Sized fractionated cDNAs were directly
                     ligated into pOTB7. Plasmid cDNA library."
ORIGIN

  Query Match            14.3%;  Score 429;  DB 2;  Length 605;
  Best Local Similarity   81.8%;  Pred. No. 1.4e-101;
  Matches  495;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy       2028 CGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAACTT 2087
             ||| |||||||||||| || || ||| ||||||| ||||| ||||| || || ||||||||
Db             1 CGCGGAGTTCACCTGTGCGCTGTTCCGGTTCATCCAGCTGACCTGCGAGGGCCACAACTT 60

Qy       2088 GGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTCAT 2147
             ||| ||||| |||||  || | || ||||| |||||||| || || ||||||||||||||
Db            61 GGAATGGCAAAACTATTTGAGGACCCAGGCGGGTAACACCACCACCGTGAACGTGGTCAT 120

Qy       2148 CTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCACTA 2207
             ||| || || || ||  |||| || ||||| ||||||||||||||||||||||||||||||
Db            121 CTGTACTGTGGATTATTTGCTTCGTCTGCAAGAGTCCATCATGGACTTCTACTGGCACTA 180

Qy       2208 CTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGT 2267
             ||| ||||| ||  | ||||| || || || || || |||||||||||||||||  ||
Db            181 CTCCAGCAAAGAGATCATCGATCCCGCTGGAAAGGCCAACTTCTTCAAGGCCATCGAAGT 240

Qy       2268 GGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAATCA 2327
             ||||  |||||||| |||||||||||||||||||| ||||| || ||||| |  |||||
Db            241 GGCTAGCCAAGTATTTAACACCCTCACTGAAGTCATCCAGGGTCCGTGTACCCTCAATCA 300

Qy       2328 GCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTC 2387
             |||||| ||||| ||||| |||||||||| || || ||||| ||||| ||||| || ||
Db            301 GCAGGCCTTGGCACACTCGAGGTTGTGGGATGCAGTTGGTGGCTTCCTCTTCCTGTTTTC 360

Qy       2388 CCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCT 2447
             |||||||||||||||| |||| |||||||||    || || || ||||| ||||||||| ||
Db            361 CCACATGCAGGACAAGCTGTCAAAGCACTCCAGCCAAGTTGATCTGCTCAAGGAACTGCT 420

Qy       2448 CAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAA 2507
             |||||||| |||||||||||| |||||||||| |||||||| ||||||||||||||||||
Db            421 GAATCTGCAAAAGGACATGATCACCATGATGCTTTCCATGCTGGAAGGAAATGTTGTTAA 480

Qy       2508 TGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAACT 2567
               || || || |||||||| |||||||||| ||||| || || |||  ||| ||||| ||
Db            481 CGGCACTATTGGCAAGCAGATGGTGGACACGCTAGTGGAGTCTGCCAGCAATGTGGAGCT 540

Qy       2568 GATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTT 2627
             ||| || || |||||||||||||||||| |||||     ||||| | |       |||||||
Db            541 GATTCTTAAGTACTTCGACATGTTCCTGAAGCTCGGCGACCTTATCGAATCGCCCAGCTT 600

Qy       2628 CCAGG 2632
             |||| |
Db            601 CCACG 605


RESULT 6
BI502728/c
LOCUS       BI502728                601 bp    mRNA    linear   EST 08-APR-2002
DEFINITION  BB170002B20G11.5 Bee Brain Normalized/Subtracted Library, BB17 Apis
            mellifera cDNA clone BB170002B20G11 5', mRNA sequence.
ACCESSION   BI502728
VERSION     BI502728.1  GI:15353102
KEYWORDS    EST.
SOURCE      Apis mellifera (honey bee)
  ORGANISM  Apis mellifera
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,
            Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
  TITLE     Annotated expressed sequence tags and cDNA microarrays for studies
            of brain and behavior in the honey bee
  JOURNAL   Genome Res. 12 (4), 555-566 (2002)
   PUBMED   11932240
COMMENT     Contact: Gene E. Robinson
            Department of Entomology
            University of Illinois
            505 S. Goodwin Ave., Urbana, IL 61801, USA
            Tel: 217 265 0309
            Fax: 217 244 3499
            Email: generobi@life.uiuc.edu
            This research was funded by the University of Illinois Critical
            Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
            Award in Functional Genomics to G.E. Robinson and an NSF
            Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Plate: BB170002B20  row: G  column: 11
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 601.
FEATURES             Location/Qualifiers
     source          1. .601
                     /organism="Apis mellifera"
                     /mol_type="mRNA"
                     /strain="mixed strains of European bees, predominantly
                     A.m. ligustica"
                     /db_xref="taxon:7460"
                     /clone="BB170002B20G11"
                     /sex="female"
                     /tissue_type="brain"
                     /dev_stage="adult worker honey bee"
                     /lab_host="DH10B"
                     /clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
                     /note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1;
                     Site_2: Not1; This BB17 cDNA library was generated by
                     subtraction of the BB16  library with 4000 previously
                     sequenced clones. The BB16 library was  contributed by the
                     Soares laboratory and it was constructed and  normalized
                     as described by Bonaldo, M.F., Lennon, G. and  Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. RNA was
                     prepared  from dissected brains of adult worker bees of
                     various ages and  various behavioral groups. "
ORIGIN

  Query Match            13.1%;  Score 392.6;  DB 3;  Length 601;
  Best Local Similarity   78.2%;  Pred. No. 5.9e-92;
  Matches  470;  Conservative    0;  Mismatches  131;  Indels    0;  Gaps    0;

Qy       2009 GAGAGAAGAACATGCATGACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCA 2068
             |||||||||||||||| || || ||||| || || || || ||  | || ||||| || |
Db             601 GAGAGAAGAACATGCACGATGCTGAGTTTACATGTGCTCTATTTCGTTTTATTCAACTGA 542

Qy       2069 CCTGTGAAGGACACAACTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGA 2128
             | || || || || ||  | ||||  ||||| || ||  |||| || || |||||||| |
Db             541 CTTGCGAGGGTCATAATCTTGACTNNCAGAATTATCTAAGAACGCAAGCTGGTAACACAA 482

Qy       2129 CAACAGTGAACGTGGTCATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCA 2188
             |||| |||||||| |||||||||||||||||| || || ||||| || || || |||||||
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Db        481 CAACGGTGAACGTAGTCATCTGCACCGTCGATTATCTACTGCGACTCCAAGAATCCATCA 422

Qy       2189 TGGACTTCTACTGGCACTACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACT 2248

Db        421 TGGACTTCTATTGGCACTATTCCAGCAAGGAACTCATCGACCCTGCCGGCAAGGCTAATT 362

Qy       2249 TCTTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGG 2308

Db        361 TTTTCAAAGCTATTGGCGTTGCCAGTCAGGTGTTCAATACCCTCACTGAGGTGATTCAAG 302

Qy       2309 GACCTTGTACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTG 2368

Db        301 GACCCTGCGCACAGAATCAACAAGCATTGGCACATTCTCGATTGTGGGACGCGGTTGGTG 242

Qy       2369 GTTTCCTGTTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGG 2428

Db        241 GATTCCTTTTCCTTTTCTCTCACATGCAAGACAAGTTGTCCAAACACTCGAGTCAGGTGG 182

Qy       2429 ACCTGCTGAAGGAACTCCTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGC 2488

Db        181 ATCTATTGAAGGAGTTGCTCAACTTGCAAAAAGATATGATCACTATGATGTTGTCTATGC 122

Qy       2489 TTGAAGGAAATGTTGTTAATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAAT 2548

Db        121 TGGAAGGTAACGTCGTAAATGGAACTATTGGAAAACAGATGGTGGACACATTGGTAGAAT 62

Qy       2549 CGGCCTCCAACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACC 2608

Db          61 CTGCGGGCAATGTCGAGTTGATTCTTAAATACTTCGACATGTTCTTGAAACTGAAAGATC 2

Qy       2609 T 2609

Db          1 T 1
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RESULT 7
CD509498
LOCUS CD509498 1169 bp mRNA linear EST 12-JUN-2003
DEFINITION CDA96-F06.x1d-t SHGC-CDA Gasterosteus aculeatus cDNA clone CDA96-F06 5', mRNA sequence.
ACCESSION CD509498
VERSION CD509498.1 GI:31440067
KEYWORDS EST.
SOURCE Gasterosteus aculeatus (three spined stickleback)
ORGANISM Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.
REFERENCE 1 (bases 1 to 1169)
AUTHORS Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.
TITLE Expressed sequence tags from Gasterosteus aculeatus
JOURNAL Unpublished (2003)
COMMENT Contact: Kingsley, DM
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
Tel: 650 725 5954
Fax: 650 725 7739
Email: kingsley@cmgm.stanford.edu
Plate: 96
High quality sequence stop: 692.
FEATURES Location/Qualifiers
source 1. .1169
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Salinas river, CA"
/db_xref="taxon:69293"
/clone="CDA96-F06"
/sex="mixed male and female"
/tissue_type="heads and internal organs combined"
/dev_stage="adult"
/clone_lib="SHGC-CDA"
/note="Vector: lambda ZAP Express/pBK-CMV; Site_1: EcoR1 (5' adaptor); Site_2: XhoI (3' linker primer); The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a a 50 bp linker primer containing an oligo dT sequence preceeded by a synthetic XhoI site. 5 prime adaptors were used containing an EcoR1 cohesive end. The finished cDNAs were inserted in to the ZAP express vector unidirectionally in the sense orientation with respect to the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for EST sequencing."
ORIGIN

Query Match 12.6%; Score 379.4; DB 6; Length 1169;
Best Local Similarity 67.6%; Pred. No. 2.2e-88;
Matches 547; Conservative 0; Mismatches 261; Indels 1; Gaps 1;

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Qy       2191 GACTTCTACTGGCACTACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTC 2250

Db          3 GACTTCTACTGGTACTACTCTGGCAAAGATATCATCGACGAGACTGGAAGAGTCAACTTC 62

Qy       2251 TTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGA 2310

Db         63 TCCAAAGCTTTGTCTGTTGCCAAGCAGATATTCAACTCACTGACTGAGTACATTCAGGGC 122

Qy       2311 CCTTGTACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGT 2370

Db        123 CCGTGCATTGGGAACCAGCAGAGTTTGGCTCACAGCAGACTTTGGGATGCAGTTGTTGGC 182

Qy       2371 TTCCTGTTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGAC 2430

Db        183 TTCCTGCATGTGTTTGCCAACATGCAAATGAAGCTGTCTCAGGACTCCAGTCAGATTGAG 242

Qy       2431 CTGCTGAAGGAACTCCTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTT 2490

Db        243 CTGTTGAAGGAGCTGATGGATTTACAGAAGGACATGATTGTGATGTTGCTGTCTCTGCTA 302

Qy       2491 GAAGGAAATGTTGTTAATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCG 2550

Db        303 GAGGGTAACGTGGTGAACGGAACAATTGGAAAGCAGATGGTTGACACCCTGGTGGAGTCT 362

Qy       2551 GCCTCCAACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTG 2610

Db        363 TCTAGCAACGTGGAGATGATCCTCAAGTTCTTTGATATGTTCCTCAAGCTAAAGGACCTG 422

Qy       2611 ACCTCCAGCGCCAGCTTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAG 2670

Db        423 ACGTCCTCCGACAACTTCCGAGAGTATGACCCCGAGTGCAAAGGCATGATCTCGAAGAAG 482

Qy       2671 GACTTCAAGGAGAAAATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTC 2730

Db        483 GAGTTCCAGAAGTCCATGGAGAGCCAGATGCAGTACAGCCAGTCGGAGATTGGATTCTTG 542

Qy       2731 CTAGCTTGCTGCGAGACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGT 2790

Db        543 CTCTCGTGCGCGGAGGCCGACGAGAACGACATGTTCAATTACAAAGAGTTTGTCGAGCGG 602

Qy       2791 TTCCACGAGCCTGCCAAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCT 2850

Db        603 TTCCACGAGCCGGCGCAAGACATCGGATTCAACATGGCGGTGCTGCTGACCAACCTGTCC 662

Qy       2851 GAACATATGCCGAACGAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTG 2910

Db        663 GAACACATGCCACACGACTCCAGACTCGCCACCTTCTTAGACCTGGCGGGGAGCGTGCTC 722

Qy       2911 AACTACTTCGAACCATTCCTGGGCCGTATCGAGATCATGGGC-GGCTCCAAGCGCATCGA 2969

Db        723 AGCTACTTTGAGCCCTATCTGGGTCGCATTGAAATCATGGGCAGTGCCCAAGCGGATCGA 782
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Qy       2970 GCGTGTCTACTTCGAGATCAAGGAGTCTA 2998
              ||| || ||||| |||||||| ||||| |
Db        783 GCGGGTGTACTTTGAGATCAACGAGTCCA 811


RESULT 8
AG926182/c
LOCUS       AG926182                599 bp    DNA     linear   GSS 01-FEB-2005
DEFINITION  Drosophila melanogaster DNA, clone: DME1-007J21.F.fa, genomic
            survey sequence.
ACCESSION   AG926182
VERSION     AG926182.1  GI:58447553
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1
  AUTHORS   Hattori,M., Toyoda,A., Murakami,K., Kuroki,Y., Fujiyama,A.,
            Toshio,T.K. and Sakaki,Y.
  TITLE     BAC end sequences of Library DME1
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 599)
  AUTHORS   Hattori,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the BAC library DME1
            For BAC library availability, please contact Masa-Toshi Yamamoto
            (yamamoto@kit.jp).
            Submitted (30-11-2004) by  Masahira Hattori,
            RIKEN, Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp,Tel:81-45-503-9111,
            Fax:81-45-503-9170)
            This work was done in collaboration with Yamamoto, M-T. Drosophila
            Genetic Resource Center
            Saga Ippongi-cho, Ukyo-ku, Kyoto 616-8354, Japan
            Tel: 81-75-873-2660 FAX: 81-75-861-0881
            PRIMERS
                 Sequencing : F
            LIBRARY
                 Vector     : pKS150
                 R.Site 1   : SacI
                 R.Site 2   : SacI.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             12.1%;  Score 364.4;  DB 10;  Length 599;
  Best Local Similarity   75.6%;  Pred. No. 1.7e-84;
  Matches  452;  Conservative    0;  Mismatches  146;  Indels    0;  Gaps    0;

Qy          50 ACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGATCTTAGGCGAGGTGG 109
               |||| |||   || |||||    || ||||| |  |||||||| ||  | | |||||| |
Db         599 ACATTATGGTCAAGATGGAGAGCTGTATGCCAAATCTAGAGACCATTCTCGCCGAGGTCG 540

Qy         110 ACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATATCATCGATGTGGTGC 169
               |||| || |||||||| |||||||| ||||| || ||||| ||||| ||||| ||| | |
Db         539 ACCAGTTTGTGGAGTCGGACAAGACATACAATGATGCGCCTCATATTATCGACGTGATCC 480

Qy         170 TGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCCTGATAATGTTACTC 229
               |||| | || || | ||| | ||||| |||||| | ||||| || |||||||| | ||
Db         479 TGCCGCTGCTTTGCGCCTATCTACCGTTTTGGTGGTCCCAGGGACCGGATAATGTCAGTC 420

Qy         230 CTACTGGCGGAAACCACGTAACAATGGTAACAGCGGAACACATGAACCAGCTCCTCAAGA 289
               | ||  | || |||||||| || ||||| ||||| || |||||||| | | | ||    |
Db         419 CCACCAGTGGCAACCACGTGACCATGGTCACAGCCGATCACATGAATCCGTTGCTGCGAA 360

Qy         290 ATGTTCTGAAGCTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCA 349
               |||| || ||  | ||||| |||||||| ||||| || ||||| || |||||||| ||||
Db         359 ATGTGCTTAAAATGATCAAGAAGAACATTGGCAACGATAACGCCCCTTGGATGACTCGCA 300

Qy         350 TCGCCACCTACACGCAGCAGATCATCATCAACAGCTCCGAGGAACTGCTGAGGGATTCCT 409
               | ||| |||| |||||||||| |||||||| |  || ||||| ||||| | |||| | |
Db         299 TTGCCGCCTATACGCAGCAGATTATCATCAATACGTCGGAGGAGCTGCTCAAGGATCCGT 240

Qy         410 TCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGA 469
               || ||||||| || || || ||     || ||||| || || ||| | || |||||||| |
Db         239 TCTTGCCGCTGGCGGAGCGGGTGAAGAAGCGCACTGAGAACATGCTGCACAAGGAGGACA 180

Qy         470 GCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATAC 529
               || || | || || || |||||| | || |||||||| || ||||| ||| | ||| | |
Db         179 GCATGCGAGGATTCATCAAGTCGGCCACGGACGACACTTCGCAGGTGGAGACCCAGCTGC 120

Qy         530 AAGAAGACTGGCAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGT 589
               | || |||||| | ||||| ||  |||||| ||||| ||||| || ||||||||||||||
Db         119 AGGAGGACTGGAATCTGCTAGTGCGAGACATATACTCGTTCTATCCCCTGCTCATCAAGT 60

Qy         590 ACGTCGACCTGCAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCT 647
               |||| || |||||| | |||||||||| | | ||||  | || ||||| || |||||
Db          59 ACGTGGATCTGCAGCGAAACCACTGGCTGAAGGACAACATACCGGAGGCCGAGGAGCT 2


RESULT 9
CX784892
LOCUS       CX784892                842 bp    mRNA    linear   EST 02-MAR-2005
DEFINITION  HESC3_40_D03.g1_A036 NIH_MGC_260 Homo sapiens cDNA clone
            IMAGE:7479224 5', mRNA sequence.
ACCESSION   CX784892
VERSION     CX784892.1  GI:58301682
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 842)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: BresaGen, Inc.
             cDNA Library Preparation: Express Genomics, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
            University of Georgia
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15795  row: h  column: 06
            Seq primer: JENREV (CAGGAAACAGCTATGACC)
            High quality sequence stop: 842.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7479224"
                     /sex="male"
                     /tissue_type="human embryonic stem cells"
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                     /cell_line="BG01"
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/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH_MGC_260"
/note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos. Cell line
id and NIH Registry designation is BGO1. Positive for
SSEA3, SSEA4, Tra 1-60, Tra 1-81, CD9, Alk Phos, Oct4 and
Nanog expression; negative for SSEA1 expression. Passage
number 21. cDNA primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH_MGC_261). It was constructed by Express Genomics
(Frederick, MD). Sequence ends have been trimmed to
exclude vector and regions below Phred quality 16. Note:
this is a Mammalian Gene Collection library."

ORIGIN

Query Match 10.8%; Score 325; DB 8; Length 842;
Best Local Similarity 69.8%; Pred. No. 4.7e-74;
Matches 439; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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Qy       2005 GCGGGAGAGAAGAACATGCATGACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAG 2064
              || |||||||||  ||||   || |  || |||||     |  || ||| | ||| | ||
Db        213 GCAGGAGAGAAGGTCATGGCGGATGATGAATTCACACAAGACCTGTTCCGATTCCTACAA 272

Qy       2065 CTCACCTGTGAAGGACACAACTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAAC 2124
                |  |||||| || |||||     || |  |||||||||| || || ||| | || |||
Db        273 TTGCTCTGTGAGGGGCACAATAATGATTTCCAGAACTACCTACGGACACAGACAGGGAAC 332

Qy       2125 ACGACAACAGTGAACGTGGTCATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCC 2184
              ||||| ||  | ||| |  |||| ||||| || ||||||||| ||||||||||||||| |||
Db        333 ACGACCACTATTAACATCATCATTTGCACTGTGGACTACCTCCTGCGGCTGCAGGAATCC 392

Qy       2185 ATCATGGACTTCTACTGGCACTACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCG 2244
              ||||  |||||||||||| |||||||  |||||||  | || ||   |  |||||  |
Db        393 ATCAGCGACTTCTACTGGTACTACTCGGGCAAGGATGTCATTGAAGAGCAGGGCAAGAGG 452

Qy       2245 AACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATA 2304
              |||||||  ||| |||||     ||||||    || || ||||||| |||||||||   |||
Db        453 AACTTCTCCAAAGCCATGTCGGTGGCTAAGCAGGTGTTCAACAGCCTCACTGAGTACATC 512

Qy       2305 CAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTC 2364
              |||||  || || ||   ||| ||||||    |||| |||    |  | |||||||| ||
Db        513 CAGGGTCCCTGCACCGGGAACCAGCAGAGCCTGGCGCACAGTCGCCTATGGGACGCAGTG 572

Qy       2365 GGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAG 2424
              |  || ||||||  | | ||| ||||||||  |   ||| |  |  || ||||    |||
Db        573 GTGGGATTCCTGCACGTGTTCGCCCACATGATGATGAAGCTCGCTCAGGACTCAAGCCAG 632

Qy       2425 GTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCC 2484
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Db        633 ATCGAGCTGCTGAAGGAGCTGCTGGATCTGCAGAAGGACATGGTGGTGATGTTGCTGTCG 692

Qy       2485 ATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTA 2544
              | || ||||| || || || || || | |||| |  ||| ||||||||||  || ||
Db        693 CTACTAGAAGGGAACGTGGTGAACGGCATGATCGCCCGGCAGATGGTGGACATGCTCGTG 752

Qy       2545 GAATCGGCCTCCAACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAG 2604
              |||||  | ||||| |||||  ||||||| || | ||||||||||||||| || || |||
Db        753 GAATCCTCATCCAATGTGGAGATGATCCTCAAGTTCTTCGACATGTTCCTGAAACTCAAG 812

Qy       2605 GACCTGACCTCCAGCGCCAGCTTCCAGGA 2633
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Db        813 GACATTGTGGGCTCTGAAGCCTTCCAGGA 841
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RESULT 10
CX786866
LOCUS CX786866 781 bp mRNA linear EST 02-MAR-2005
DEFINITION HESC3_65_H01.g1_A036 NIH_MGC_260 Homo sapiens cDNA clone IMAGE:7482075 5', mRNA sequence.
ACCESSION CX786866
VERSION CX786866.1 GI:58303656
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 781)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: BresaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics, University of Georgia
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM15802 row: o column: 01
Seq primer: JENREV (CAGGAAACAGCTATGACC)
High quality sequence stop: 781.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7482075"
/sex="male"
/tissue_type="human embryonic stem cells"
/cell_type="human embryonic stem cells"
/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH_MGC_260"
/note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos. Cell line
id and NIH Registry designation is BGO1. Positive for
SSEA3, SSEA4, Tra 1-60, Tra 1-81, CD9, Alk Phos, Oct4 and
Nanog expression; negative for SSEA1 expression. Passage
number 21. cDNA primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH_MGC_261). It was constructed by Express Genomics
(Frederick, MD). Sequence ends have been trimmed to
exclude vector and regions below Phred quality 16. Note:
this is a Mammalian Gene Collection library."

ORIGIN

Query Match 10.7%; Score 320.8; DB 8; Length 781;
Best Local Similarity 70.6%; Pred. No. 6e-73;
Matches 427; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

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Qy       2005 GCGGGAGAGAAGAACATGCATGACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAG 2064
              || |||||||||  ||||   || |  || |||||     |  || ||| | ||| | ||
Db         165 GCAGGAGAGAAGGTCATGGCGGATGATGAATTCACACAAGACCTGTTCCGATTCCTACAA 224

Qy       2065 CTCACCTGTGAAGGACACAACTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAAC 2124
                |  |||||| || |||||     || |  |||||||||| || || ||| | || |||
Db         225 TTGCTCTGTGAGGGGCACAATAATGATTTCCAGAACTACCTACGGACACAGACAGGGAAC 284

Qy       2125 ACGACAACAGTGAACGTGGTCATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCC 2184
              ||||| ||  | ||| |  |||| ||||| || ||||||||| ||||||||||||||| |||
Db         285 ACGACCACTATTAACATCATCATTTGCACTGTGGACTACCTCCTGCGGCTGCAGGAATCC 344

Qy       2185 ATCATGGACTTCTACTGGCACTACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCG 2244
              ||||  |||||||||||| |||||||  |||||||  | || ||   |  |||||  |
```

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Db        345 ATCAGCGACTTCTACTGGTACTACTCGGGCAAGGATGTCATTGAAGAGCAGGGCAAGAGG 404

Qy       2245 AACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATA 2304

Db        405 AACTTCTCCAAAGCCATGTCGGTGGCTAAGCAGGTGTTCAACAGCCTCACTGAGTACATC 464

Qy       2305 CAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTC 2364

Db        465 CAGGGTCCCTGCACCGGGAACCAGCAGAGCCTGGCGCACAGTCGCCTATGGGACGCAGTG 524

Qy       2365 GGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAG 2424

Db        525 GTGGGATTCCTGCACGTGTTCGCCCACATGATGATGAAGCTCGCTCAGGACTCAAGCCAG 584

Qy       2425 GTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCC 2484

Db        585 ATCGAGCTGCTGAAGGAGCTGCTGGATCTGCAGAAGGACATGGTGGTGATGTTGCTGTCG 644

Qy       2485 ATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTA 2544

Db        645 CTACTAGAAGGGAACGTGGTGAACGGCATGATCGCCCGGCAGATGGTGGACATGCTCGTG 704

Qy       2545 GAATCGGCCTCCAACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAG 2604

Db        705 GAATCCTCATCCAATGTGGAGATGATCCTCNAGTTCTTCGACATGTTCCTGAAACTCAAG 764

Qy       2605 GACCT 2609

Db        765 GACAT 769
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RESULT 11
BB639430
LOCUS BB639430 684 bp mRNA linear EST 26-OCT-2001
DEFINITION BB639430 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630095L05 5', mRNA sequence.
ACCESSION BB639430
VERSION BB639430.1 GI:16474825
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 684)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES Location/Qualifiers
source 1. .684
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A630095L05"
/tissue_type="thymus"
/dev_stage="3 days neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 3 days neonate thymus"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 10.6%; Score 319.6; DB 2; Length 684;
Best Local Similarity 68.8%; Pred. No. 1.2e-72;
Matches 439; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

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Qy       1933 TCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAGGCTGAAGGTCTGGGCGTGGGT 1992

Db         47 TTCGTCCTGGACCTCAATGCCTTCGAGAGGCAGAACAAGGCAGAGGGGCTGGGCATGGTG 106

Qy       1993 CTGGAAGGTGCGGCGGGAGAGAAGAACATGCATGACGCCGAGTTCACCTGCGCACTCTTC 2052

Db        107 AACGAGGACGGAACTGGAGAGAAAGTCATGGCGGATGACGAGTTCACACAGGACCTGTTC 166

Qy       2053 AGGTTCATTCAGCTCACCTGTGAAGGACACAACTTGGACTGGCAGAACTACCTGCGAACT 2112

Db        167 CGCTTCCTGCAGCTGCTCTGCGAGGGGCACAACAATGATTTCCAAAACTACCTACGGACA 226

Qy       2113 CAGGCCGGTAACACGACAACAGTGAACGTGGTCATCTGCACCGTCGACTACCTGCTGCGG 2172

Db        227 CAGACTGGGAACACGACCACCATCAATATCATTATCTGCACAGTGGACTACCTCCTGCGG 286

Qy       2173 CTGCAGGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAACTGATCGACCCG 2232

Db        287 CTGCAGGAATCCATCAGTGACTTCTACTGGTATTACTCGGGCAAGGATGTCATCGAGGAA 346

Qy       2233 GCCGGCAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTC 2292

Db        347 CAGGGAAAGAGAAACTTCTCCAAAGCCATGTCGGTAGCTAAACAAGTGTTCAACAGCCTC 406

Qy       2293 ACTGAAGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTG 2352
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```
Db        407 ACCGAGTACATCCAGGGACCCTGCACCGGAAACCAGCAGAGTCTGGCGCACAGTCGCCTC 466

Qy       2353 TGGGACGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAG 2412

Db        467 TGGGATGCCGTGGTGGGCTTCCTGCACGTGTTCGCGCACATGATGATGAAGCTGGCTCAG 526

Qy       2413 CACTCGTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAGGACATGATCCCC 2472

Db        527 GACTCCAGCCAGATAGAGCTGCTGAAGGAGCTGCTGGACCTACAGAAGGACATGGTGGTG 586

Qy       2473 ATGATGCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGCAAGCAAATGGTG 2532

Db        587 ATGCTGCTGTCCCTCCTGGAAGGAAACGTGGTGAACGGTATGATCGCGCGGCAGATGGTG 646

Qy       2533 GACACACTAGTAGAATCGGCCTCCAACGTGGAACTGAT 2570

Db        647 GACATGCTCGTGGAGTCTTCGTCCAATGTGGAGATGAT 684
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RESULT 12
BG409436

```
LOCUS       BG409436                964 bp    mRNA    linear   EST 13-MAR-2003
DEFINITION  GKP2-34 GKP2 subtraction cDNA library Mus musculus cDNA clone
            GKP2-34 5' and 3', mRNA sequence.
ACCESSION   BG409436
VERSION     BG409436.1  GI:28933771
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 964)
  AUTHORS   Woo,J.T., Asai,Y., Zhu,M., Moates,J.M. and Magnuson,M.A.
  TITLE     Identification of thirty-six genes whose expression is markedly
            affected by beta cell differentiation and de-differentiation
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Magnuson, M.A.
            Department of Molecular Physiology and Biophysics
            Vanderbilt University
            747 LH, 21st Ave at Garland Ave. Nashville, TN 37232-0615, USA
            Fax: 615 322 7236
            Email: mark.magnuson@mcmail.vanderbilt.edu
            similar to mouse ryanodine receptor cDNA sequences (GenBank
            Accession No.; AF071003.1)
            PCR PRimers
            FORWARD: M13 forward
            BACKWARD: M13 reverse
            Insert Length: 964   Std Error: 0.00
            Seq primer: T7, M13 reverse, custom
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .964
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J x DBA/2"
                     /db_xref="taxon:10090"
                     /clone="GKP2-34"
                     /cell_type="Pancreatic endocrine tumor"
                     /cell_line="GKP2"
                     /lab_host="TOP10 (Invitrogen, Carlsbad, CA)"
                     /clone_lib="GKP2 subtraction cDNA library"
                     /note="Organ: Pancreas; Vector: pCR 2.1-TOPO (Invitrogen,
                     Carlsbad, CA); Site_1: EcoR1; Site_2: BamH1; mRNA from
                     GKP2 and GKP4 cells was used to perform subtraction
                     suppression hybridization. Genes that are more highly
                     expressed in  GKP2 cells (an insulinoma derived cell),
                     compared to GKP4 cells (a  precursor cell line) were
                     cloned pCR 2.1-TOPO and transformed into  TOP10 competent
                     bacteria."
ORIGIN
```

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  Query Match           10.6%;  Score 317.6;  DB 2;  Length 964;
  Best Local Similarity   66.9%;  Pred. No. 4.5e-72;
  Matches  452;  Conservative    0;  Mismatches  224;  Indels    0;  Gaps    0;

Qy       2323 AATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTA 2382

Db          7 AATCAGCAGAGCCTGGCACACAGCAGGCTGTGGGATGCTGTTGTGGGCTTCCTTCATGTA 66

Qy       2383 TTCTCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAA 2442

Db         67 TTTGCACACATGCAAATGAAGCTGTCTCAGGATTCCAGCCAGATTGAGCTCTTAAAAGAA 126

Qy       2443 CTCCTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTT 2502

Db        127 CTTATGGATCTCCAGAAGGACATGGTGGTCATGCTGCTGTCTATGCTAGAAGGTAATGTG 186

Qy       2503 GTTAATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTG 2562

Db        187 GTGAACGGAACAATAGGCAAACAGATGGTGGCCATGCTTGTGGAGTCGTCCAACAACGTG 246

Qy       2563 GAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCC 2622

Db        247 GAGATGATCCTCAAGTTCTTTGACATGTTTCTGAAGCTGAAGGACTTAACATCCTCTGAC 306

Qy       2623 AGCTTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAG 2682

Db        307 ACATTCAAAGAGTATGACCCTGATGGCAAAGGGGTCATTTCCAAGAGAGACTTCCACAAA 366

Qy       2683 AAAATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGC 2742

Db        367 GCCATGGAGAGCCACAAGCACTACACCCAGTCAGAGACTGAGTTCCTGCTGTCCTGTGCA 426

Qy       2743 GAGACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCT 2802

Db        427 GAGACAGATGAAAACGAGACACTTGACTATGAAGAGTTTGTCAAGAGGTTCCATGAGCCT 486

Qy       2803 GCCAAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACATATGCCG 2862

Db        487 GCCAAGGACATCGGCTTCAACGTGGCTGTTCTGCTGACCAACCTCTCAGAGCACATGCCC 546

Qy       2863 AACGAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAA 2922

Db        547 AATGACACGAGGCTGCAGACCTTCTTGGAGTTGGCAGAGAGTGTCCTCAACTACTTCCAA 606

Qy       2923 CCATTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTC 2982

Db        607 CCTTTCCTGGGTCGCATTGAGATCATGGGCAGTGCCAAGCGCATCGAAAGGGTCTATTTT 666

Qy       2983 GAGATCAAGGAGTCTA 2998

Db        667 GAGATCAGCGAATCCA 682
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RESULT 13
DT063789

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LOCUS       DT063789                813 bp    mRNA    linear   EST 11-AUG-2005
DEFINITION  AGENCOURT_56115410 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:8003748
            5', mRNA sequence.
ACCESSION   DT063789
VERSION     DT063789.1  GI:72363038
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 813)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
```

Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM17172 row: c column: 10
High quality sequence stop: 680.

FEATURES Location/Qualifiers
source 1. .813
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:8003748"
/tissue_type="whole body"
/lab_host="DH10B"
/clone_lib="NIH_ZGC_10"
/note="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV; Bulk tissue was collected from a whole adult individual from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1 kb fragments. A normalized version of this library is also available (NIH_ZGC_7). Library was constructed by Open Biosystems (Huntsville, AL)."

ORIGIN

Query Match 9.6%; Score 287.8; DB 8; Length 813;
Best Local Similarity 63.6%; Pred. No. 3.2e-64;
Matches 456; Conservative 0; Mismatches 257; Indels 4; Gaps 1;

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Qy       2257 GCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGT 2316
Db          1 GCAATCAATGTAGCCAAACAAGTCTTCAACACTCTTACAGAGTACATTCAGGGTCCCTGC 60

Qy       2317 ACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTG 2376
Db         61 ACCGGGAATCAGCAGAGTCTGGCTCACAGTCGCCTGTGGGATGCGGTTGTTGGTTTCCTG 120

Qy       2377 TTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTG 2436
Db        121 CATGTTTTTGCACATATGCAGATGAAGCTCTCTCAGGACTCAAGCCAAATCGAGCTACTG 180

Qy       2437 AAGGAACTCCTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGA 2496
Db        181 AAGGAGCTGATGGATCTTCAGAAGGACATGGTCGTGATGCTCTTGTCCATGTTGGAAGGA 240

Qy       2497 AATGTTGTTAATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCC 2556
Db        241 AATGTTGTGAATGGCACTATTGGCAAGCAGATGGTGGACATGTTAGTGGAGTCCTCGAAT 300

Qy       2557 AACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCC 2616
Db        301 AACGTGGAGATGATCCTGAAGTTCTTTGACATGTTCCTCAAACTAAAAGACCTGACGTCG 360

Qy       2617 AGCGCCAGCTTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTC 2676
Db        361 TCGGACGCCTTCAAAGAGTACGACCCCGATGGCAAAGGCGTCATTTCCAAACGAGATTTC 420

Qy       2677 AAGGAGAAAATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCT 2736
Db        421 CACAAGGCAATGGAGAGCCATAAGCACTACACCCAATCCGAGACGGAGTTCCTGCTCTCC 480

Qy       2737 TGCTGCGAGACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCAC 2796
Db        481 TGTGCGGAAACAGATGAGAATGAGCTCTTAGACTACGAAGAGTTCGTCGAACGATTTCAC 540

Qy       2797 GAGCCTGCCAAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAACAT 2856
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Db        541 GAACCGGCGAAGGATATCGGTTTTAACGTGGCTGTTCTTCTAACCAATCTCTCAGAGCAC 600

Qy       2857 ATGCCGAACGAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAACTAC 2916
Db        601 ATGCCGCATGATTCTCGCCTCCAGACGTTCCTGGAGTTGGCGGAGAGCGTGCTGAATATT 660

Qy       2917 TTCGAACCATTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGT 2973
Db        661 TCCAGCCTATCTGGGCGC----TCGAGATCATGGGCACGCCAGAGATCGACGAGTGT 713
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RESULT 14
BM645859
LOCUS BM645859 569 bp mRNA linear EST 26-FEB-2002
DEFINITION 17000687317474 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone 19600449655747 5', mRNA sequence.
ACCESSION BM645859
VERSION BM645859.1 GI:18945370
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.
REFERENCE 1 (bases 1 to 569)
AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
TITLE Celera Anopheles gambiae EST project
JOURNAL Unpublished (2002)
COMMENT Contact: Holt R.A.
Celera Genomics
45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU01004A9T row: F column: 01
Seq primer: M13 Reverse.

FEATURES Location/Qualifiers
source 1. .569
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449655747"
/dev_stage="Adult"
/lab_host="DH10b"
/clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN

Query Match 9.2%; Score 276.8; DB 3; Length 569;
Best Local Similarity 79.1%; Pred. No. 2.3e-61;
Matches 329; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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Qy       2586 CATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGATGCCAA 2645
Db          11 CGTGTTCCTGAAGCTGAAGGATCTGACCTCCACGCCAAGCTTCATGGAGATTGATAGCAA 70

Qy       2646 TAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAGAGTTA 2705
Db          71 CGGGGACGGTTGGATTATGCCGAAAGATTTCCGCGAAAAGATGGAACAGCAGAAGAGCTA 130

Qy       2706 TACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGCAAGTT 2765
Db         131 CACGCCGGAGGAGATCGACTTCCTGCTCGCTTGCTGCGAGACCAACCATGACGGAAAGAT 190

Qy       2766 AGACTACATCGGTTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTTAACTT 2825
```

```
                ||||||||||||||   ||| || ||||||||||| |||||||||| || || ||  |
Db        191 CGACTACATCGGTTTTGTCGATCGGTTCCACGAGCCGGCCAAGGAGATTGGTTTCAATCT 250

Qy       2826 GGCCGTGTTACTGACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCACGTTT 2885
                ||||||  | ||||| ||| |||| || || |||||||||| ||  | ||||| || ||
Db        251 GGCCGTCCTGCTGACGAACCTGTCCGAGCACATGCCGAACGAACCGCGGTTGGCCCGGTT 310

Qy       2886 CCTGGAGACGGCAGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATCGAGAT 2945
                ||| |||||||| ||||| || ||||||||||||||  | ||| ||||||||||||| ||
Db        311 CCTCGAGACGGCCGGTTCCGTGCTGAACTACTTCGAGTCGTTCTTGGGCCGTATCGAAAT 370

Qy       2946 CATGGGCGGCTCCAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAATA 3001
                  ||||||   |||||||||||||||| || |||||||| ||||||||  | || |
Db        371 TATGGGCTCGTCCAAGCGCATCGAGCGCGTGTACTTCGAAATCAAGGAAGCGAACA 426


RESULT 15
CZ533566
LOCUS       CZ533566               887 bp    DNA     linear   GSS 13-MAY-2005
DEFINITION  SRAA-aac85h09.b1 Strongyloides ratti whole genome shotgun library
            (SRAAGSS 004) Strongyloides ratti genomic, genomic survey sequence.
ACCESSION   CZ533566
VERSION     CZ533566.1  GI:64647729
KEYWORDS    GSS.
SOURCE      Strongyloides ratti
  ORGANISM  Strongyloides ratti
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Panagrolaimoidea; Strongyloididae; Strongyloides.
REFERENCE   1  (bases 1 to 887)
  AUTHORS   Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D.,
            Ritter,E., Martin,J., Wylie,T., Dante,M., Waterston,R.H.,
            Clifton,S.W. and Wilson,R.
  TITLE     Genome Survey sequences from the rat parasitic nematode
            Strongyloides ratti
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Mitreva M
            Washington University in St. Louis
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: nematode@watson.wustl.edu
            Genomic DNA was provided by Fiona Thompson
            (F.Thompson@bristol.ac.uk) and Mark Viney
            (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol,
            UK.
            Class: shotgun.
FEATURES             Location/Qualifiers
     source          1. .887
                     /organism="Strongyloides ratti"
                     /mol_type="genomic DNA"
                     /strain="Isofemale line ED321 heterogonic"
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                     /dev_stage="infective larval stage (iL3)"
                     /lab_host="GS10"
                     /clone_lib="Strongyloides ratti whole genome shotgun
                     library (SRAAGSS 004)"
                     /note="Vector: pOTW13; Site_1: BstX1; Site_2: BstX1;
                     Strongyloides ratti genomic DNA was randomly sheared,
                     end-repaired and size fractioned to enrich for 2-4 kb
                     fragments. Genomic DNA was provided by Fiona Thompson
                     (F.Thompson@bristol.ac.uk) and Mark Viney
                     (Mark.Viney@bristol.ac.uk) at the University of Bristol,
                     Bristol, UK. Sequencing by Washington University Genome
                     Sequencing Center, St. Louis, MO."
ORIGIN

  Query Match             9.2%;  Score 276.2;  DB 10;  Length 887;
  Best Local Similarity   58.7%;  Pred. No. 3.8e-61;
  Matches  516;  Conservative    0;  Mismatches  358;  Indels    5;  Gaps    2;

Qy       1970 AGGCTGAAGGTCTGGGCGTGGGTCTGGAAGGTGCGGCGGGAGAGA----AGAACATGCAT 2025
                | |||||||||| | ||  |||||   |||   || || ||||| |    | ||  || ||

Db          6 AAGCTGAAGGTTTAGGTATGGGTGCAGAATTGGCTGCTGGAGAAACACCAAAATTTGAAT 65

Qy       2026 GACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGTGAAGGACACAAC 2085
                || || || || || || |    | || || ||| |||| | || |||||||| || ||
Db         66 GATGCAGAATTTACATGTGATTTATTTAGATTCCTTCAATTAACATGTGAAGGGCATAAT 125

Qy       2086 TTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGTC 2145
                || || |  || || || || || || || ||  | ||  | || || |  || ||| |  |
Db        126 TTAGATTTTCAAAATTATCTTCGTACACAACCAGGACATACAACTAGTGTTAACTTAATA 185

Qy       2146 ATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTACTGGCAC 2205
                |  || |  || || ||  |  |  | || || ||      | ||||| ||||| |||||
Db        186 AATTGTATTGTTGATTATTTATTAAGACTTCAAGAAAGTGTTATGGATTTCTATTGGCAT 245

Qy       2206 TACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTCAAGGCCATTGGC 2265
                ||||||   || ||| |||| ||    |  || ||||   | |||||    || ||
Db        246 TACTCATCAAAAGAAATGATTGATGAAGGTGGGAAAGAATATTTCTTACGTGCTATACAA 305

Qy       2266 GTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCTTGTACGCAGAAT 2325
                ||   |   || ||||| || ||  | || |||   || || ||||| |||      |||
Db        306 GTTTGTAGTCAGGTATTTAATACATTAACAGAATCAATTCAAGGACCATGTGTTGGTAAT 365

Qy       2326 CAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTCCTGTTCCTATTC 2385
                ||   | | || ||| | || || || ||||| ||  |   |||||||| | ||| ||||
Db        366 CAAATGACATTAGCTAATTCAAGATTATGGGATGCAATTAATGGTTTCTTTTTCTTATTT 425

Qy       2386 TCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTGCTGAAGGAACTC 2445
                | || |||  ||| || | |  ||  |      | ||  | || ||  ||| ||| |
Db        426 GCTCATATGATGGAAAAACTTTATAAAAATAGTACACAATTAGAACTTTTGAGAGAATTT 485

Qy       2446 CTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAAGGAAATGTTGTT 2505
                | ||| | || || || ||||     | ||| | || ||||||||||||||||||| |
Db        486 TTAAATTTACAAAAAGATATGATTGTTTTAATGTTATCTATGCTTGAAGGAAATGTTTTA 545

Qy       2506 AATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCCTCCAACGTGGAA 2565
                |||||  |||| || || || ||||| ||  || |||| |||||           || |||
Db        546 AATGGAGCAATTGGTAAACAGATGGTTGATGCATTAGTTGAATCACAACAATGTGTAGAA 605

Qy       2566 CTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACCTCCAGCGCCAGC 2625
                ||||  | ||||  |  || |||||  | ||  | ||| ||  | |||  |
Db        606 ATGATATTAAAATTTTCAGATATGTTTTTAAAATTAAAAGATTTAACAACATCACAAGCT 665

Qy       2626 TTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGACTTCAAGGAGAAA 2685
                || || ||  ||||| | ||||| || || ||| |    || || || ||| |  |
Db        666 TTTCAAGATTTTGATACTAATAAAGATGGTTGGATATCACCAAAAGAATTCCAAAAAGCT 725

Qy       2686 ATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTAGCTTGCTGCGAG 2745
                ||||||   || ||||  ||| |    ||||||||     |   |  |    ||    ||
Db        726 ATGGAAAGTCAAAAGATGTATTCAGTTGAAGAAATTACATATTTAATGATGTGTACTGAT 785

Qy       2746 ACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTCCA-CGAGCCTGC 2804
                ||  | || || ||  | || || || ||  | | |     | ||||    | || ||
Db        786 GTTAATAATGATGGTAAAGTTGATTATATGGGAATTTACTGAAGATTCCATTAATCCAGC 845

Qy       2805 CAAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAA 2843
                ||  || || || ||| | |    | || |  | | |
Db        846 CAGAGATATTGGTTTTTAATCTAGCCTGGTTTTTATTTA 884


Search completed: April 14, 2006, 20:56:18
Job time : 11362.5 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2006, 14:57:45 ; Search time 1272.5 Seconds
(without alignments)
9499.034 Million cell updates/sec

Title: US-10-668-767-127_COPY_10000_13000
Perfect score: 3001
Sequence: 1 cagttctccttgctgaacag.....cgagatcaaggagtctaata 3001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
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10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
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13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	732.2	24.4	15564	14	US-11-000-688-1500	Sequence 1500, Ap
2	724.4	24.1	10129	14	US-11-044-111-21	Sequence 21, Appl
3	644	21.5	14620	14	US-11-044-111-17	Sequence 17, Appl
4	63.8	2.1	1786	6	US-09-925-065A-73529	Sequence 73529, A
5	63.8	2.1	1786	6	US-09-925-065A-73530	Sequence 73530, A
6	63.8	2.1	1786	6	US-09-925-065A-73531	Sequence 73531, A
7	63.8	2.1	1786	9	US-10-301-480-174768	Sequence 174768,
8	63.8	2.1	1786	9	US-10-301-480-174769	Sequence 174769,
9	63.8	2.1	1786	9	US-10-301-480-174770	Sequence 174770,
10	63.8	2.1	1786	10	US-10-301-480-788177	Sequence 788177,
11	63.8	2.1	1786	10	US-10-301-480-788178	Sequence 788178,
12	63.8	2.1	1786	10	US-10-301-480-788179	Sequence 788179,
13	61.8	2.1	578	10	US-10-301-480-550750	Sequence 550750,
14	61.8	2.1	578	10	US-10-301-480-1164159	Sequence 1164159,
c 15	55.4	1.8	1556	8	US-10-750-185-28292	Sequence 28292, A
c 16	55.4	1.8	1556	8	US-10-750-623-28292	Sequence 28292, A
c 17	53	1.8	639	10	US-10-301-480-574146	Sequence 574146,
c 18	53	1.8	639	10	US-10-301-480-1187555	Sequence 1187555,
c 19	52.8	1.8	618	8	US-10-750-185-41205	Sequence 41205, A
c 20	52.8	1.8	618	8	US-10-750-623-41205	Sequence 41205, A
21	52.4	1.7	5940	9	US-10-893-483-106	Sequence 106, App
22	51.8	1.7	648	6	US-09-925-065A-712572	Sequence 712572,
c 23	51.8	1.7	208765	9	US-10-330-773-407	Sequence 407, App
c 24	50.2	1.7	2227	6	US-09-925-065A-720983	Sequence 720983,
c 25	50.2	1.7	2227	6	US-09-925-065A-720984	Sequence 720984,
c 26	50.2	1.7	2227	6	US-09-925-065A-720986	Sequence 720986,
c 27	49.8	1.7	640	10	US-10-301-480-574144	Sequence 574144,
c 28	49.8	1.7	640	10	US-10-301-480-1187553	Sequence 1187553,
29	49.8	1.7	971	10	US-10-301-480-579957	Sequence 579957,
30	49.8	1.7	971	10	US-10-301-480-1193366	Sequence 1193366,
c 31	49.6	1.7	372	9	US-10-932-182A-174580	Sequence 174580,
c 32	49.6	1.7	372	9	US-10-932-182A-174580	Sequence 174580,
c 33	49.6	1.7	489	6	US-09-925-065A-578773	Sequence 578773,
34	49.6	1.7	1908	9	US-10-932-182A-82752	Sequence 82752, A
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c 37	49.2	1.6	640	10	US-10-301-480-574141	Sequence 574141,
c 38	49.2	1.6	640	10	US-10-301-480-574142	Sequence 574142,
c 39	49.2	1.6	640	10	US-10-301-480-574143	Sequence 574143,
c 40	49.2	1.6	640	10	US-10-301-480-1187550	Sequence 1187550,
c 41	49.2	1.6	640	10	US-10-301-480-1187551	Sequence 1187551,
c 42	49.2	1.6	640	10	US-10-301-480-1187552	Sequence 1187552,
c 43	49	1.6	191350	8	US-10-857-780-4	Sequence 4, Appli
c 44	48.8	1.6	1691140	14	US-11-091-018-1	Sequence 1, Appli
45	48.6	1.6	589	6	US-09-925-065A-399065	Sequence 399065,

ALIGNMENTS

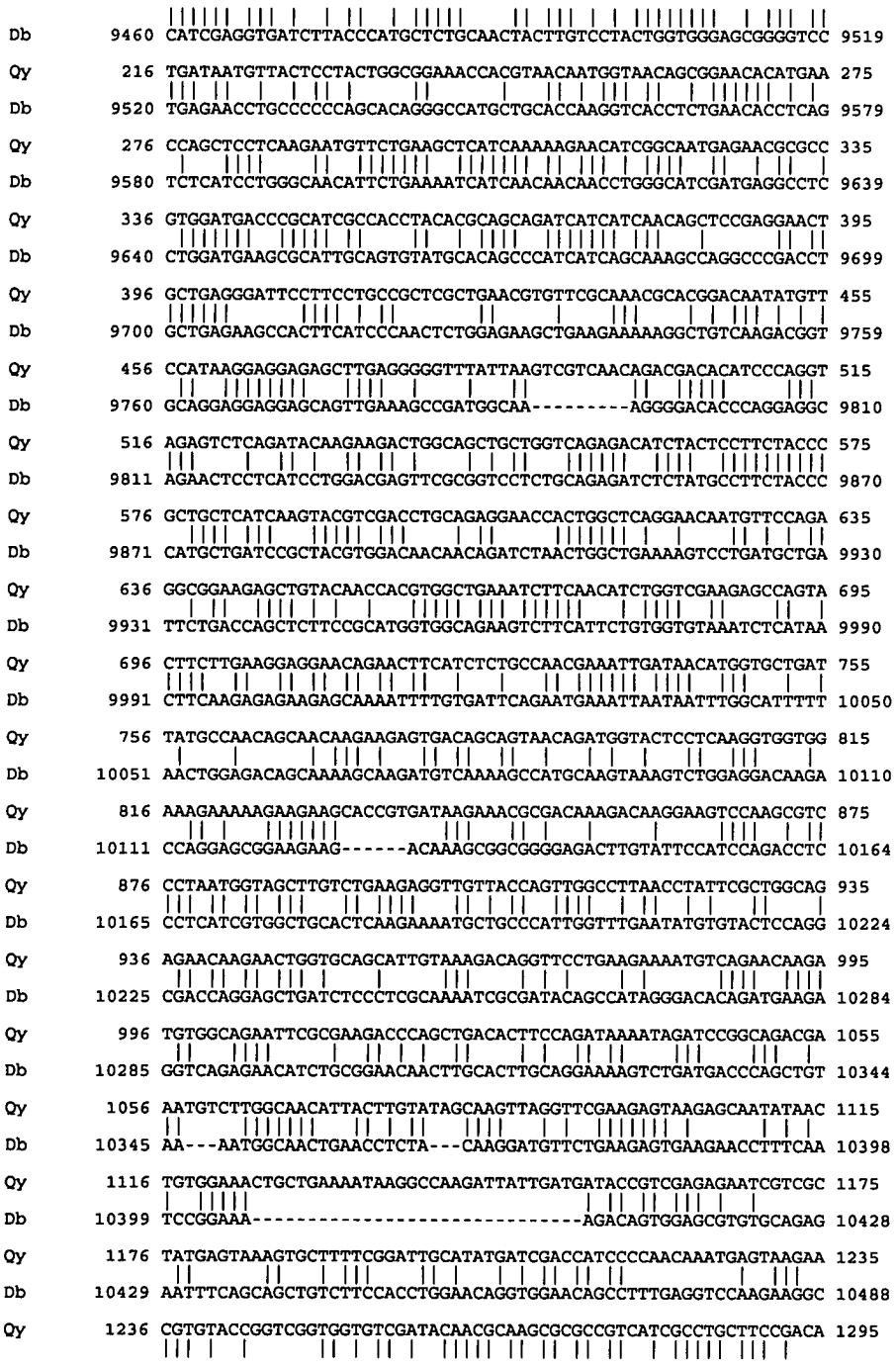
RESULT 1
US-11-000-688-1500
; Sequence 1500, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1500
; LENGTH: 15564
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15564)
; OTHER INFORMATION: ryanodine receptor 3(RYR3) gene.
US-11-000-688-1500

Query Match 24.4%; Score 732.2; DB 14; Length 15564;
Best Local Similarity 55.7%; Pred. No. 3.8e-192;
Matches 1661; Conservative 0; Mismatches 1208; Indels 114; Gaps 9;

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Qy         36 TTTGGAAGCCCAAGACATAATGCAGAAAATGGAACAATGCATGCCGACGCTAGAGACGAT 95
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Db       9340 TCTGGGGATGCCAGACACGGTAGAAGACATGTGTCCTGACATCCCCCAGCTGGAAGGCCT 9399

Qy         96 CTTAGGCGAGGTGGACCAATTCGTGGAGTCAGACAAGACGTACAACGAGGCGCCGCATAT 155
                |    ||  |  || |  | |  |||||||       |||||  |||  ||| ||| |
Db       9400 GATGAAGGAAATCAACGACCTGGCCGAGTCAGGGGCCCGGTACACAGAGATGCCCCATGT 9459

Qy        156 CATCGATGTGGTGCTGCCTTTACTCTGTTCTTATTTGCCGTTCTGGTGGGCACAGGGGCC 215
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Db 9460 CATCGAGGTGATCTTACCCATGCTCTGCAACTACTTGTCCTACTGGTGGGAGCGGGGTCC 9519
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Db 9640 CTGGATGAAGCGCATTGCAGTGTATGCACAGCCCATCATCAGCAAAGCCAGGCCCGACCT 9699
Qy 396 GCTGAGGGATTCCTTCCTGCCGCTCGCTGAACGTGTTCGCAAACGCACGGACAATATGTT 455
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Qy 456 CCATAAGGAGGAGAGCTTGAGGGGGTTTATTAAGTCGTCAACAGACGACACATCCCAGGT 515
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Qy 636 GGCGGAAGAGCTGTACAACCACGTGGCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTA 695
Db 9931 TTCTGACCAGCTCTTCCGCATGGTGGCAGAAGTCTTCATTCTGTGGTGTAAATCTCATAA 9990
Qy 696 CTTCTTGAAGGAGGAACAGAACTTCATCTCTGCCAACGAAATTGATAACATGGTGCTGAT 755
Db 9991 CTTCAAGAGAGAAGAGCAAAATTTTGTGATTCAGAATGAAATTAATAATTTGGCATTTTT 10050
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Db 10051 AACTGGAGACAGCAAAAGCAAGATGTCAAAAGCCATGCAAGTAAAGTCTGGAGGACAAGA 10110
Qy 816 AAAGAAAAAGAAGAAGCACCGTGATAAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTC 875
Db 10111 CCAGGAGCGGAAGAAG------ACAAAGCGGCGGGGAGACTTGTATTCCATCCAGACCTC 10164
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Db 10165 CCTCATCGTGGCTGCACTCAAGAAAATGCTGCCCATTGGTTTGAATATGTGTACTCCAGG 10224
Qy 936 AGAACAAGAACTGGTGCAGCATTGTAAAGACAGGTTCCTGAAGAAAATGTCAGAACAAGA 995
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Qy 1056 AATGTCTTGGCAACATTACTTGTATAGCAAGTTAGGTTCGAAGAGTAAGAGCAATATAAC 1115
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Db 10399 TCCGGAAA----------AGACAGTGGAGCGTGTGCAGAG 10428
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Qy 1836 CGGCAATATTGATATACAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGG 1895
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Db 11284 CCTACAGTTACTTTGTGAGGGACATAACAGTGACTTTCAGAACTTCCTGCGGACTCAGAT 11343
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; Publication No. US20050272362A1
; GENERAL INFORMATION:
;  APPLICANT: Chiang, Wen
;  APPLICANT:  Strasburg, Gale
;  APPLICANT:  Linz, John
;  TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
;  FILE REFERENCE: MSU-09308
;  CURRENT APPLICATION NUMBER: US/11/044,111
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
;   LENGTH: 10129
;   TYPE: DNA
;   ORGANISM: Meleagris gallopavo
US-11-044-111-21

  Query Match           24.1%;  Score 724.4;  DB 14;  Length 10129;
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Qy        295 CTGAAGCTCATCAAAAAGAACATCGGCAATGAGAACGCGCCGTGGATGACCCGCATCGCC 354
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Db       5812 GTGTTCGCTCAGCCCATCGTCAGCAAGGCGAAGCCGGAGCTGCTGCGCACCCACTTCATC 5871

Qy        415 CCGCTCGCTGAACGTGTTCGCAAACGCACGGACAATATGTTCCATAAGGAGGAGAGCTTG 474
Db       5872 CCCACGATGGAGAAGCTGAAGAAGCGGGCAGGGAAGGTGGTGTCGGAGGAGGAGCAGCTG 5931

Qy        475 AGGGGGTTTATTAAGTCGTCAACAGACGACACATCCCAGGTAGAGTCTCAGATACAAGAA 534
Db       5932 CGCATGGAGGCGAAGGCGGAGGCCGAGGAC---------GCCGAGCTGCTCATCCGCGAC 5982

Qy        535 GACTGGCAGCTGCTGGTCAGAGACATCTACTCCTTCTACCCGCTGCTCATCAAGTACGTC 594
Db       5983 GAGTTCTCCGTGCTCTGCCGCGACCTCTACGCCCTGTACCCTCTGCTCATCCGCTACGTC 6042

Qy        595 GACCTGCAGAGGAACCACTGGCTCAGGAACAATGTTCCAGAGGCGGAAGAGCTGTACAAC 654
Db       6043 GACAACAGCCGGGCCAAGTGGCTGACGGAGCCCAACGCGGACGCGGAGGAGCTGTTCCGC 6102

Qy        655 CACGTGGCTGAAATCTTCAACATCTGGTCGAAGAGCCAGTACTTCTTGAAGGAGGAACAG 714
Db       6103 ATGGTGGGAGAGGTCTTCATCTACTGGTCCAAATCCCACAACTTTAAGCGCGAGGAGCAG 6162

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Qy        775 AGAGTGACAGCAGTAACAGATGGTACTCCTCAAGGTGGTGGAAAGAAAAAGAAGAAGCAC 834
Db       6223 AAGATGGCCAAGTCCGGAGACGGC------CAGGGCGGTGGCTCGGAGCAGGAGCGCACC 6276

Qy        835 CGTGATAAGAAACGCGACAAAGACAAGGAAGTCCAAGCGTCCCTAATGGTAGCTTGTCTG 894
Db       6277 AAGAAGAAGCGCCGCGGCGACCGTTACTCCATCCACACCTCCCTGATCGTGGCCACCCTG 6336

Qy        895 AAGAGGTTGTTACCAGTTGGCCTTAACCTATTCGCTGGCAGAGAACAAGAACTGGTGCAG 954
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Db       6457 AACAACCTGCACCTGCAGGGCAAGTGTGAGAACTCGTCGGCCATGCGCTGGCAGCTGGCT 6516

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Db       6667 TCCAAGCAGCGGCGCCGCGCCGTGGTCGCCTGTTTCCGAATGACGCCGCTCTACAACCTG 6726

Qy       1315 CCGAGACATCGAGCGTGTAACATCTTCGCTCGCACGTACTACGAGCTCTGGTTGG---AA 1371
Db       6727 CCCAGGCATCGCGCCTGCAATATGTTCCTGGAGGCCTACAAGCTGCTGTGGTTGGTGACG 6786

Qy       1372 GAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAAGACGCA 1431
Db       6787 GAGGAGCATCCCTTCGAGGACCGCATGATTGACGACCTGGCGAAATCA---------GGG 6837

Qy       1432 GAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCAGCTG 1491
Db       6838 GAGGAGGAGGAGGAGGAGGAAGAGGAGAAGGACAAGAAGCCAGACCCGCTGCATCAGCTC 6897

Qy       1492 GTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGATCCT 1551
Db       6898 ATCCTGCACTTCAGCCGCACGGCGCTGACCGAGA---AAAGCAAGTTGGAGAAGGATCAC 6954

Qy       1552 CTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGG 1611
Db       6955 CTGTACATGGCGTACGCGGGTATCATGGCCAAGAGCTGTCACATTGAAGAAG-GGAATGA 7013

Qy       1612 GGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGT 1671
Db       7014 AGAGGAGAAGGAGGAGAAGAAGGAGGAGGAGGACCCGGAGGATTCG-------------- 7059

Qy       1672 ATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGGCGGAC 1731
Db       7060 TTTGAGGAGAAGGAGATGGAGAAGCAGAAGCTGCTGTACCAGCAGTCGCGGCTGCACACG 7119

Qy       1732 CGTGGGGTTGCCGAAATGGTGTTGCTGCACATCTCCGCGTCCAAAGGCCTGCCCAGCGAG 1791
Db       7120 AGGGGAGCAGCTGAGATGGTGCTGCAGATGATCAGCGCCTGCAAAGGGGAGCGGGGGGAG 7179

Qy       1792 ATGGTCATGAAGACTTTACAGCTCGGTATTAGTATACTGAGGGGCGGCAATATTGATATA 1851
Db       7180 ATGGTTTCCTCCACGCTGAAGTTGGGGATCTCCATCCTCAACGGGGGAAACGCCGATGTG 7239

Qy       1852 CAGATGGGTATGTTGAACCACTTGAAAGACAAGAAAGACGTGGGCTTCTTTACGTCCATC 1911
Db       7240 CAGCAGAAAATGTTGGATTACCTGAAGGAGAAACGTGAGATCGGATTCTTCCAAAGCGTC 7299

Qy       1912 GCCGGCCTCATGAACTCCTGCTCCGTGCTCGATCTTGACGCCTTCGAGAGGAACACCAAG 1971
Db       7300 CAGGCGCTGATGCAGACCTGCAGCGTCCTGGACCTGAACGCCTTTGAGCGGCAGAACAAA 7359

Qy       1972 GCTGAAGGTCTGGGCGTGGGTCTGGAAG----------------GTGCGGCGGGAGAG 2013
Db       7360 GCGGAGGGGCTGGGGATGGTGACGGAGGAGGGGACGATCATCAGCCGTGAGAACGGGGAG 7419

Qy       2014 AAGAACATGCATGACGCCGAGTTCACCTGCGCACTCTTCAGGTTCATTCAGCTCACCTGT 2073
Db       7420 AAGGTGATGTCGGATGATGAGTTCACGCAGGATCTGTTCCGGCTGCTGCAGCTGCTGTGC 7479

Qy       2074 GAAGGACACAACTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACA 2133
Db       7480 GAGGGGCACAACAACGACTTCCAGAATTACCTCCGCACGCAGACGGGCAACACCACCACC 7539

Qy       2134 GTGAACGTGGTCATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGAC 2193
Db       7540 ATCAACATCATCATCTGCACCGTGGATTACCTGCTGCGCCTGCAGGAGTCCATCAGCGAT 7599

Qy       2194 TTCTACTGGCACTACTCAAGCAAGGAACTGATCGACCCGGCCGGCAAAGCGAACTTCTTC 2253
Db       7600 TTCTATTGGTATTACTCGGGGAAGGACGTCATCGACGAGCAGGGAAAGCGCAACTTCTCC 7659

Qy       2254 AAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTCACTGAAGTCATACAGGGACCT 2313
Db       7660 AAGGCCATGGCTGTGGCCAAGCAGGTCTTCAACAGCCTCACCGAGTACATCCAGGGTCCG 7719

Qy       2314 TGTACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGACGCTGTCGGTGGTTTC 2373
Db       7720 TGCACGGGGAACCAGCAGAGCCTGGCTCACAGCCGCCTGTGGGACGCCGTGGTCGGATTC 7779

Qy       2374 CTGTTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAGCACTCGTCGCAGGTGGACCTG 2433
Db       7780 CTGCACGTCTTCGCACACATGATGAAGAAGTTGGCACAGGACTCCAGCCAGATCGGGCTG 7839

Qy       2434 CTGAAGGAACTCCTCAATCTGCAGAAGGACATGATCCCCATGATGCTGTCCATGCTTGAA 2493
Db       7840 CTGAAGGAGCTGCTGGACCTGCAGAAGGACATGGTGGTGATGCTGCTGTCCCTGCTGGAA 7899

Qy       2494 GGAAATGTTGTTAATGGTACAATCGGCAAGCAAATGGTGGACACACTAGTAGAATCGGCC 2553
Db       7900 GGCAATGTGGTGAACGGGACGATCGCACGGCAGGTGGTGGACATGCCGGTGGAGTCGTCC 7959

Qy       2554 TCCAACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAAGCTGAAGGACCTGACC 2613
Db       7960 AGCAACGTCACCATGATCCTGAAGTTCTTCGATATGTTCCTGAAGCTGCGCGACATCGTG 8019

Qy       2614 TCCAGCGCCAGCTTCCAGGAGATTGATGCCAATAACGACGGCTGGGTGCTGCCCAAGGAC 2673
Db       8020 GCCTCCGACGCCTTCCGCGATTACGTGACGGACCCGCGGGGGCTCATCTCCAAAAAGGAC 8079

Qy       2674 TTCAAGGAGAAAATGGAACAACAGAAGAGTTATACTCCCGAAGAAATCGAGTTCCTCCTA 2733
Db       8080 TTCCAGAAGGCCATGGACAGCCAGAAGCAGTACGAGCCGTCCGAGGTGCAGTTCCTGCTC 8139

Qy       2734 GCTTGCTGCGAGACGAACCACGACGGCAAGTTAGACTACATCGGTTTCTGCGACCGTTTC 2793
Db       8140 TCGTGCTCGGAGGCGGACGAGAACGAGATGATCGACGTGGAGGCGTTCGTCGGGCGCTCC 8199

Qy       2794 CACGAGCCTGCCAAGGAGATCGGGTTTAACTTGGCCGTGTTACTGACTAACTTGTCTGAA 2853
Db       8200 CAGGAGCCGGCTCGCGACATCGGCTTCAACGTGGCGGTGCTGCTGACCAACCTGGCCGAG 8259

Qy       2854 CATATGCCGAACGAGCCTAGATTGGCACGTTTCCTGGAGACGGCAGGTTCAGTCCTGAAC 2913
Db       8260 CACGTCCCCCACGACCAGAGGCTGCGCACCTTTTTGGAGCAGGCCGCCAGCATCCTGGAG 8319

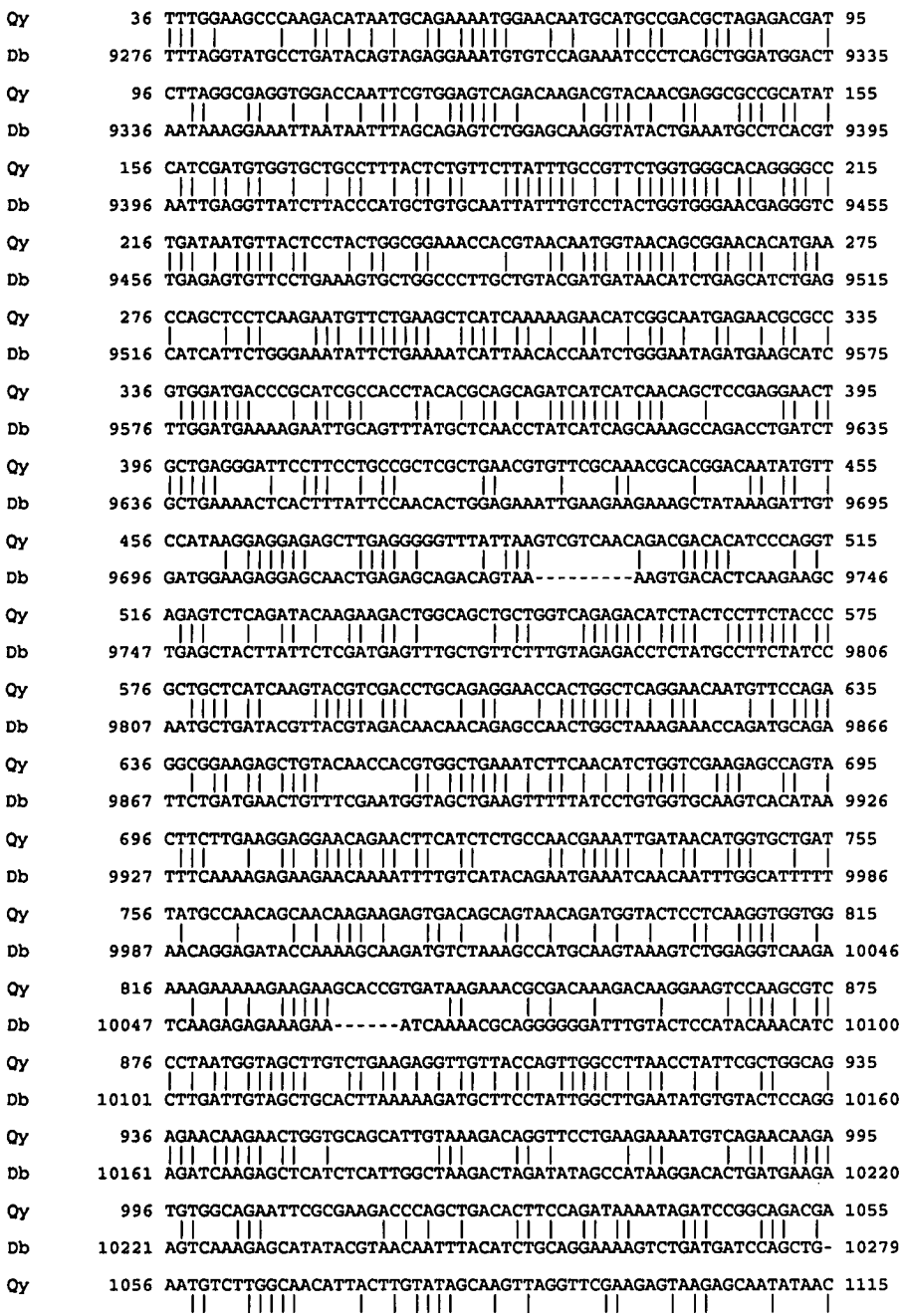
Qy       2914 TACTTCGAACCATTCCTGGGCCGTATCGAGATCATGGGCGGCTCCAAGCGCATCGAGCGT 2973
Db       8320 TATTTCCGGCCGTTTCTGGGCCGCATCGAGATCATGGGAGCGGCGCGGCGCATCGAGCGC 8379

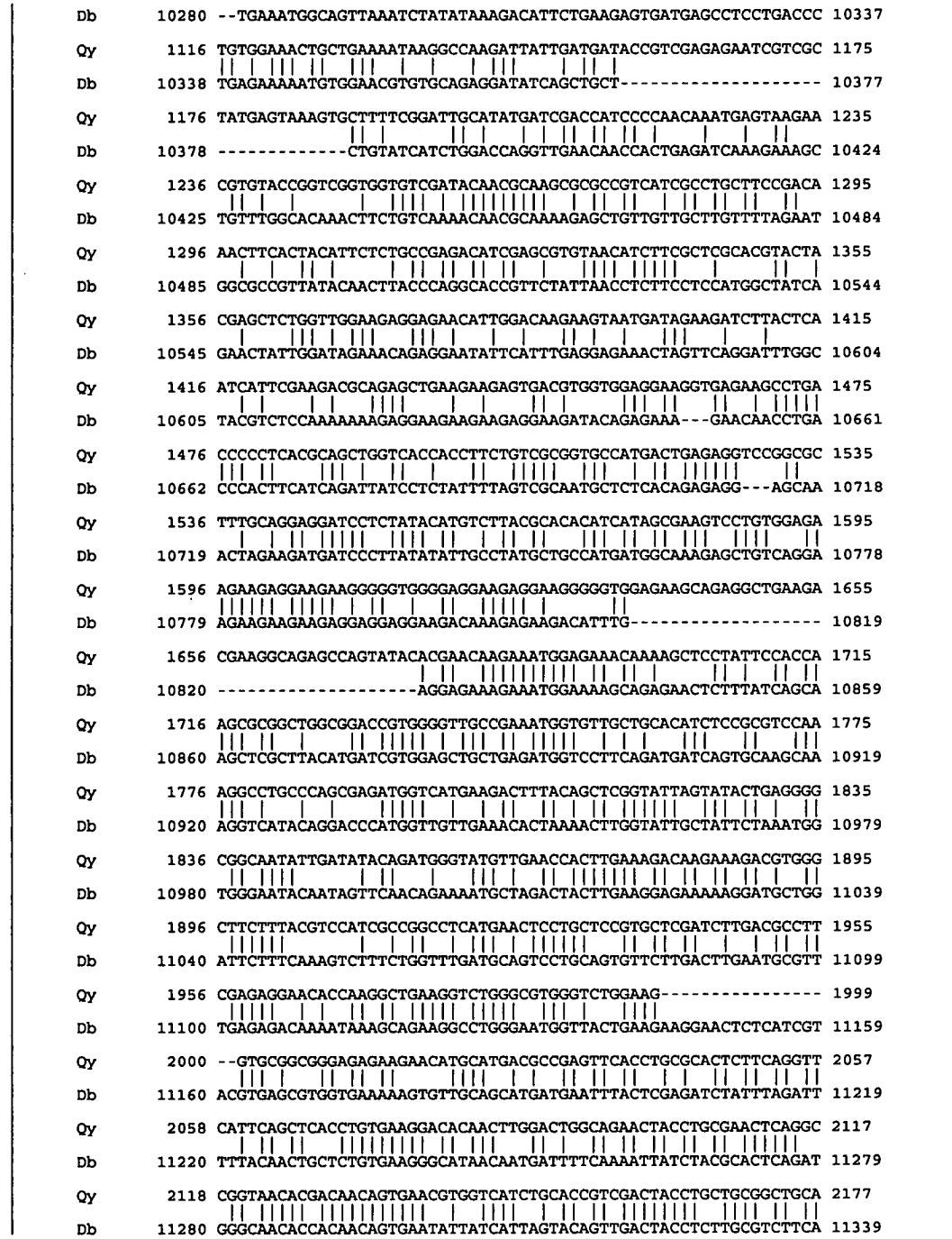
Qy       2974 GTCTACTTCGAGATCAAGGAGTCTAATA 3001
Db       8380 CTCTACTTCGAGATCAGCGCGGCCAACA 8407
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RESULT 3
US-11-044-111-17
; Sequence 17, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasburg, Gale
; APPLICANT: Linz, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 14620
; TYPE: DNA
; ORGANISM: Meleagris gallopavo
US-11-044-111-17

Query Match 21.5%; Score 644; DB 14; Length 14620;

Best Local Similarity 53.6%; Pred. No. 1.2e-167;
Matches 1600; Conservative 0; Mismatches 1270; Indels 114; Gaps 8;





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Qy       2178 GGAGTCCATCATGGACTTCTACTGGCACTACTCAAGCAAGGAACTGATCGACCCGGCCGG 2237
Db      11340 GGAATCAATCAGTGACTTCTATTGGTACTATTCAGGAAAAGAGTTTATTGATGAATCAGG 11399

Qy       2238 CAAAGCGAACTTCTTCAAGGCCATTGGCGTGGCTTCCCAAGTATTCAACACCCTCACTGA 2297
Db      11400 ACAACGTAACTTCTCTAAAGCTCTGGCTGTCACCAAACAAATATTCAATTCCCTTACCGA 11459

Qy       2298 AGTCATACAGGGACCTTGTACGCAGAATCAGCAGGCTTTGGCTCACTCCAGGTTGTGGGA 2357
Db      11460 ATATATACAGGGACCTTGCATCGGTAACCAACAGAGTCTGGCTCATAGTAGGCTGTGGGA 11519

Qy       2358 CGCTGTCGGTGGTTTCCTGTTCCTATTCTCCCACATGCAGGACAAGTTGTCGAAGCACTC 2417
Db      11520 TGCAGTTGTTGGATTTCTTCATGTATTTGCCAATATGCAGATGAAACTTTCACAGGACTC 11579

Qy       2418 GTCGCAGGTGGACCTGCTGAAGGAACTCCTCAATCTGCAGAAGGACATGATCCCCATGAT 2477
Db      11580 TGCTCAGATTGAACTGCTTAAGGAACTGCTAGATCTGCTAAAGGATATGGTTGTGATGTT 11639

Qy       2478 GCTGTCCATGCTTGAAGGAAATGTTGTTAATGGTACAATCGGCAAGCAAATGGTGGACAC 2537
Db      11640 GTTGTCATTACTTGAAGGTAACGTTGTAAATGGAACAATTGGAAAACAAATGGTCGATAC 11699

Qy       2538 ACTAGTAGAATCGGCCTCCAACGTGGAACTGATCCTGAAATACTTCGACATGTTCCTCAA 2597
Db      11700 ACTTGTAGAATCATCTAGCAACGTAGAATTAATCTTGAAGTTTTTTGACATGTTTCTCAA 11759

Qy       2598 GCTGAAGGACCTGACCTCCAGCGCCAGCTTCCAGGAGATTGATGCCAATAACGACGGCTG 2657
Db      11760 ATTAAAAGATTTAACTAACTCGGATGCTTTCAAGGAGCATGACCCAGATGGTAAGGGCAT 11819

Qy       2658 GGTGCTGCCCAAGGACTTCAAGGAGAAAATGGAACAACAGAAGAGTTATACTCCCGAAGA 2717
Db      11820 CATTTCAAAGAAGGATTTCCAGAAGTCAATGGAGGCTCAAAAACAATATATACAATCAGA 11879

Qy       2718 AATCGAGTTCCTCCTAGCTTGCTGCGAGACGAACCACGACGGCAAGTTAGACTACATCGG 2777
Db      11880 GATTGAATTCCTGTTGTCATGTACGGAAGCTGATGAAAATGATATGTTCAACTACATTGA 11939

Qy       2778 TTTCTGCGACCGTTTCCACGAGCCTGCCAAGGAGATCGGGTTTAACTTGGCCGTGTTACT 2837
Db      11940 TTTTGTAGAAAGATTCCATGAACCAGCCAAAGATATTGGCTTTAATGTAGCAGTTTTGCT 11999

Qy       2838 GACTAACTTGTCTGAACATATGCCGAACGAGCCTAGATTGGCACGTTTCCTGGAGACGGC 2897
Db      12000 AACAAACCTTTCAGAGCATATGCCTAATGACTCACGCCTTCAGAGCTTACTTGAACCTGC 12059

Qy       2898 AGGTTCAGTCCTGAACTACTTCGAACCATTCCTGGGCCGTATCGAGATCATGGGCGGCTC 2957
Db      12060 AGAAAGTGTTCTTAATTACTTTGAACCATACCTTGGCCGTATTGAAATAATGGGTGGAGC 12119

Qy       2958 CAAGCGCATCGAGCGTGTCTACTTCGAGATCAAGGAGTCTAATA 3001
Db      12120 CAAGAAAATAGAAAGAGTTTACTTTGAAATCAGTGAATCCAGTA 12163
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RESULT 4
US-09-925-065A-73529
; Sequence 73529, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73529
; LENGTH: 1786
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73529

Query Match 2.1%; Score 63.8; DB 6; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
Db       1561 CTCAGACTTTCAGAACTTCCTGCGGACTCAGATGGGCAACACCACCACCGTGAATGTCAT 1620

Qy       2145 CATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTAC 2199
Db       1621 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTGAGTGGGAGGGCCTTGGAC 1675
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RESULT 5
US-09-925-065A-73530
; Sequence 73530, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73530
; LENGTH: 1786
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73530

Query Match 2.1%; Score 63.8; DB 6; Length 1786;
Best Local Similarity 72.2%; Pred. No. 7.7e-07;
Matches 83; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
Db       1561 CTCAGACTTTCAGAACTTCCTGCGGACTCAGATGGGCAACACCACCACCGTGAATGTCAT 1620

Qy       2145 CATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTAC 2199
Db       1621 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTGAGTGGGAGGGCCTTGGAC 1675
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RESULT 6
US-09-925-065A-73531
; Sequence 73531, Application US/09925065A
; Publication No. US20040181048A1

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; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73531
;   LENGTH: 1786
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-73531

  Query Match             2.1%;  Score 63.8;  DB 6;  Length 1786;
  Best Local Similarity   72.2%;  Pred. No. 7.7e-07;
  Matches   83;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
             ||  ||||  ||||||| ||||||  ||||||    || |||||  || ||  |||||  ||  |
Db       1561 CTCAGACTTTCAGAACTTCCTGCGGACTCAGATGGGCAACACCACCACCGTGAATGTCAT 1620

Qy       2145 CATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTAC 2199
              ||||  ||||  ||  ||||||||  |||||  |||||||  |       |  ||  |||   ||
Db       1621 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTGAGTGGGAGGGCCTTGGAC 1675


RESULT 7
US-10-301-480-174768
; Sequence 174768, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174768
;   LENGTH: 1786
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-174768

  Query Match             2.1%;  Score 63.8;  DB 9;  Length 1786;
  Best Local Similarity   72.2%;  Pred. No. 7.7e-07;
  Matches   83;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
             ||  ||||  ||||||| ||||||  ||||||    || |||||  || ||  |||||  ||  |
Db       1561 CTCAGACTTTCAGAACTTCCTGCGGACTCAGATGGGCAACACCACCACCGTGAATGTCAT 1620

Qy       2145 CATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTAC 2199
              ||||  ||||  ||  ||||||||  |||||  |||||||  |       |  ||  |||   ||
Db       1621 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTGAGTGGGAGGGCCTTGGAC 1675


RESULT 8
US-10-301-480-174769
; Sequence 174769, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174769
;   LENGTH: 1786
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-174769

  Query Match             2.1%;  Score 63.8;  DB 9;  Length 1786;
  Best Local Similarity   72.2%;  Pred. No. 7.7e-07;
  Matches   83;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
             ||  ||||  ||||||| ||||||  ||||||    || |||||  || ||  |||||  ||  |
Db       1561 CTCAGACTTTCAGAACTTCCTGCGGACTCAGATGGGCAACACCACCACCGTGAATGTCAT 1620

Qy       2145 CATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTAC 2199
              ||||  ||||  ||  ||||||||  |||||  |||||||  |       |  ||  |||   ||
Db       1621 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTGAGTGGGAGGGCCTTGGAC 1675


RESULT 9
US-10-301-480-174770
; Sequence 174770, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174770
;   LENGTH: 1786
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-174770

  Query Match             2.1%;  Score 63.8;  DB 9;  Length 1786;
  Best Local Similarity   72.2%;  Pred. No. 7.7e-07;
  Matches   83;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
             ||  ||||  ||||||| ||||||  ||||||    || |||||  || ||  |||||  ||  |
Db       1561 CTCAGACTTTCAGAACTTCCTGCGGACTCAGATGGGCAACACCACCACCGTGAATGTCAT 1620

Qy       2145 CATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTAC 2199
              ||||  ||||  ||  ||||||||  |||||  |||||||  |       |  ||  |||   ||
Db       1621 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTGAGTGGGAGGGCCTTGGAC 1675
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RESULT 10
US-10-301-480-788177
; Sequence 788177, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 788177
;   LENGTH: 1786
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-788177

  Query Match             2.1%;  Score 63.8;  DB 10;  Length 1786;
  Best Local Similarity   72.2%;  Pred. No. 7.7e-07;
  Matches   83;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
              ||  ||||  ||||||| ||||||  ||||||    || |||||  || ||  |||||  ||  |
Db       1561 CTCAGACTTTCAGAACTTCCTGCGGACTCAGATGGGCAACACCACCACCGTGAATGTCAT 1620

Qy       2145 CATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTAC 2199
              ||||  ||||  ||  ||||||||  |||||  |||||||  |       |  ||  |||   ||
Db       1621 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTGAGTGGGAGGGCCTTGGAC 1675


RESULT 11
US-10-301-480-788178
; Sequence 788178, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 788178
;   LENGTH: 1786
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-788178

  Query Match             2.1%;  Score 63.8;  DB 10;  Length 1786;
  Best Local Similarity   72.2%;  Pred. No. 7.7e-07;
  Matches   83;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
              ||  ||||  ||||||| ||||||  ||||||    || |||||  || ||  |||||  ||  |
Db       1561 CTCAGACTTTCAGAACTTCCTGCGGACTCAGATGGGCAACACCACCACCGTGAATGTCAT 1620

Qy       2145 CATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAGTCCATCATGGACTTCTAC 2199
              ||||  ||||  ||  ||||||||  |||||  |||||||  |       |  ||  |||   ||
Db       1621 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTGAGTGGGAGGGCCTTGGAC 1675


RESULT 12
US-10-301-480-788179
; Sequence 788179, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 788179
;   LENGTH: 1786
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-788179

  Query Match             2.1%;  Score 63.8;  DB 10;  Length 1786;
  Best Local Similarity   72.2%;  Pred. No. 7.7e-07;
  Matches   83;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
              ||  ||||  ||||||| ||||||  ||||||    || |||||  || ||  |||||  ||  |
Db       1561 CTCAGACTTTCAGAACTTCCTGCGGACTCAGATGGGCAACACCACCACCGTGAATGTCAT 1620

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Db       1621 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTGAGTGGGAGGGCCTTGGAC 1675


RESULT 13
US-10-301-480-550750
; Sequence 550750, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
;  TITLE OF INVENTION:  in the Human Genome
;  FILE REFERENCE: 108827.137
;  CURRENT APPLICATION NUMBER: US/10/301,480
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US 10/215,598
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: US 60/311,695
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 1226818
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550750
;   LENGTH: 578
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-301-480-550750

  Query Match             2.1%;  Score 61.8;  DB 10;  Length 578;
  Best Local Similarity   77.3%;  Pred. No. 1.7e-06;
  Matches   75;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy       2085 CTTGGACTGGCAGAACTACCTGCGAACTCAGGCCGGTAACACGACAACAGTGAACGTGGT 2144
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Qy       2145 CATCTGCACCGTCGACTACCTGCTGCGGCTGCAGGAG 2181
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Db        541 CATCAGCACTGTGGACTACCTTCTGCGTCTGCAGGTG 577


RESULT 14
US-10-301-480-1164159
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; Sequence 1164159, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1164159
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1164159

Query Match 2.1%; Score 61.8; DB 10; Length 578;
Best Local Similarity 77.3%; Pred. No. 1.7e-06;
Matches 75; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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; Sequence 28292, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 28292
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Bovine 19866880905269
US-10-750-185-28292

Query Match 1.8%; Score 55.4; DB 8; Length 1556;
Best Local Similarity 62.8%; Pred. No. 0.00016;
Matches 86; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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GenCore version 5.1.7
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SUMMARIES

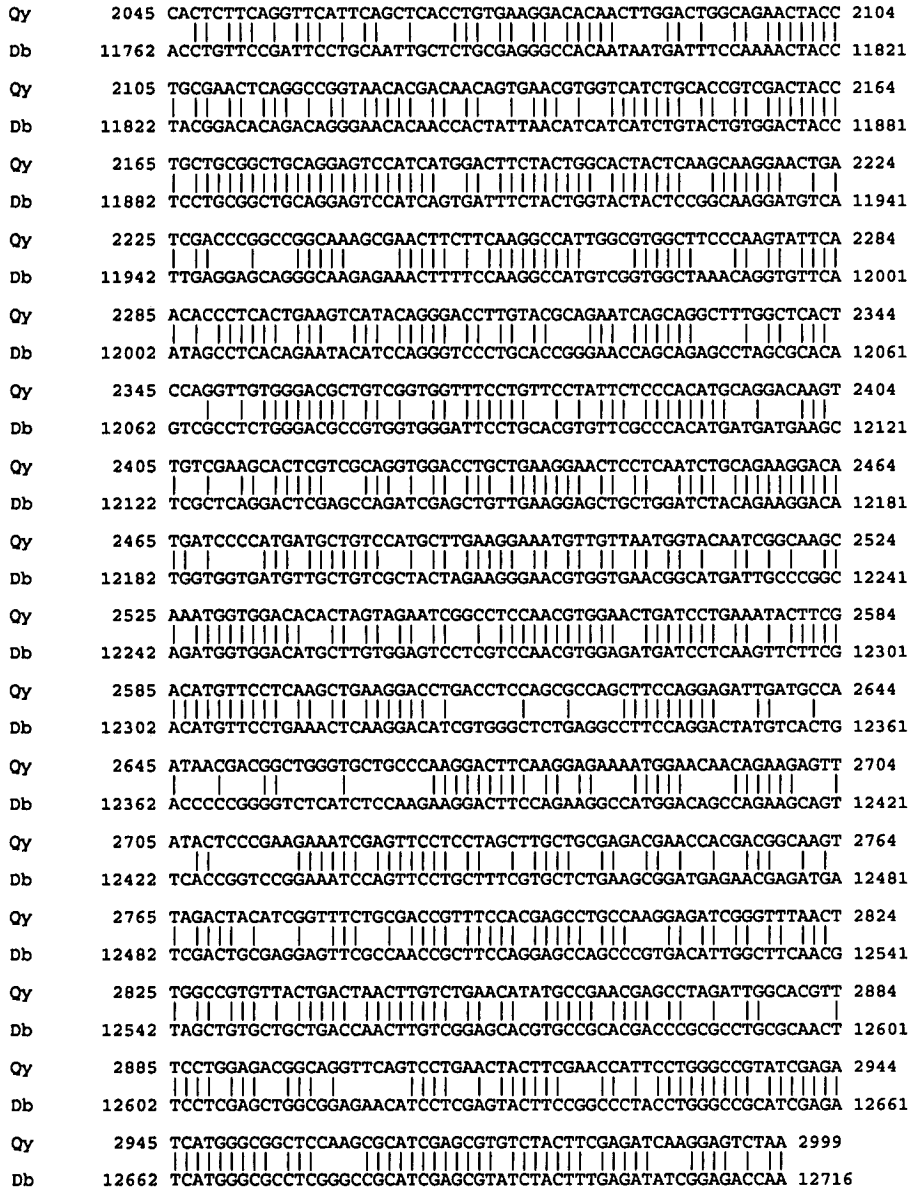
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	2	715	23.8	15572	3	US-09-424-783-1	Sequence 1, Appli
c	3	69.8	2.3	7218	2	US-08-232-463-14	Sequence 14, Appl
c	4	54	1.8	64309	3	US-09-949-016-14581	Sequence 14581, A
c	5	49.4	1.6	12695	3	US-09-949-016-16775	Sequence 16775, A
	6	48.6	1.6	49931	3	US-09-949-016-13727	Sequence 13727, A
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c	19	46.6	1.6	2150	2	US-08-861-464-13	Sequence 13, Appl
c	20	46.6	1.6	2150	2	US-08-396-001-13	Sequence 13, Appl
c	21	46.6	1.6	2150	3	US-09-323-433A-13	Sequence 13, Appl
c	22	46.6	1.6	2150	3	US-09-826-752-13	Sequence 13, Appl
	23	46.6	1.6	2343	3	US-09-252-991A-2275	Sequence 2275, Ap
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c	38	45	1.5	188	3	US-09-935-247-1	Sequence 1, Appli
c	39	45	1.5	405	2	US-08-299-074A-1	Sequence 1, Appli
c	40	45	1.5	405	3	US-09-399-773-1	Sequence 1, Appli
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	45	44.4	1.5	601	3	US-09-949-016-31807	Sequence 31807, A

ALIGNMENTS

RESULT 1
US-08-785-420-1
; Sequence 1, Application US/08785420
; Patent No. 6001976
; GENERAL INFORMATION:
; APPLICANT: MacLennan, David H
; APPLICANT: O'Brien, Peter J.
; TITLE OF INVENTION: DIAGNOSIS FOR PORCINE MALIGNANT
; TITLE OF INVENTION: HYPERTHERMIA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: P.O. Drawer 34009
; CITY: Charlotte,
; STATE: No. 6001976th Carolina 28234
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,388
; FILING DATE:
; APPLICATION NUMBER: US 08/030,159
; FILING DATE: 15-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Layton,Jr., Samuel G.
; REGISTRATION NUMBER: 22807
; REFERENCE/DOCKET NUMBER: 3477-73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 704-377-1561
; TELEFAX: 704-334-2014
; TELEX: 57-5102
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

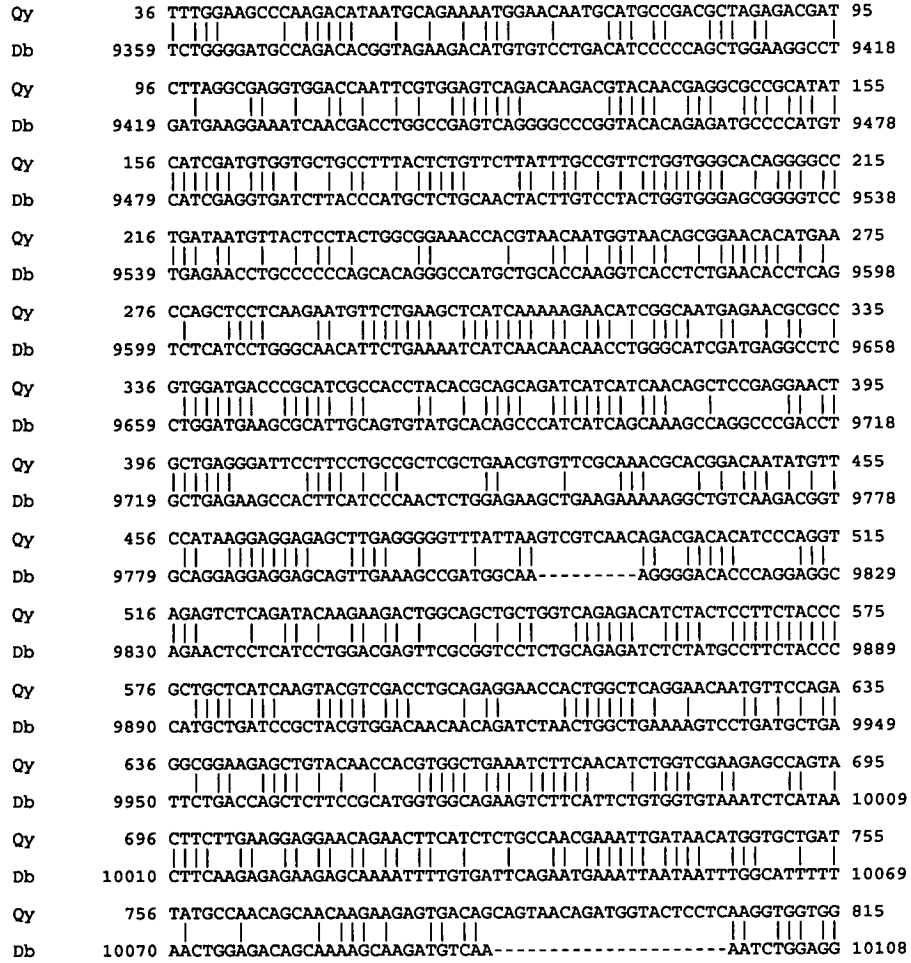
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;    POSITION IN GENOME:
;      UNITS:  bp
US-08-785-420-1

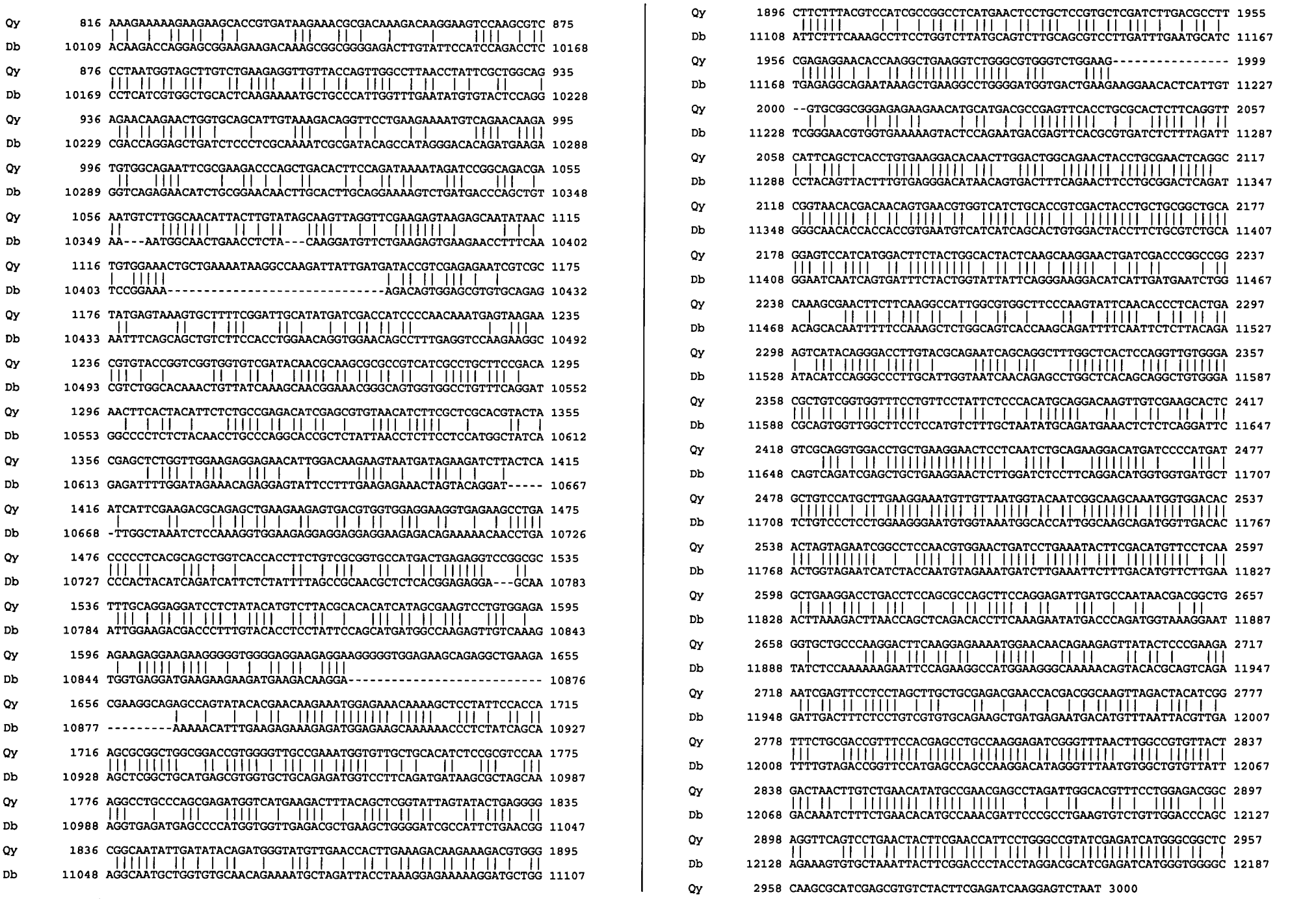
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US-09-424-783-1
; Sequence 1, Application US/09424783
; Patent No. 6780608
; GENERAL INFORMATION:
;  APPLICANT: Hakamata, Yasuhiro
;  APPLICANT:  Nishimura, Seiichiro
;  APPLICANT:  Barsoumian, Edward Leon
;  TITLE OF INVENTION: Human Type 3 Ryanodine Receptor Protein
;  TITLE OF INVENTION:  and DNA Molecules Coding Therefor
;  FILE REFERENCE: 0652.2000000
;  CURRENT APPLICATION NUMBER: US/09/424,783
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: PCT/EP98/02926
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: DE 197 22 317.6
;  PRIOR FILING DATE: 1997-05-28
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 15572
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-424-783-1

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RESULT 3
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; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             2.3%;  Score 69.8;  DB 2;  Length 7218;
  Best Local Similarity   4.7%;  Pred. No. 7.7e-08;
  Matches   17;  Conservative  215;  Mismatches  127;  Indels    0;  Gaps    0;

Qy       1368 GGAAGAGGAGAACATTGGACAAGAAGTAATGATAGAAGATCTTACTCAATCATTCGAAGA 1427
              :::::::::::: :  ::: :::::: :: :: ::::::    :   ::  :   :::::
Db       1392 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1333

Qy       1428 CGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTCACGCA 1487
               : ::::  ::::::::: :: : :: ::::::::: ::::::   ::       : : :
Db       1332 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1273

Qy       1488 GCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAGGAGGA 1547
              :  ::  :  :      :  : :: :  : ::  ::::::   :: :    : :::::::
Db       1272 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1213

Qy       1548 TCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGA 1607
                    : : :    : : : : :  : :: ::::    : ::::::::::::::::
Db       1212 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1153

Qy       1608 AGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGC 1667
              :::::: :::::::::::::::::::: ::::::: :::::  ::::: ::::: ::::
Db       1152 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1093

Qy       1668 CAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGGCTGG 1726
               :: : : : ::: :::::: :::::| |  |||||||     |    |||   ||| |
Db       1092 RRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAAGCTCG 1034


RESULT 4
US-09-949-016-14581/c
; Sequence 14581, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14581
;   LENGTH: 64309
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(64309)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14581

  Query Match             1.8%;  Score 54;  DB 3;  Length 64309;
  Best Local Similarity   64.3%;  Pred. No. 0.0039;
  Matches   81;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy       1575 CATAGCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGG 1634
              || ||||||    |  || |||||||||| || ||||| |  |  || ||||||||||  |
Db      24085 CAGAGCGAAACTCCATGAAGAAGAAGAAGATGAAGGAGAAGAAGAAGAAGAGGAAGAAGA 24026

Qy       1635 TGGAGAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAA 1694
              | ||| | |||||  |||||| ||||    ||  |    | | ||| |||||   ||  |
Db      24025 GGAAGAGGAAGAGGAAGAAGAGGAAGAAGAAGAAAAAGAAGAAGAAGAAGAAGAAGAAGA 23966

Qy       1695 ACAAAA 1700
              | || |
Db      23965 AGAAGA 23960


RESULT 5
US-09-949-016-16775/c
; Sequence 16775, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16775
;   LENGTH: 12695
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16775

  Query Match             1.6%;  Score 49.4;  DB 3;  Length 12695;
  Best Local Similarity   46.8%;  Pred. No. 0.03;
  Matches  155;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy       1423 GAAGACGCAGAGCTGAAGAAGAGTGACGTGGTGGAGGAAGGTGAGAAGCCTGACCCCCTC 1482
              || || | ||||  | || ||   || | || ||||||||  ||| ||   ||
Db       9608 GAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAG 9549

Qy       1483 ACGCAGCTGGTCACCACCTTCTGTCGCGGTGCCATGACTGAGAGGTCCGGCGCTTTGCAG 1542
                | ||  ||                  | |    |   |||  |   | |    | ||
Db       9548 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAG 9489

Qy       1543 GAGGATCCTCTATACATGTCTTACGCACACATCATAGCGAAGTCCTGTGGAGAAGAAGAG 1602
              |||||       |   |    | |   |       || | ||      | ||| || |||
Db       9488 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAG 9429

Qy       1603 GAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCTGAAGACGAAGGC 1662
              || |||| ||  | ||||||||||||| | ||  | ||| |  ||||  ||||| || |
Db       9428 GAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAG 9369

Qy       1663 AGAGCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTCCACCAAGCGCGG 1722
                ||        | ||| | ||   |||| || |  ||          | ||| |  |
Db       9368 GAAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAAGAGGAG 9309

Qy       1723 CTGGCGGACCGTGGGGTTGCCGAAATGGTGT 1753
                || ||||   | | |      | || |||
Db       9308 GAGGAGGACGAGGAGTTGTTGTTAGTGTTGT 9278


RESULT 6
US-09-949-016-13727
; Sequence 13727, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13727
;   LENGTH: 49931
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(49931)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13727

  Query Match             1.6%;  Score 48.6;  DB 3;  Length 49931;
  Best Local Similarity   57.6%;  Pred. No. 0.097;
  Matches   87;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy       1591 GGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCT 1650
              | |||| |||| ||||  | ||  || |||||||| |||| ||  |  |||| ||| |
Db      32552 GAAGAAAAAGAAGAAGTGGAGGAAGGAGAGGAAGAAGAAGAGGAAGAGGAAGAAGAAGAG 32611

Qy       1651 GAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTC 1710
              |||| ||||    ||        | ||| |||||    ||   || | ||||  |
Db      32612 GAAGAGGAAGAAGAAGAGGAAGAGGAAGAAGAAGAAGAAAAGCTGCACATGCTCACAAAG 32671

Qy       1711 CACCAAGCGCGGCTGGCGGACCGTGGGGTTG 1741
              | ||    ||    | | ||   |||||| |
Db      32672 CCCCTGAAGCACAGGCCAGAATCTGGGGTCG 32702


RESULT 7
US-09-949-016-13728
; Sequence 13728, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13728
;   LENGTH: 49931
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(49931)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13728

  Query Match             1.6%;  Score 48.6;  DB 3;  Length 49931;
  Best Local Similarity   57.6%;  Pred. No. 0.097;
  Matches   87;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy       1591 GGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCT 1650
              | |||| |||| |||| | ||  || |||||||| |||| ||  |  |||| ||| |
Db      32552 GAAGAAAAAGAAGAAGTGGAGGAAGGAGAGGAAGAAGAAGAGGAAGAGGAAGAAGAAGAG 32611

Qy       1651 GAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTC 1710
              |||| ||||    ||        | ||| |||||    ||   || | ||||  |
Db      32612 GAAGAGGAAGAAGAAGAGGAAGAGGAAGAAGAAGAAGAAAAGCTGCACATGCTCACAAAG 32671

Qy       1711 CACCAAGCGCGGCTGGCGGACCGTGGGGTTG 1741
              | ||    ||    | | ||   |||||| |
Db      32672 CCCCTGAAGCACAGGCCAGAATCTGGGGTCG 32702


RESULT 8
US-09-949-016-13729
; Sequence 13729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13729
;   LENGTH: 49931
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(49931)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13729

  Query Match             1.6%;  Score 48.6;  DB 3;  Length 49931;
  Best Local Similarity   57.6%;  Pred. No. 0.097;
  Matches   87;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy       1591 GGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCT 1650
              | |||| |||| |||| | ||  || |||||||| |||| ||  |  |||| ||| |
Db      32552 GAAGAAAAAGAAGAAGTGGAGGAAGGAGAGGAAGAAGAAGAGGAAGAGGAAGAAGAAGAG 32611

Qy       1651 GAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTATTC 1710
              ||||| ||||    ||          | ||| |||||    ||   || | ||||  |
Db      32612 GAAGAGGAAGAAGAAGAGGAAGAGGAAGAAGAAGAAGAAAAGCTGCACATGCTCACAAAG 32671

Qy       1711 CACCAAGCGCGGCTGGCGGACCGTGGGGTTG 1741
              | ||    ||    | | ||   |||||| |
Db      32672 CCCCTGAAGCACAGGCCAGAATCTGGGGTCG 32702


RESULT 9
US-09-949-016-14113
; Sequence 14113, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14113
;   LENGTH: 7044
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14113

  Query Match             1.6%;  Score 48;  DB 3;  Length 7044;
  Best Local Similarity   64.3%;  Pred. No. 0.053;
  Matches   72;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy       1589 GTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGG 1648
              | ||||||| ||| | |||||| |  || ||||||||||||| ||  |  |||| || |
Db       1277 GAGGAGAAGGAGAAGGAGAAGGAGAAGGAGAGGAAGAGGAAGAGGAAGAGGAAGAGGAAG 1336

Qy       1649 CTGAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACAAAA 1700
              |||||  ||||    ||       | | ||| |||||   ||  || || |
Db       1337 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 1388


RESULT 10
US-08-688-376-1
; Sequence 1, Application US/08688376
; Patent No. 6018039
;  GENERAL INFORMATION:
;    APPLICANT:  Satow, Hiroyasu
;    TITLE OF INVENTION:  NOVEL PROCESS FOR PRODUCING SUBSTANCES
;    TITLE OF INVENTION:  IN MAMMARY GLAND OF TRANSGENIC ANIMAL BY USING MC26 GENE
;    TITLE OF INVENTION:  EXPRESSION-REGULATORY REGION
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DILWORTH & BARRESE
;      STREET:  4350 LaJolla Village Drive, Suite 300
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/688,376
;      FILING DATE:  30-JUL-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pepper, Frederick W.
;      REGISTRATION NUMBER:  31,286
;      REFERENCE/DOCKET NUMBER:  567-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-546-4410
;      TELEFAX:  619-453-2839
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5394 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CAAT_signal
;      LOCATION:  2234..2243
;    FEATURE:
;      NAME/KEY:  TATA_signal
;      LOCATION:  2275..2281
;    FEATURE:
;      NAME/KEY:  polyA_signal
;      LOCATION:  4607..4612
US-08-688-376-1

  Query Match             1.6%;  Score 47.6;  DB 3;  Length 5394;
  Best Local Similarity   62.7%;  Pred. No. 0.059;
  Matches   74;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy       1591 GGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAAGCAGAGGCT 1650
              | |||||||| |||||||  |  |  || ||||| ||||  |  | ||||| ||| |
Db       1439 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA 1498

Qy       1651 GAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACAAAAGCTCCTAT 1708
              |||||  ||||    ||       | | | | |  || |||| ||| |||||   || |
Db       1499 GAAGAAGAAGAAGAAGAAGAAGAAAAGGGAAATTAATTGGAAAAAGAAAAGGAACTCT 1556


RESULT 11
US-08-574-959A-8
; Sequence 8, Application US/08574959A
; Patent No. 5962224
;  GENERAL INFORMATION:
;    APPLICANT:  Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
;    APPLICANT:  and Jack L. Strominger
;    TITLE OF INVENTION:  p62 POLYPEPTIDES, RELATED POLYPEPTIDES
;    TITLE OF INVENTION:  AND USES THEREFOR
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
```

```
;       ZIP:  02109-1875
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/574,959A
;       FILING DATE:  19-DEC-95
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mandragouras, Amy E.
;       REGISTRATION NUMBER:  36,207
;       REFERENCE/DOCKET NUMBER:  DFN-008
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3211 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  439..3157
US-08-574-959A-8

  Query Match             1.6%;  Score 47.2;  DB 2;  Length 3211;
  Best Local Similarity   62.9%;  Pred. No. 0.059;
  Matches   73;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy       1582 AAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAA 1641
              ||   | |||  ||||| ||||| ||||  || |  |||||||| ||||  |  | ||||
Db       2386 AACAGCAGTGATGAAGAGGAGGAGGAAGAAGGAGAAGAGGAAGAAGAAGAAGAAGAAGAA 2445

Qy       1642 GCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACA 1697
              | |||||  ||||| ||||    ||       | | ||  ||||  | ||| || |
Db       2446 GAAGAGGAAGAAGAAGAAGAGGAAGAAGAGGAAGAGGAGGAAGACTTTGAGGAAGA 2501


RESULT 12
US-09-357-014-8
; Sequence 8, Application US/09357014
; Patent No. 6291645
;   GENERAL INFORMATION:
;       APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
;                  and Jack L. Strominger
;       TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
;                           AND USES THEREFOR
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: LAHIVE & COCKFIELD
;            STREET: 60 State Street, Suite 510
;            CITY: Boston
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02109-1875
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/357,014
;            FILING DATE: 19-Jul-1999
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/574,959
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mandragouras, Amy E.
;            REGISTRATION NUMBER: 36,207
;            REFERENCE/DOCKET NUMBER: DFN-008
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)227-7400
;            TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3211 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  439..3157
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-357-014-8

  Query Match             1.6%;  Score 47.2;  DB 3;  Length 3211;
  Best Local Similarity   62.9%;  Pred. No. 0.059;
  Matches   73;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy       1582 AAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAA 1641
              ||   | |||  ||||| ||||| ||||  || |  |||||||| ||||  |  | ||||
Db       2386 AACAGCAGTGATGAAGAGGAGGAGGAAGAAGGAGAAGAGGAAGAAGAAGAAGAAGAAGAA 2445

Qy       1642 GCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACA 1697
              | |||||  ||||| ||||    ||       | | ||  ||||  | ||| || |
Db       2446 GAAGAGGAAGAAGAAGAAGAGGAAGAAGAGGAAGAGGAGGAAGACTTTGAGGAAGA 2501


RESULT 13
US-08-574-959A-6
; Sequence 6, Application US/08574959A
; Patent No. 5962224
;  GENERAL INFORMATION:
;    APPLICANT:  Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
;    APPLICANT:  and Jack L. Strominger
;    TITLE OF INVENTION:  p62 POLYPEPTIDES, RELATED POLYPEPTIDES
;    TITLE OF INVENTION:  AND USES THEREFOR
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/574,959A
;      FILING DATE:  19-DEC-95
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  DFN-008
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3901 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  439..3847
US-08-574-959A-6
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  Query Match             1.6%;  Score 47.2;  DB 2;  Length 3901;
  Best Local Similarity   62.9%;  Pred. No. 0.065;
  Matches   73;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy       1582 AAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAA 1641
             ||   | |||  ||||| ||||| ||||  || |  |||||||| ||||  |  | ||||
Db       3076 AACAGCAGTGATGAAGAGGAGGAGGAAGAAGGAGAAGAGGAAGAAGAAGAAGAAGAAGAA 3135

Qy       1642 GCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACA 1697
             | |||||  ||||| ||||    ||       | | ||  ||||  | ||| || |
Db       3136 GAAGAGGAAGAAGAAGAAGAGGAAGAAGAGGAAGAGGAGGAAGACTTTGAGGAAGA 3191


RESULT 14
US-09-357-014-6
; Sequence 6, Application US/09357014
; Patent No. 6291645
;  GENERAL INFORMATION:
;       APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
;                  and Jack L. Strominger
;       TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
;                           AND USES THEREFOR
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: LAHIVE & COCKFIELD
;            STREET: 60 State Street, Suite 510
;            CITY: Boston
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02109-1875
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/357,014
;            FILING DATE: 19-Jul-1999
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/574,959
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mandragouras, Amy E.
;            REGISTRATION NUMBER: 36,207
;            REFERENCE/DOCKET NUMBER: DFN-008
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)227-7400
;            TELEFAX: (617)227-5941
;  INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3901 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  439..3847
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-357-014-6

  Query Match             1.6%;  Score 47.2;  DB 3;  Length 3901;
  Best Local Similarity   62.9%;  Pred. No. 0.065;
  Matches   73;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy       1582 AAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGAGAA 1641
             ||   | |||  ||||| ||||| ||||  || |  |||||||| ||||  |  | ||||
Db       3076 AACAGCAGTGATGAAGAGGAGGAGGAAGAAGGAGAAGAGGAAGAAGAAGAAGAAGAAGAA 3135

Qy       1642 GCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACA 1697
             | |||||  ||||| ||||    ||       | | ||  ||||  | ||| || |
Db       3136 GAAGAGGAAGAAGAAGAAGAGGAAGAAGAGGAAGAGGAGGAAGACTTTGAGGAAGA 3191


RESULT 15
US-09-248-796A-5393
; Sequence 5393, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5393
;   LENGTH: 843
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-09-248-796A-5393

  Query Match             1.6%;  Score 46.8;  DB 3;  Length 843;
  Best Local Similarity   61.5%;  Pred. No. 0.039;
  Matches   75;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy       1579 GCGAAGTCCTGTGGAGAAGAAGAGGAAGAAGGGGGTGGGGAGGAAGAGGAAGGGGGTGGA 1638
             | |||| |   || | ||||||| | |||||  |  |  || ||||| ||||  |  | |
Db        181 GAGAAGCCAACTGTACAAGAAGAAGGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA 240

Qy       1639 GAAGCAGAGGCTGAAGACGAAGGCAGAGCCAGTATACACGAACAAGAAATGGAGAAACAA 1698
             |||| ||| |  ||||| ||||     |||  || |  | ||  | ||||    |  || ||
Db        241 GAAGAAGAAGAAGAAGAAGAAGAATTAGCTGGTTTTGAAGATGATGAAAATAATCAAGAA 300

Qy       1699 AA 1700
              |
Db        301 GA 302


Search completed: April 14, 2006, 15:14:17
Job time : 502.5 secs
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